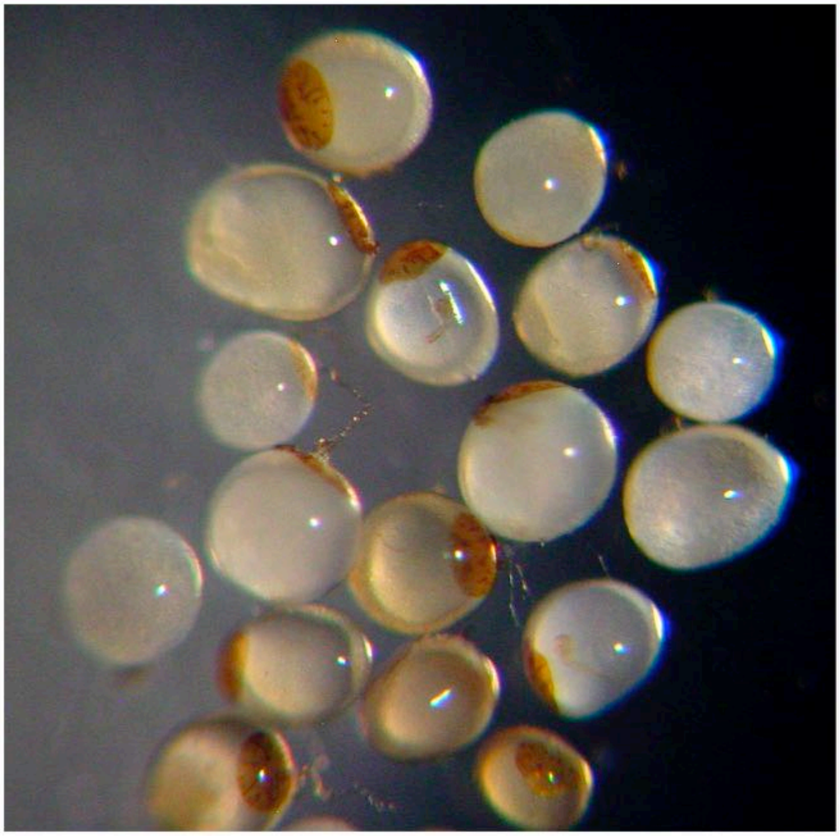
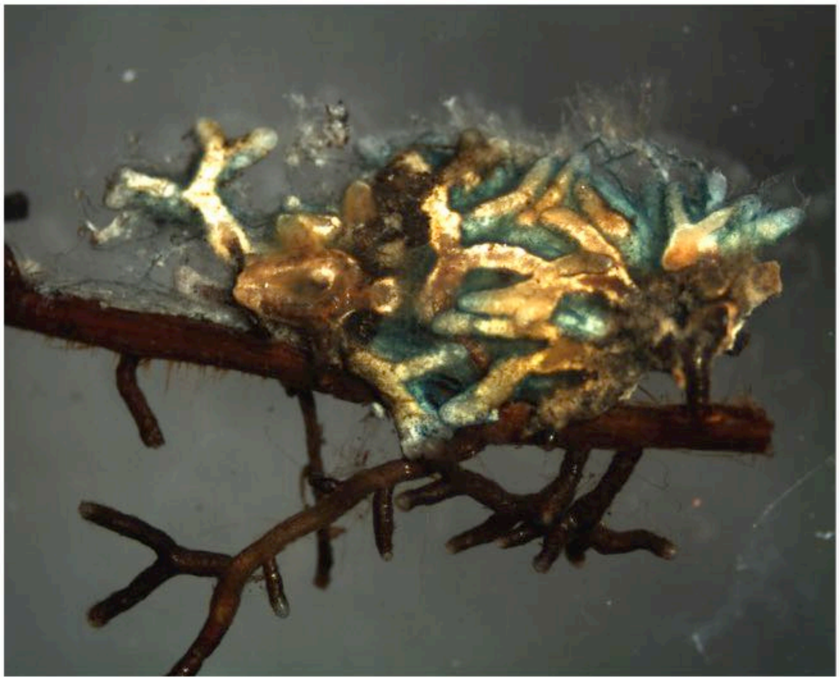
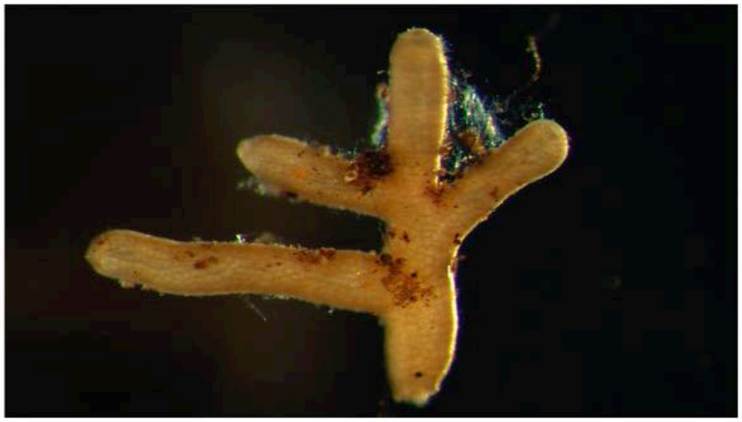
icom10

International Conference on Mycorrhiza
Merida, Mexico 2019.

Mycorrhizae for a Sustainable World







Conference program

Acknowledgements

New Phytologist Trust

IMS

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WELCOME TO icom10!

We are very pleased to welcome you to the 10th International Conference on Mycorrhiza (ICOM 10) in Mérida, Mexico. We are very happy because it is the first time that this important conference takes place in Mexico.

ICOM 10 wishes to encourage innovation in the researchers, students, companies and organizations that study the mycorrhizal symbiosis in order to generate basic and applied knowledge in a way committed to sustainable development. We hope you will enjoy this week of scientific and social interactions and feel enriched by the presentations and conversations with colleagues and friends from almost 40 countries. We have made our best to provide an excellent scientific program and make you feel at home. We also encourage you to go out and experience the Mayan culture. We are confident that ICOM 10 will be very successful because you are coming to join us.

On behalf of the Local Organizing Committee
Dr. Javier Álvarez-Sánchez (Chair)
Dr. Mayra E. Gavito (Co-Chair)

INTERNATIONAL MYCORRHIZA SOCIETY
WELCOME MESSAGE

Dear Colleagues,

I am very pleased to welcome you to the 10th International Conference on Mycorrhiza in Mérida, Mexico.

Scientists working on mycorrhizal symbioses have known for more than a century that plant-associated microbes, such as mycorrhizal fungi, take center stage in terrestrial ecosystems. A century of research has clarified the nature of what is undoubtedly the commonest and most important symbiosis in terrestrial ecosystems. Simply stated, nearly all families of plants form root symbiotic associations, named mycorrhizas, with soil fungi. The importance of this symbiosis in promoting plant nutrient status and growth is now well established, and mycorrhizas are used worldwide to develop sustainable agriculture and forestry.

Primary research papers in the last few years since ICOM9 in Prague have broken the ground for new lines of research, from regulation of gene expression to the ecological relevance of mycorrhizal symbioses. They have provided detailed insights into the complexity of mycorrhizal fungal communities and populations, offering exciting prospects for elucidation of the processes that structure their communities and biogeography.

There is no doubt that ICOM10 sessions and workshops will be fertile ground for novel hypotheses that will advance our general perspective on plant and fungal ecology and evolution, and will provide new insights on the biological dynamics that mediate the flux of matter and energy in terrestrial ecosystems through mycorrhizal interfaces.

It is hoped that the ICOM10 will stimulate further research, and will encourage younger scientists in our community to look to future challenges that lie ahead.

I would like to thank Professor Javier Álvarez Sánchez, the Local Organizing Committee and the International Scientific Committee for putting together very exciting scientific and social programs.

On behalf of the Board of Directors of the International Mycorrhiza Society

Dr. Francis M. Martin
President of the International Mycorrhiza Society

COMMITTEES

Local Organizing Committee

Javier Álvarez-Sánchez, Universidad Nacional Autónoma de México

Mayra E. Gavito Pardo, Universidad Nacional Autónoma de México

Irene Sánchez-Gallen, Universidad Nacional Autónoma de México

Roberto Garibay-Orijel, Universidad Nacional Autónoma de México

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Diana Martínez Almaguer, Universidad Nacional Autónoma de México

International Scientific Committee

IMS scientific committee

Francis Martin (general coordinator), Marcel van der Heijden (scientific board coordinator)

Local committee

Mayra E. Gavito (scientific program coordinator), Ignacio Maldonado Mendoza, Roberto Garibay Orijel, Rosalva García Sánchez, Rocío Vega Frutis (session coordinators), Irene Sánchez Gallén, América Baleón-Sepúlveda, Isaac Acevedo Rojas (communication coordinators).

IMS Awards

John Klironomos (IMS awards coordinator)

Session Chairs

Alok Adholeya
Petr Baldrian
Jim Bever
Martin Bidartondo
Jan Colpaert
Tatsu Ezawa
Katie Field
Gu Feng
Miranda Hart
Marcel van der Heijden
David Johnson
Nancy Johnson
Annegret Kohler
Thom Kuyper
Luisa Lanfranco
Jonathan Plett
Ignacio Querejeta
Sidney Stürmer
Leho Tedersoo
Camille Truong

Organizing Secretariat

International Meeting Services, S.A. de C.V.
Eje 10 sur Río Magdalena No. 326, Office 201 and 202.
Col. La Otra Banda C.P. 01090 Álvaro Obregón, Mexico City, Mexico.
www.intermeeting.com.mx
Tel. (52) 55 5661-7905
Nataly Juárez, Claudia García

OPENING GUEST SPEAKER

Julia Carabias, UNAM (Mexico)

Sunday afternoon guest speaker

She completed her undergraduate and postgraduate studies (1973-1981) in the Faculty of Sciences of the Universidad Nacional Autónoma de México (UNAM). She is a Full-time Professor in the Department of Ecology and Natural Resources of the Faculty of Sciences.

She has taught courses since 1977, as well as in other academic institutions, in subjects such as Plant Ecology, Natural Resources Management, Environmental Restoration and Public Entreprises. Her research has been published in a large number of journals and textbooks on the topics of tropical forest regeneration, environmental restoration, natural resource management, ecology and production systems, global change, poverty and the environment, water management, conservation of ecosystems and environmental policy.

Some of the texts she has written and in which she has collaborated are: Ecology and Food Self-sufficiency; Rural Production in Mexico: Ecological Alternatives; For Earth's Sake; Management of Natural Resources and Rural Poverty; Water, Environment and Society; Climate change; and One hundred successful cases of conservation of the natural heritage; Usumacinta: bases for integral management.

Between 1984 and 1994, she coordinated the Rural Research and Development Program for the Integral Use of Natural Resources (PAIR), an inter-institutional program in which the UNAM, the federal government and four state governments participated, as well as rural organizations and private initiative, aimed at rural communities in extreme poverty in four regions of Mexico. The objective was the search for alternatives to use natural resources that improve the living conditions of the population without detriment to the environment. She is founder of the Latin American Training Center for the Conservation of Biodiversity in the Lacandona Selva region, Chiapas.

She was a member of the Commission on Developing Countries and Global Change, which produced the report of For Earth's Sake, for the United Nations Conference on Environment and Development, held in Brazil in 1992. She was also a member of the High Level Panel on Global Sustainability of the General Secretary of the United Nations, which prepared the report Resilient People, Resilient Planet: a future worth choosing, for the Summit of Sustainable Development to be held in Rio de Janeiro in June 2012.

In February 1994, she was appointed President of the National Institute of Ecology, a decentralized agency of the Ministry of Social Development. In December 1994 she was invited by the President of Mexico to be Secretary of the Environment, Natural Resources and Fisheries, of which she was head of the Government until 2000.

She was a member of the Commission on Developing Countries and Global Change and Chairman of the Scientific Technical Panel of the Global Environmental Fund (GEF). In 2000 she received the Getty Prize awarded by Word Wildlife Fund; In 2004 the Cosmos International Prize, in 2005 the United Nations Environment Program awarded Julia the "Champions of the Earth" Prize and in 2011 the recognition "Nature, Territory and Society: Alexander Von Humboldt" awarded by the University of Guadalajara, Mexico.

CONFERENCE KEYNOTE SPEAKERS

A plenary talk will be given on morning and afternoon (Monday and Thursday) or just morning (Tuesday and Friday) of the conference by a leader in the field of mycorrhizal research.

Annegreth Kohler (INRA, France)

Monday morning keynote speaker (evolution)

Annegret Kohler is a researcher in the "Tree-microbe interactions" research group at INRA Grand-Est Nancy in France. Her research is focused on the biology of trees and the associated forest fungi and their role in forest ecosystems. She is particularly interested in mycorrhizal symbiosis and in characterizing the molecular mechanisms established during development and functioning of this mutualistic interaction, as well as to understand the evolution of symbiotic fungi from saprotrophic ancestors.

Annegret Kohler received a PhD in plant physiology and molecular biology at the University of Kaiserslautern/Germany in 1996. During her postdoctoral research she worked on Priming as a mechanism in induced systemic resistance in plants. In 2000 she joined the INRA group, first as a postdoctoral fellow, since 2006 as a permanent staff member. During the last 10 years she was involved in many genomic projects and in particular in charge of the transcriptomic analyses within these projects. She published over 50 scientific papers related to transcriptomics, genomics and tree-microbe interactions.

María José Pozo (Estación Experimental del Zaidín, CSIC, Spain)

Monday afternoon keynote speaker (interactions)

Maria J. Pozo is biologist and a scientific researcher at the Estación Experimental del Zaidín from the CSIC, the Spanish National Research Council, in Granada, Spain. Her group is interested on how beneficial soil fungi, and in particular arbuscular mycorrhizal fungi, boost plant immunity inducing systemic resistance against pathogens and pests. She is particularly interested in the molecular mechanisms regulating plant defenses by the symbiosis, their impact in multitrophic interactions, and the context dependency of the symbiosis impact on plant health. The final aim is to optimize mycorrhizal applications for sustainable crop protection. Please see their webpage for more information: www.eez.csic.es/mycorrhizaandbioticstresslab

During her PhD at Granada University, under the supervision of Prof. José Miguel Barea and Prof. Concepción Azcón-Aguilar she studied mycorrhiza induced resistance of tomato plants against the soil borne pathogen *Phytophthora parasitica*. Then she was a Postdoc at Prof. Kenerley´s lab in Texas A&M University, studying functional genomics of the biocontrol fungus *Trichoderma virens*. Later she was a Marie Curie Postdoctoral fellow at Prof. Pieterse lab at Utrecht University, The Netherlands, studying the signaling pathways regulating defense priming and induced resistance by beneficial soil bacteria in *Arabidopsis*. Currently she is head of the mycorrhiza and biotic stress lab within the Mycorrhiza group at the department of Soil Microbiology and Symbiotic Systems, Estación Experimental del Zaidín, CSIC, in Granada, Spain.

Jan Jansa (Czech Academy of Sciences, Czech Rep.)

Tuesday morning keynote speaker (physiology/ecology)

Jan Jansa graduated in biology at Charles University in Prague (Czech Republic) in 1997, then continued with doctoral studies in agricultural sciences at the Federal Institute of Technology (ETH) in Zurich, Switzerland (1999-2002). He spent one year (2003-2004) at the University of Adelaide (Australia) with Prof. Sally Smith before returning to Switzerland, where he worked at ETH Zurich until 2011. Thereafter, he moved back to Czech Republic where he currently heads the Laboratory of Fungal Biology at the Institute of Microbiology, Czech Academy of Sciences. He is interested, among others, in large-scale biogeography of mycorrhizal fungi, cost and benefits in mycorrhizal symbiosis, trading of nutrients for carbon between symbiotic partners, and utilization of organic nitrogen by arbuscular mycorrhizal fungi and their associated host plants, in concert with associated hyphosphere microbiome.

Matthias Rillig (Freie Universität Berlin, Germany)

Thursday morning keynote speaker (global change)

Matthias Rillig studied biology at Universität Kaiserslautern (Germany) and University of Edinburgh (Scotland), and then moved to the US, where he earned his Ph.D. at University of California Davis/ San Diego State University. After a postdoc at the Carnegie Institution of Washington, Stanford, he moved to University of Montana, where he was assistant and then associate professor of Microbial Ecology. In 2007, he relocated to Freie Universität Berlin, where he is professor of plant ecology and director of the Berlin-Brandenburg Institute of Advanced Biodiversity Research.

Matthias' group works on soil ecology in general, with a focus on fungi, including arbuscular mycorrhizal fungi. The group works on numerous topics, including the role of biota in soil aggregation, and the effects of global change on soils.

Richard Phillips (Indiana University, USA)

Friday morning keynote speaker (ecosystem processes)

Dr. Phillips' research program focuses on how plants and microbes mediate energy flow and nutrient dynamics in temperate forests – the largest terrestrial sinks for carbon globally. While there is a rich history of empirical research and theory on how and why forests differ in their functioning, much of this research has been shaped by a "surface bias", such that processes occurring in soils are often not considered explicitly. Dr. Phillips´ research addresses this gap by focusing on the hidden half of ecosystems, where roots and associated microbes (including symbiotic fungi) interact with soil minerals and soil organic matter (SOM) to control how energy, nutrients and water are cycled and linked.

Nearly all tree species associate with a single type of mycorrhizal fungi: AM *vs* ECM fungi. Plants that associate with AM fungi differ from plants that associate with ECM fungi in a suite of nutrient use traits. Likewise, AM and ECM fungi differ in their nutrient use traits. Given well-established links between trait variation and putative "biogeochemical syndromes" in ecosystems, Dr. Phillips proposed the Mycorrhizal-Associated Nutrient Economy (or MANE) hypothesis, which predicts that trees and microbes that associate with different types of mycorrhizal fungi possess an integrated suite of stoichiometrically-constrained traits that both reflect and determine biogeochemical variation across landscapes or within regions. Research in the Philips lab has sought to test this hypothesis using a complementary suite of field experiments, mesocosms and mathematical trait-based models.

AWARDS

David Read

Eminent Mycorrhiza Researcher Award

David Read is Emeritus Professor of Plant Sciences at the University of Sheffield, and a Fellow of the Royal Society of London, where he has served as Biological Secretary and Vice President. He graduated from the University of Hull with a PhD in forest pathology, and was appointed to the University of Sheffield in 1963 where he has spent his career. His research has encompassed studies of the functioning of all major groups of mycorrhizas, including pioneering contributions to understanding ericoid, monotropoid, orchid, ecto and arbuscular mycorrhizas. His work was pivotal in broadening awareness of the multifunctionality of mycorrhizas beyond their roles in phosphorus nutrition, especially with his demonstrations of the importance of mycorrhizas in utilization of organic nitrogen, and the roles of mycorrhizas as conduits for carbon flow through mycelial networks interconnecting plants. He co-authored with Sally Smith the second and third edition of the seminal work Mycorrhizal Symbiosis. He has published over 180 papers that have been highly influential and advanced the field in multiple ways. He has trained and mentored a diverse set of research students, postdocs, research fellows, colleagues and national and international collaborators with a generosity of spirit, wisdom and insight and good humor that has made him legendary as a scientist.

Sally E. Smith

Eminent Mycorrhiza Researcher Award

Sally E. Smith is an Emeritus Professor at the University of Adelaide. She holds BA, MA and PhD degrees from The University of Cambridge and a DSc from the University of Adelaide. She is a world authority on arbuscular mycorrhizas, having co-authored all three editions of the definitive text *Mycorrhizal Symbiosis*. She is also a Hi-Cite researcher. In addition to being elected as Fellow of the Australian Academy of Science, she has won numerous awards including the J.K. Taylor, OBE, Gold Medal in Soil Science awarded by the Soil Science Society of Australia. She is also Honorary Professor at the Research Centre for Eco-Environmental Sciences, Chinese Academy of Sciences, and Honorary Research Professor at the Chinese Agricultural University.

Jim M. Trappe

Eminent Mycorrhiza Researcher Award

Jim M. Trappe is currently a Professor of Forest Ecosystems and Botany-Plant Pathology at Oregon State University. After receiving his PhD in Forestry in 1962 from Washington University Jim began a long and distinguished career with the United States Forest Service Pacific Northwest Research Station as project leader for the Mycorrhizal research team. With over 500 mycorrhizal scientific publications dating back since 1960 Jim continues his research activity today. Jim's work in fungal taxonomy and mycophagy has been ground-breaking. Over the course of his career Jim has been author or joint author of one new order, three new families, 42 new genera/subgenera, 215 new species and 168 new species combinations. Jim has 18 fungi named in his honor. Jim brings passion, insight and humor to the Mycorrhizal community. He is respected and loved by the hundreds of students, visiting scientists and friends he has influenced and nurtured over his remarkable career.

Anne Pringle

Mid-Career Mycorrhiza Research Excellence Award

Anne Pringle is a Professor of Botany and Bacteriology at the University of Wisconsin-Madison. After receiving an undergraduate honors degree from the University of Chicago and a PhD from Duke University, she then conducted post-doctoral research at the University of California Berkeley, was a faculty member at Harvard University, and then moved to the University of Wisconsin-Madison, where she is currently a Professor. She has received many awards and fellowships for her research on fungi, and is currently the president of the Mycological Society of America. Anne is a very creative and accomplished fungal ecologist and evolutionary biologist. Her research has great breadth, integrating theoretical insights from population and physical modeling with demographic, physiological, community ecology and phylogenetic experimental approaches to answering a range of questions from ecology and evolution of invasion to stability of mutualisms to physiology and physics of dispersal. On mycorrhizas, her research has had major impact on our understanding of the evolution of the mycorrhizal habit within the Amanitaceae, and on fungal invasion biology.

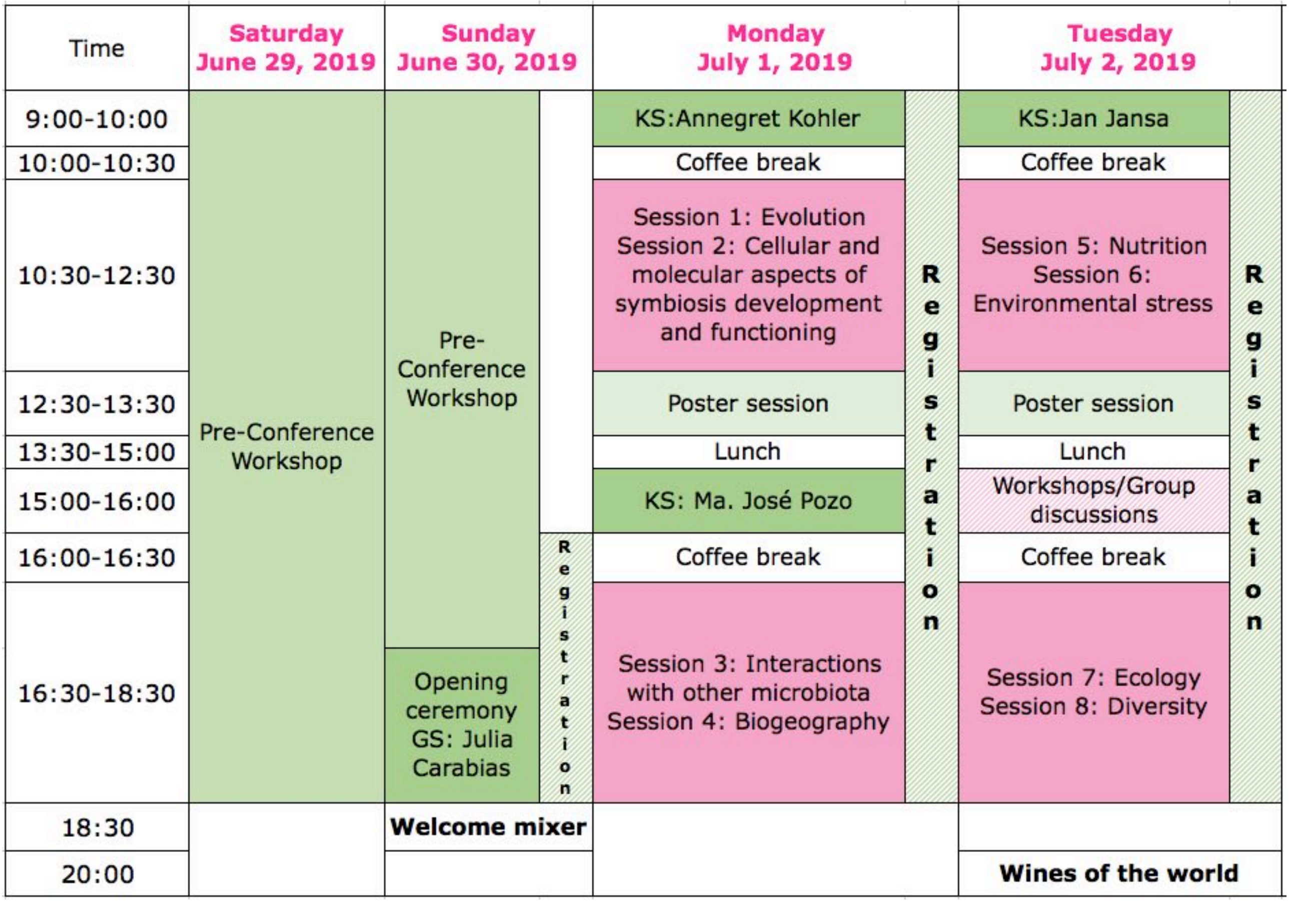
Lin Zhang, China Agricultural University

Student Publication Award

Lin Zhang, Gu Feng and Stéphane Declerck. 2018. Signal beyond nutrient, fructose, exuded by an arbuscular mycorrhizal fungus triggers phytate mineralization by a phosphate solubilizing bacterium. ISME Journal 12: 2339-2351. doi.org/10.1038/s41396-018-0171-4

PROGRAM AT A GLANCE

Saturday June 29 to Tuesday July 2, 2019

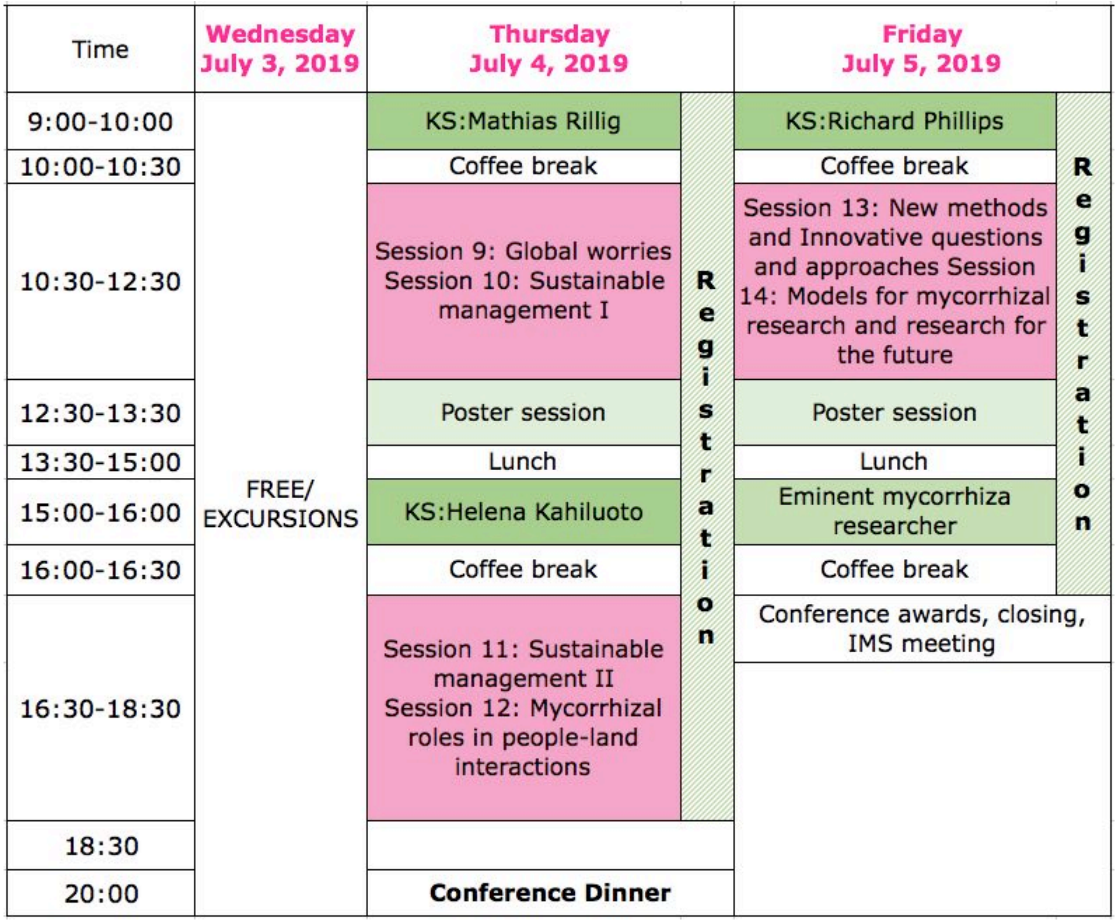


Time	Saturday June 29, 2019	Sunday June 30, 2019		Monday July 1, 2019		Tuesday July 2, 2019	
9:00-10:00	Pre-Conference Workshop	Pre-Conference Workshop		KS:Annegret Kohler	Registration	KS:Jan Jansa	Registration
10:00-10:30				Coffee break		Coffee break	
10:30-12:30				Session 1: Evolution Session 2: Cellular and molecular aspects of symbiosis development and functioning		Session 5: Nutrition Session 6: Environmental stress	
12:30-13:30				Poster session		Poster session	
13:30-15:00				Lunch		Lunch	
15:00-16:00				KS: Ma. José Pozo		Workshops/Group discussions	
16:00-16:30			Registration	Coffee break		Coffee break	
16:30-18:30		Opening ceremony GS: Julia Carabias		Session 3: Interactions with other microbiota Session 4: Biogeography		Session 7: Ecology Session 8: Diversity	
18:30		**Welcome mixer**					
20:00						**Wines of the world**	

The lunch will be served at Fiesta Americana Hotel

PROGRAM AT A GLANCE

Wednesday July 3 to Friday July 5, 2019



Time	**Wednesday July 3, 2019**	**Thursday July 4, 2019**		**Friday July 5, 2019**	
9:00-10:00	FREE/ EXCURSIONS	KS:Mathias Rillig	**Registration**	KS:Richard Phillips	**Registration**
10:00-10:30		Coffee break		Coffee break	
10:30-12:30		Session 9: Global worries Session 10: Sustainable management I		Session 13: New methods and Innovative questions and approaches Session 14: Models for mycorrhizal research and research for the future	
12:30-13:30		Poster session		Poster session	
13:30-15:00		Lunch		Lunch	
15:00-16:00		KS:Helena Kahiluoto		Eminent mycorrhiza researcher	
16:00-16:30		Coffee break		Coffee break	
16:30-18:30		Session 11: Sustainable management II Session 12: Mycorrhizal roles in people-land interactions		Conference awards, closing, IMS meeting	
18:30					
20:00		**Conference Dinner**			

The lunch will be served at Fiesta Americana Hotel

PRE-CONFERENCE WORKSHOP

Taxonomic identification of mycorrhizal fungi through molecular analysis: *"I already have my sequences, Now what do I do?"*

Taxonomic identification can be based solely on morphology, on molecular data, or a combination of both. The purpose of this course is to update researchers on the tools available for the molecular identification of fungi, both for individual isolates by Sanger sequencing and for metagenomes of fungal communities through Next Generation Sequencing (NGS). In particular, we will discuss (1) the three nuclear ribosomal regions most commonly used in the identification of fungi and the potential advantages and limitations of the ITS region, which is the official DNA barcode marker for the identification of fungi at the level of species; (2) how to do homology searches using BLAST for DNA barcodes and their limitations; (3) cured molecular databases of fungal sequences; (4) the various protein coding genes used to complement the ITS data in the species-level identification of certain fungal groups; and (5) the methods used in the construction of phylogenetic trees from DNA sequences to facilitate the identification of fungal species.

Dr. Jorge Ramírez-Prado
Centro de Investigaciones Científicas de Yucatán

PROGRAM DAY BY DAY

Sunday June 30, 2019

Time	Room	Activities
9:00-17:00	Casa Colón	Pre-Conference Workshop
17:00-18:30	26, International Conference Center (ICC)	**Opening ceremony** Chair: Javier Álvarez-Sánchez *Guest Speaker* **Julia Carabias** Mycorrhizas and environmental sustainability for development
18:30-20:30	Terrace, ICC	**Welcome mixer**

Monday July 1, 2019

Time	Event	Room	Activities
9:00-10:00	Keynote Lecture	26	The evolution of mycorrhizal genomes and transcriptomes **Annegret Kohler**
10:00-10:30		Foyer	Coffee break
10:30-12:30	Concurrent sessions	26A	**Session 1: Evolution** Chairs: Martin Bidartondo and Katie Field
10:30-12:30	Concurrent sessions	26B	**Session 2: Cellular and molecular aspects of symbiosis development and functioning** Chairs: Luisa Lanfranco and Jonathan Plett
12:30-13:30	Posters	Foyer	Poster session
13:30-15:00		Fiesta Americana	Lunch
15:00-16:00	Keynote Lecture	26	Increased metabolic plasticity underlies enhanced stress resistance in mycorrhizal plants **María José Pozo**
16:00-16:30		Foyer	Coffee break
16:30-18:30	Concurrent sessions	26A	**Session 3: Interactions with other microbiota** Chair: David Johnson
16:30-18:30	Concurrent sessions	26B	**Session 4: Biogeography** Chair: Camille Truong
18:30			
20:00			

Tuesday July 2, 2019

Time	Event	Room	Activities
9:00-10:00	Keynote Lecture	26	Mycorrhizal benefits and costs - do we understand enough to design more sustainable agroecosystems? **Jan Jansa**
10:00-10:30		Foyer	Coffee break
10:30-12:30	Concurrent sessions	26A	**Session 5: Nutrition** Chair: Feng Gu
10:30-12:30	Concurrent sessions	26B	**Session 6: Environmental stress** Chair: Jan Colpaert
12:30-13:30	Posters	Foyer	Poster session
13:30-15:00		Fiesta Americana	Lunch
15:00-16:00	Workshops	26	Workshops/Group discussions
16:00-16:30		Foyer	Coffee break
16:30-18:30	Concurrent sessions	26A	**Session 7: Ecology** Chair: Miranda Hart
16:30-18:30	Concurrent sessions	26B	**Session 8: Diversity** Chair: Sidney Stürmer
18:30-19:30			
20:00		**Terrace Fiesta Americana**	**Wines of the world**

Thursday July 4, 2019

Time	Event	Room	Activities
9:00-10:00	Keynote Lecture	26	Mycorrhiza and Global Change **Mathias Rillig**
10:00-10:30		Foyer	Coffee break
10:30-12:30	Concurrent sessions	26A	**Session 9: Global worries** Chair: Nancy Johnson
10:30-12:30	Concurrent sessions	26B	**Session 10: Sustainable management I** Chair: Alok Adholeya
12:30-13:30	Posters	Foyer	Poster session
13:30-15:00		Fiesta Americana	Lunch
15:00-16:00			
16:00-16:30		Foyer	Coffee break
16:30-18:30	Concurrent sessions	26A	**Session 11: Sustainable management II** Chair: Marcel van der Heijden
16:30-18:30	Concurrent sessions	26B	**Session 12: Mycorrhizal roles in people-land interactions** Chair: Thom Kuyper
18:30-19:30			
20:00		**Hacienda Chenkú**	**Conference Dinner**

Friday July 5, 2019

Time	Event	Room	Activities
9:00-10:00	Keynote Lecture	26	Seeing the forest beneath the trees: Mycorrhizal Fungi as trait integrators of ecosystem services **Richard Phillips**
10:00-10:30		Foyer	Coffee break
10:30-12:30	Concurrent sessions	26A	**Session 13: New methods and Innovative questions and approaches** Chairs: Annegret Kohler, Leho Tedersoo, Tatsu Ezawa and Petr Baldrian
10:30-12:30	Concurrent sessions	26B	**Session 14: Models for mycorrhizal research and research for the future** Chairs: Jim Bever and Ignacio Querejeta
12:30-13:30	Posters	Foyer	Poster session
13:30-15:00		Fiesta Americana	Lunch
15:00-16:00	Keynote Lecture	26	**Eminent mycorrhiza researcher Award**
16:00-16:30		Foyer	Coffee break
16:30-18:30	Plenary Session	26	IMS meeting, Wines of the World scores, Student Awards Chair: Jan Jansa Closing Ceremony Chair: Javier Álvarez-Sánchez

OPENING GUEST SPEAKER

Julia Carabias
Mycorrhizas and environmental sustainability for development
Sunday June 30, 17:30 - 18:30, ICC room 26

CONFERENCE KEYNOTE SPEAKERS

Annegreth Kohler
The evolution of mycorrhizal genomes and transcriptomes
Monday July 1, 9:00 - 10:00, ICC room 26

María José Pozo
Increased metabolic plasticity underlies enhanced stress resistance in mycorrhizal plants
Monday July 1, 15:00 - 16:00, ICC room 26

Jan Jansa
Mycorrhizal benefits and costs - do we understand enough to design more sustainable agroecosystems?
Tuesday July 2, 9:00 - 10:00, ICC room 26

Matthias Rillig
Mycorrhiza and Global Change
Thursday July 4, 9:00 - 10:00, ICC room 26

Richard Phillips
Seeing the forest beneath the trees: Mycorrhizal Fungi as trait integrators of ecosystem services
Friday July 5, 9:00 - 10:00, ICC room 26

CONDENSED PROGRAM ORAL SESSIONS

Presentation day	Time	Session	Oral modality	ID
Monday, July 1	10:30-12:30	1	15 minutes	312, 316, 132, 55
			10 minutes	112, 65, 203
		2	15 minutes	83, 189, 105, 176
			10 minutes	182, 21, 22, 235
	16:30-18:30	3	15 minutes	8, 26, 31, 63
			10 minutes	25, 45, 74, 124, 174
		4	15 minutes	47, 82, 145, 192
			10 minutes	183, 12, 257
Tuesday, July 2	10:30-12:30	5	15 minutes	173, 80, 129, 42
			10 minutes	34, 66, 171, 44, 106, 110
		6	15 minutes	49, 136, 103, 62
			10 minutes	86, 107, 93, 191
	16:30-18:30	7	15 minutes	20, 87, 10, 29
			10 minutes	77, 163, 43, 166, 186
		8	15 minutes	151, 89, 40, 137
			10 minutes	46, 90, 104
Thursday, July 4	10:30-12:30	9	15 minutes	161, 121, 60, 223
			10 minutes	113, 111, 71, 19, 37, 277
		10	15 minutes	313, 11, 48, 180
			10 minutes	123, 120, 95, 27, 201, 178
	16:30-18:30	11	15 minutes	91, 138, 308,32
			10 minutes	75, 59, 73, 53, 264, 269
		12	15 minutes	72, 184, 88, 142
			10 minutes	28, 179, 299, 217, 56, 302
Friday, July 5	10:30-12:30	13	15 minutes	38, 64, 307, 30
			10 minutes	35, 216, 41, 108, 79
		14	15 minutes	133, 177, 39, 172
			10 minutes	36, 78, 169, 18, 284

DETAILED PROGRAM ORAL SESSIONS

Monday July 1, 2019

Oral Session 1 "Evolution"

International Conference Center, room 26A, 10:30-12:30
Chairs: Martin Bidartondo and Katie Field

10:30 - 10:45 **ID 312** - Plant-Mucoromycotina mutualisms: a nitrogen affair? **Silvia Pressel**, Martin Bidartondo, Jeffrey Duckett, Grace Hoysted, Jill Jowal, William Rimington, Jonathan Leake, Katie Field

10:45 - 11:00 **ID 316** - Mycorrhiza-like symbioses and Earth's early climate. **Katie Field**, Sarah A. Batterman, Khushboo Gurung, Grace A. Hoysted, Silvia Pressel, Martin I. Bidartondo, Benjamin J. W. Mills

11:00 - 11:15 **ID 132** - How are contemporary outcomes of mycorrhizal interactions shaped by early and ongoing evolution? **Jason Hoeksema**

11:15 - 11:30 **ID 55** - Genomic differentiation of an ectomycorrhizal fungus (*Laccaria trichodermophora*) in Mexican sky-islands. **Christian Armando Quintero Corrales**, Rodolfo Ángeles-Argáiz, Juan Pablo Jaramillo-Correa, Daniel Piñero, Roberto Garibay-Orijel, Alicia Mastretta-Yanes

11:30 - 11:40 **ID 112** - Population genomics of toxins genes in *Amanita phalloides*. **Samantha Harrow**, Yen-Wen Wang, Jaqueline Hess, Anne Pringle

11:40 - 11:50 **ID 65** - Variation in plant and fungal traits indicates mycorrhizal mediated selection for *Pinus radiata*. **Megan Rúa**, Jason Hoeksema

11:50 - 12:00 **ID 203** - Association with arbuscular mycorrhizal fungi modifies phenotypic natural selection of fruit production in *Ruellia nudiflora* (Acanthaceae) **José Ramos-Zapata**, Victor Parra-Tabla, Blanca Mejía-Alva

Oral Session 2 "Cellular and molecular studies on symbiosis development and functioning"

International Conference Center, room 26B, 10:30-12:30
Chairs: Luisa Lanfranco and Jonathan Plett

10:30 - 10:45 **ID 83** - Nutrient availability and the impact on host receptivity to ectomycorrhizal fungi: separating host from fungal influences on symbiosis. **Jonathan Plett**, V. R. Singan, M. Wang, V. Ng. I. V. Grigoriev, F. Martin, I. C. Anderson

10:45 - 11:00 **ID 189** - *In silico* analysis of fungal small RNA accumulation reveals putative plant mRNA targets in the symbiosis between an arbuscular mycorrhizal fungus and its host plant. **Luisa Lanfranco**, Alessandro Silvestri, Valentina Fiorilli, Laura Miozzi, Gian Paolo Accotto, Massimo Turina

11:00 - 11:15 **ID 105** - Tracing fungal nitrogen and host carbon in arbuscular mycorrhizal symbiosis by correlative ultrastructural TEM observation and high-resolution secondary ion mass spectrometry imaging. **Yukari Kuga**, Wu Ting-Di, Sakamoto Naoya, Nagata Kosuke, Katsuyama Chie, Yurimoto Hisayoshi

11:15 - 11:30 **ID 176** - Interactions between arbuscular mycorrhizal fungi and non-host plant **Marco Rebeca Cosme**, Ivan Fernández, Maryline Calonne-Salmon, Ioannis A. tringlis, Ke Yu, Ronnie De Jonge, Saskia C.M. Van Wees, María J. Pozo, Stéphane Declerck, Marcel Van Der Heijden, M.J. Corné

11:30 - 11:40 **ID 182** - Cellulose content increase as a possible mechanism of priming in shoots of mycorrhizal tomato. Amada Zule Rodríguez-Corral, Ana Belén Mendoza-Soto, **Melina López-Meyer**

11:40 - 11:50 **ID 21** - Structural variation in the genomes of AMF. **Joaq uim Cruz Corella**

11:50 - 12:00 **ID 22** - *Tricholoma*-spruce ectomycorrhiza: phytohormones and volatiles. **Oluwatosin Abdulsalam**, Katrin Krause, Erika Kothe

12:00 - 12:10 **ID 235** - Phosphate acquisition through the mycorrhizal pathway upregulates the genes involved in arbuscule development and Pi homeostasis in the host. **Asaeda Satoshi**, Hayato Maruyama, Tatsuhiro Ezawa

Oral Session 3 "Interactions with other biota"

International Conference Center, room 26A, 16:30-18:30
Chair: David Johnson

16:30 - 16:45 **ID 8** - Ectomycorrhizal symbiosis buffers responses to above/belowground biotrophic interactions governed by endogenous rhythmic growth in trees. **Sylvie Herrmann**, Frank Fleischmann, Thorsten Grams, Liliane Ruess, Martin Schaedler, Stefan Scheu, Silvia Schrey, Mika Tarkka, Francois Buscot

16:45 - 17:00 **ID 26** - Cooperation with hyphosphere microbiome helps arbuscular mycorrhizal community assembling in the root system. **Jiachao Zhou**

17:00 - 17:15 **ID 31** - Signal beyond nutrient – Fructose exuded by an arbuscular mycorrhizal fungus triggers phytate mineralization by a phosphate solubilizing bacterium. **Lin Zhang**, Gu Feng, Stéphane Declerck

17:15 - 17:30 **ID 63** - Aphid herbivory decouples of carbon-for-nutrient exchange in the AM symbiosis. **Michael Charters**, Steven Sait, Katie Field

17:30 - 17:40 **ID 25** - The adversaries of arbuscular mycorrhizal fungi. **Carla Cruz-Paredes**, Marie Davey, Iver Jakobsen, Ole Nybroe

17:40 - 17:50 **ID 45** - Characterization of mycorrhizal seed treatments on rice growth, yield, and tolerance to rice water weevil injury. **Lina Bernaola**, Michael Stout

17:50 - 18:00 **ID 74** - The enemy of my enemy is my friend: using dual inoculation of beneficial above - and belowground fungal symbionts to save the endangered Hawaiian mint *Phyllostegia kaalaensis* from a foliar fungal pathogen. **Nicole Hynson**, Cameron Egan

18:00 - 18:10 **ID 124** - Plant-fungus-animal-virus interactions: arbuscular mycorrhiza affects grapevine fanleaf virus transmission by the nematode vector *Xiphinema index*. **Zhipeng Hao**, Diederik van Tuinen, Léon Fayolle, Odile Chatagnier, Xiaolin Li, Baodong Chen, Silvio Gianinazzi, Vivienne Gianinazzi-Pearson

18:10 - 18:20 **ID 174** - Interaction between arbuscular mycorrhizae, plant growth promoting bacteria and bacterial metabolites in growth and development of *Phaseolus vulgaris* var *canario centenario*. Rocio Calsina, Miriam Mememza, Ricar Santos, **Marcia Toro**, Doris Zuñiga

Oral Session 4 "Biogeography"

International Conference Center, room 26B, 16:30-18:30
Chair: Camille Truong

16:30 - 16:45 **ID 47** - Environment and host as large-scale controls of ectomycorrhizal fungi. **Martin I. Bidartondo**, Laura M. Suz, C. David L. Orme, Filipa Cox, Henning Andreae, Endla Asi, Bonnie Atkinson, Sue Benham, Christopher Carroll, Nathalie Cools, Bruno De Vos, Hans-Peter Dietrich, Johannes Eichhorn, Joachim

16:45 - 17:00 **ID 82 -** Does the biogeographic origin of ectomycorrhizal fungi differ among non native woody plants species? **Miroslav Vosátka**, Leho Tedersoo, Tomáš Antl, Tomáš Větrovský, Kessy Abarenkov, Jan Pergl, Jana Albrechtová, Petr Pyšek, Petr Baldrian, Petr Kohout

17:00 - 17:15 **ID 145** - Does plant mycorrhizal trait assignment method matters for biogeographic analyses? **Guillermo Bueno**, Reeta Sharma

17:15 - 17:30 **ID 192** - Biogeography of plant mycorrhizal traits along a latitudinal gradient in the Southern Hemisphere. **Patricia Silva-Flores**, Guillermo Bueno

17:30 - 17:40 **ID 183** - Biogeography of ectomycorrhizal fungi associated with Nothofagaceae in the Southern Hemisphere. **Camille Truong**, Marisol Sánchez-García, B. Mujic Alija, Rosanne Healy, Francisco Kuhar, Eduardo Nouhra, Andrew Wilson, Don Pfister, Brandon Matheny P., E. Smith Matthew

17:40 - 17:50 **ID 12** - Ectomycorrhizal fungal communities associated with Betulaceae in Chinese secondary forest ecosystems. **Liang-Dong Guo**, Gao Cheng, Cheng Liang, Ji Niu-Niu, Wu Bin-Wei, Li Xing-Chun, Lv Peng-Peng, Yong Zheng

17:50 - 18:00 **ID 257** - Patterns of global distribution of families in Glomeromycota related to soil properties and biomes. **Sidney L. Stürmer**, James D. Bever

Tuesday July 2, 2019

Oral Session 5 "Nutrition and resource allocation"

International Conference Center, room 26A, 10:30-12:30
Chair: Gu Feng

10:30 - 10:45 **ID 173** - Friend or foe – how does a host plant distinguish among high and low benefit AM fungi? **Heike Bücking**, Kevin Garcia, Kevin Cope, Arjun Kafle

10:45 - 11:00 **ID 80** - Exploring the secrets of hyphosphere processes. Fei Wang, Lin Zhang, **Gu Feng**

11:00 - 11:15 **ID 129** - Polyphosphate metabolism in arbuscular mycorrhizal fungi in relation to P transfer to the host. **Saito Katsuharu**

11:15 - 11:30 **ID 42** - Are ectomycorrhizal networks associated with greater growth of adult interior Douglas-fir? **Joseph Cooper**, Suzanne Simard, Justine Karst

11:30 - 11:40 **ID 34** - Field evidence for higher specific contribution of AMF to oats P uptake under long-term conservation agriculture than under conventional tillage **Mayra E. Gavito**, Iver Jakobsen

11:40 - 11:50 **ID 66** - Changes in atmospheric CO_2 induce cultivar-specific carbon-for-nutrient exchange responses in wheat arbuscular mycorrhizal fungal symbioses. **Tom Thirkell**, Daria Pastok, Katie Field

11:50 - 12:00 **ID 171** - Ericaceous root enzymes are more sensitive than ectomycorrhizal to nutrient addition in Arctic tundra. **Haley Dunleavy**, Mack Michelle

12:00 - 12:10 **ID 44** - Arbuscular mycorrhiza reduces rhizosphere priming effects on the decomposition of soil organic matter. **Johanna Pausch**, Jie Zhou, Sebastian Loeppmann, Matthias Gube

12:10 - 12:20 **ID 106** - How arbuscular mycorrhizal fungi and rhizobia compete for host carbon resources in tripartite interactions of *Medicago truncatula*? **Jaya Krishna Yakha**, Richard C. Kevin, Arjun Kafle, Kevin Garcia, Xiurong Wang, E. Philip Pfeffer, D. Gary Strahan, Heike Bucking

12:20 - 12:30 **ID 110** - Can we increase wheat growth and nutrient uptake using AMF inoculum? **Ashleigh Elliott**, Katie Field

Oral Session 6 "Environmental stress"

International Conference Center, room 26B, 10:30-12:30
Chair: Jan Colpaert

10:30 - 10:45 **ID 49** - Arbuscular mycorrhiza and altered plant drought responses – Soil water flow resistances are mitigated beyond the ambit of roots. **Michael Bitterlich**, Jan Graefe, Philipp Franken, Richard Pauwels

10:45 - 11:00 **ID 136** - Drought stress leads to differential gene expression in both plant and fungus in arbuscular mycorrhizal symbiosis. **Michelle Keller-Pearson**, Luke Willems, Annika Peterson, Erin M. Silva, Jean-Michel Ané

11:00 - 11:15 **ID 103** - Above the tree line: Drivers of ectomycorrhizal fungal communities in the European Alps. **Ricardo Arraiano Castilho**, Martin I. Bidartondo, Tuula Niskanen, James J. Clarkson, Ivano Brunner, Stephan Zimmermann, Beat Frey, Beatrice Senn-Irlet, Tanja Mrak, Ursula Peintner, Laura Martínez Suz

11:15 - 11:30 **ID 62** - Zn tolerance in *Suillus luteus* is linked to a high transcription of a CDF transporter gene through extensive gene multiplication and differences in cis-regulation. Michiel Op De Beeck, Natascha Arnauts, François Rineau, Joske Ruytinx, **Jan Colpaert**

11:30 - 11:40 **ID 86** - Mycorrhizal symbiosis induces divergent patterns of uptake, transport and partitioning of Cd and Zn in *Populus trichocarpa*. **Mark Tibbett**, Vinicius Henrique De Oliveira, Ihsan Ullah, Jim M. Dunwell,

11:40 - 11:50 **ID 107** - Kin recognition in Douglas-fir through mycorrhizal networks in response to neighbor plant stress. **Monika Gorzelak**, Brian Pickles, Suzanne Simard, Susan Dudley

11:50 - 12:00 **ID 93** - Characterization of soil-fungus-plant transfer of 238U and 232Th in a natural contaminated environment. **Jeanette Rosas-Moreno**, Jon K. Pittman, Clare H. Robinson

12:00 - 12:10 **ID 191** - Phenanthrene dissipation by wheat plants inoculated with *Funneliformis mosseae* and *Trichoderma viride*. **Cesar Arriagada**

WORKSHOP/GROUP DISCUSSIONS

How to diagnose mycorrhizal plants and (why) does it matter?

International Conference Center, room 26A, 15:00-16:00

Organizers: C. Guillermo Bueno, Maarja Öpik, Mari Moora, Ylva Lekberg, Laura Aldrich-Wolfe

The ability to characterize plants in terms of association with mycorrhizal fungi (plant mycorrhizal traits) is fundamental to understand the ecology of mycorrhizal symbiosis, especially at large scales. Mycorrhizal type, - such as: arbuscular (AM), ecto- (ECM), ericoid (ERM) or orchid (ORM) - and mycorrhizal status - obligately (OM), facultatively (FM) or non-mycorrhizal (NM) -, are the main plant species-level mycorrhizal traits (Smith and Read 2008; Moora 2014). However, the use of the same terms with different conceptual meanings creates misunderstanding and impedes constructing coherent and solid knowledge about the mycorrhizal properties of plant species. Proper consideration of plant mycorrhizal relations is paramount for understanding the effects of mycorrhizal symbiosis on plant distribution and vegetation processes across environmental gradients. Currently, different interpretations exist for some key plant mycorrhizal traits and are reflected in respective criteria and guidelines to diagnose mycorrhizal and non-mycorrhizal plant species (Brundrett and Tedersoo 2019; Bueno et al. In press). For example, to distinguish whether the mycorrhizal type of a plant is AM or NM plants, or whether a plant has a “consistent” fungal mycorrhizal colonization or not, depends on the aspect referred, context and the concepts of AM, NM, FM or OM used. Thus, efforts to discuss and understand these differences will pave the way to refine our understanding and to lay a solid ground for current and future research. In this open discussion we will briefly present the different perspectives on diagnosing mycorrhizas, their optimal proposed use, along with the relevance and consequences of using different diagnostic criteria to open the discussion. Our goal is (1) to collect the varying perceptions, (2) to discuss a general framework to understand the different approaches and their validation with empirical evidences, and (3) to determine the critical steps for reaching a consensus on those concepts.

Agenda:

10 min. Introduction of the different perspectives and main questions of the debate

50 min. Diagnostic criteria for NM, AM, FM plants. Suggestions and comments

Oral Session 7 "Ecology"

International Conference Center, room 26A, 16:30-18:30
Chair: Miranda Hart

16:30 - 16:45 **ID 20** - Fungal biofertilizers - establishment and spread. **Miranda Hart**, Vasilis Kokkoris, Corrina Thomsen, Daniel Rosa

16:45 - 17:00 **ID 87** - Relationship of plant mycorrhizal benefits and the quantitative composition of arbuscular mycorrhizal fungal communities. **Martina Janouskova**, Alena Voriskova, David Puschel, Miroslav Vosatka, Jan Jansa

17:00 - 17:15 **ID 10** - Mycorrhizal fungi influence global plant biogeography. **Camille Delavaux**, Patrick Weigelt, Jessica Duchicela, Peggy Schultz, Holger Kreft, James D. Bever.

17:15 - 17:30 **ID 29** - Taxonomic variation in aerial dispersal of AM fungi – testing trait-based predictions. **Bala Chaudhary**, Cameron Egan

17:30 - 17:40 **ID 77** - Arbuscular mycorrhizal fungi colonize leaf litter in ectomycorrhizal forests. **Rebecca Bunn**, Dylan Simpson, Lorinda Bullington, Ylva Lekberg, David Janos

17:40 - 17:50 **ID 163** - Primary succession of AM fungal communities on newly formed islands. **SØren Rosendahl**, Álvaro López-García, Camilla Maciel Rabelo Pereira, Rasmus Kjøller

17:50 - 18:00 **ID 43** - Mycobiomes of boreal forest soils: Unraveling patterns in fungal communities following natural and anthropogenic disturbances. **Jean Carlos Rodriguez Ramos**, Jonathan A. Cale, Suzanne W. Simard, James F. Cahill, Justine Karst, Nadir Erbilgin

18:00 - 18:10 **ID 166** - Changes in plant community mycorrhization along a productivity gradient in temperate grasslands in Estonia. **Daniela León**, Martin Zobel, Mari Moora, Jonathan Bennett, Kersti Riibak, Meelis Pärtell, Guillermo Bueno

18:10 - 18:20 **ID 186** - Functional traits of arbuscular mycorrhizal fungal communities along succession in a tropical dry forest. **Silvia Margarita Carrillo Saucedo**, Mayra Elena Gavito Pardo

Oral Session 8 "Diversity"

International Conference Center, room 26B, 16:30-18:30
Chair: Sidney Stürmer

16:30 - 16:45 **ID 151** - Benefits of native mycorrhizal amendments to grassland restoration increases with field inoculation density. **Elizabeth Koziol**, James D. Bever

16:45 - 17:00 **ID 89** - Fungal competition and host quality – two underappreciated factors driving AMF diversity? **Ylva Lekberg**, Ariel Lavoie, Rebecca A. Bunn, Lauren P. Waller

17:00 - 17:15 **ID 40** - The ecology and diversity of the genus *Clavulina* (Cantharellales, Basidiomycota) across tropical and temperate forests in Mexico. **Eduardo Pérez-Pazos**, Roberto Garibay-Orijel, Margarita Villegas-Ríos, Rodolfo Salas-Lizana, Noemi Matías-Ferrer, Adriana Corrales

17:15 - 17:30 **ID 137** - *Rhizoscyphus ericae* = *Hyaloscypha hepaticicola*: consequences for taxonomy, ecology and evolution of the youngest mycorrhizal symbiosis. **Martin Vohnik**, Martina Reblova, Judith Fehrer

17:30 - 17:40 **ID 46** - Diversity of *Rhizopogon* in the Madrean Sky Islands, Southwestern United States and Northwestern Mexico. **Carolina Piña Páez**, Adam Carson, Jessica Martin, Joseph Spatafora

17:40 - 17:50 **ID 90** - Assessing inter- and intraspecific diversity of AM fungi in association with maize in Mexico and France. **Arthur QuyManh Maës**, Pilar Ortega-Larrocea, Francis Carbonne, Guillaume Bécard, Nathalie Séjalon-Delmas

17:50 - 18:00 **ID 104** - Rescuing the ectomycorrhizal diversity from south American Nothofagaceae forest and unraveling confusing identities: the case of *Cortinarius magellanicus* complex. **María Eugenia Salgado Salomón**, Carolina Barroetaveña, Ursula Peintner

Thursday July 4, 2019

Oral Session 9 "Global worries"

International Conference Center, room 26A, 10:30-12:30
Chair: Nancy Johnson

10:30 - 10:45 **ID 161** - The effect of land use change on the arbuscular mycorrhizal fungi community in a tropical rainforest, Los Tuxtlas, Veracruz, Mexico. América Baleón Sepúlveda, Viviana Rodríguez-Galicia, **Manuel Casariego-Martínez**, Carla Hudler-Schimpf, Yesenia Flores-Gómez, Irma Cervantes-Salgado, Laura Hernández-Cuevas, Irene Sánchez-Gallen, Javier Álvarez-Sánchez

10:45 - 11:00 **ID 121** - Restoration of arbuscular mycorrhizal fungal communities in response to conversion from arable cultivation to grass/clover leys. **Thorunn Helgason**

11:00 - 11:15 **ID 60** - Arbuscular mycorrhizal fungi in agriculture and restoration: consider the species pool. **Maarja Öpik**

11:15 - 11:30 **ID 223** - Mechanisms of local adaptation in mycorrhizal systems. **Nancy C. Johnson**, Bob Maxwell Stevens, Daniel Revillini, Gail Wilson, R. Michael Miller

11:30 - 11:40 **ID 113** - Diversity indices using arbuscular mycorrhizal fungi to evaluate the soil state in banana and coffee crops in Colombia and Mexico. **Raúl Hernando Posada Almanza**

11:40 - 11:50 **ID 111** - Effect of drought and season on arbuscular mycorrhizal fungi in a subtropical secondary forest. **Yong Zheng**, Li Xing-Chun, Zhou Xu-Hui, Liang-Dong Guo

11:50 - 12:00 **ID 71** - Mycorrhizas shape plant communities: Lessons from cross-continental grassland studies. **Gail Wilson**, Adam Cobb, Jiqiong Zhou, Yingjun Zhang

12:00 - 12:10 **ID 19** - Rooting for the home team: Belowground allocation and root traits in native and nonnative woody species. **Alex Ebert**, A. Frank Douglas, D. Fridley Jason

12:10 - 12:20 **ID 37** - Networking South American mycorrhizal research. **César Marín**

12:20 - 12:30 **ID 277** - Unexpectedly deep mycorrhizal fungi may mediate plant acquisition of permafrost nitrogen. Rebecca E. Hewitt, M. Rae DeVan, Michelle C. Mack, **D. Lee Taylor**

Oral Session 10 "Sustainable management I"

International Conference Center, room 26B, 10:30-12:30
Chair: Alok Adholeya

10:30 - 10:45 **ID 313** - Seed coating of mycorrhiza: A technique to a technology. **Alok Adholeya**

10:45 - 11:00 **ID 11** - Towards the effective breeding and development of improved microbial inocula for better cassava yields in Africa. **Ricardo Alexander Peña Venegas**, Moses Thuita, Cargele Masso, Alia Rodriguez, Peter Mlay, Ian R. Sanders

11:00 - 11:15 **ID 48** - Arbuscular mycorrhizal fungal communities of 31 durum wheat cultivars (*Triticum turgidum* L. var. *durum*) under field conditions in Eastern Canadian **Mohamed Hijiri**, Chantal Hamel

11:15 - 11:30 **ID 180** - Importance of arbuscular mycorrhizas in a maize-green manure rotation. **David A. Ortiz-Salgado**, Felipe García-Oliva, Alejandro Alarcón, John Larsen

11:30 - 11:40 **ID 123** - Interactive effects of mycorrhization, daytime and/or nighttime eCO2 on plant performance are host-species (N2-fixing vs. non-N2-fixing) or cropping pattern (mono-culture vs. intercropping) dependent. Miao Wen, Songmei Shi, Lu Zhang, Xinshui Dong, Sharifullah Sharifi, **Xinhua He**

11:40 - 11:50 **ID 120** - Artificial cultivation of *Tricholoma matsutake* using the matsutake-infected pine seedlings. **Rhim Ryoo**, Ka Kang-Hyeon, Yeongseon Jang, Hyun Park

11:50 - 12:00 **ID 95** - Tracking introduced arbuscular mycorrhizal fungus in root of *Allium fistulosum* and its effect on phosphorus uptake and growth under field with or without indigenous fungi. **Keitaro Tawaraya**, Rieko Niwa, Tatsuhiro Ezawa, Shusei Sato, Hideki Hirakawa, Shigenobu Yoshida, Weiguo Cheng

12:00 - 12:10 **ID 27** - Methodology and efficacy of the *Zea mays* seed coating (maize) with the arbuscular mycorrhizal fungus, *Glomus iranicum* var. *tenuihypharum*. **Rocío Torres Vera**, Bernabé García Antonio, Ana Vila Martínez, Héctor Alejandro Carmona Álvarez Bahamonde, Francisco José Fernández, Félix Martín

12:10 - 12:20 **ID 201** - Effect of *Funneliformis mosseae* on physiological and antioxidant response of *Physalis peruviana* under phosphorus stress. L. P. Moreno, **M. Ramírez-Gómez**

12:20 - 12:30 **ID 178** - Living and dead nurse trees facilitate oak regeneration in the xeric woodlands of central Texas. **Brian John Pickles**, Monika A. Gorzelak, Cristina M. Campbell, Laurel L. Moulton, Lisa O'Donnell

Oral Session 11 "Sustainable management II"

International Conference Center, room 26A, 16:30-18:30
Chair: Marcel van der Heijden

16:30 - 16:45 **ID 91** - Effects of long-term fertilization of a young spruce plantation on soil organic matter chemistry, ectomycorrhizal fungal communities, and exoenzyme activities. Valerie Ward, **Melanie Jones**

16:45 - 17:00 **ID 138** - Soil ecological engineering with arbuscular mycorrhizal fungi and their role as keystone taxa in agro-ecosystems. **Marcel van der Heijden**, Sam Banerjee, Franz Bender, Julia Hess, Natacha Bodenhausen, Klaus Schläppi, Alain Held, Romina Demarmels, Florian Walder

17:00 - 17:15 **ID 308** - The fungal Champions League: Pathogens versus Mycorrhizas. **David Johnson**, Marina Semchenko, Richard Bardgett, Shixiao Yu, Minxia Liang, Xubing Liu

17:15 - 17:30 **ID 32** - Genetic variation in *Rhizophagus irregularis* influences soil respiration and soil structure in tropical soils under cassava cultivation. **Diego Camilo Peña Quemba**, Alia Rodriguez, Ian R. Sander

17:30 - 17:40 **ID 75** - Missing links: the lack of host specific arbuscular mycorrhizal fungi and keystone species contributes to ecosystem retrogression in native Hawaiian forest restoration experiment. **Cameron Egan**, Sean Swift, Nicole Hynson

17:40 - 17:50 **ID 59** - Arbuscular mycorrhizae versus Ectomycorrhizae: Changes in community composition after revegetation in riparian ecosystems. **Vicky Waymouth**, Rebecca Miller, Fiona Ede, Cristina Aponte

17:50 - 18:00 **ID 73** - Mycotrophic capacity and diversity of native arbuscular mycorrhizal fungi isolated from degraded soils. **Winston Franz Ríos Ruiz**, Lleny Barrios-López, José Carlos Rojas-García, Renzo Alfredo Valdez-Nuñez

18:00 - 18:10 **ID 53** - Host response of nine coffee varieties to AMF. Dora Trejo Aguilar, Marco Zilli, Yahaira Baeza, Wendy Sangabriel, **Jacob Bañuelos**

18:10 - 18:20 **ID 264** - Understanding AM community assembly to increase plant community restoration success. **Shabana Hoosein**, Trivedi Pankaj, Cameron Egan, Mark Paschke

18:20 - 18:30 **ID 269** - Legacy effects of nursery practices on arbuscular mycorrhizal fungal (AMF) communities in seedling transplants of the imperiled Mulanje cedar (*Widdringtonii wrighteii*; Cupressaceae). **Louise Egerton-Warburton**, Lynnaun Johnson, Kirsty Shaw, Gurleen Kaur, Carl Bruessow, Tembo Chanyenga, Henry Chinthuli, Chamwala Kondwani, Paul Smith

Oral Session 12 "Mycorrhizal roles in people land interactions"

International Conference Center, room 26B, 16:30-18:30
Chair: Thom Kuyper

16:30 - 16:45 **ID 72** - Resilience of *Rhizopogon*-Douglas-fir mycorrhizal networks 25 years after selective logging. **Daniel Durrall**, Carrie Van Dorp, Suzanne W. Simard

16:45 - 17:00 **ID 184** - Linking management decisions, mycorrhizal abundance, soil quality and pasture productivity in an agroforest frontier in the humid tropics of Mexico. **Rocío Aguilar**, Mayra E. Gavito, Thom Kuyper, Marielos Peña-Claros, Mirjam Pulleman

17:00 - 17:15 **ID 88** - Impact of introduction of arbuscular mycorrhizal fungi on the root microbial community in agricultural fields. Rieko Niwa, Hideki Hirakawa, Hayato Maruyama, Takumi Sato, Takae Suzuki, Ayako Fukunaga, Takashi Sato, Shigenobu Yoshida, Keitaro Tawaraya, **Masanori Saito**, Tatsuhiro Ezawa, Shusei Sato

17:15 - 17:30 **ID 142** - Arbuscular mycorrhizal fungi role in the sustainability of coastal environments from Yucatan, Mexico. **Patricia Guadarrama**, Aida M. Vasco-Palacios

17:30 - 17:40 **ID 28** - Mycorrhiza smart breeding and agroecosystem management to optimize food production and nutrition. **Adam Cobb**, Nancy C. Johnson, Gail W.T. Wilson

17:40 - 17:50 **ID 179** - Metagenomic analysis of arbuscular mycorrhizal fungi associated to native maize landraces in a Mexican traditional polyculture. Rocío G. Cervantes-Gámez, Ofelda Peñuelas-Rubio, Karla Y. Leyva-Madrigal, Arantxa Angulo-Ross, Simoneta Negrete-Yankelevich, Alejandra Núñez-de la Mora, Guadalupe Amescua-Villela, **Ignacio E. Maldonado-Mendoza**

17:50 - 18:00 **ID 299** - The genetic basis of mycorrhizal growth responses in spring wheat. Tom Thirkell, **Tim Daniell**, Katie Field, Lucy James

18:00 - 18:10 **ID 217** - Ancient Amerindian modification of Amazonian ferralsols changes community composition of arbuscular mycorrhizal fungi but does not affect cassava root mycorrhization. **Clara Peña**, Thomas W. Kuyper, John Davison, Teele Jairus, Martti Vasar, Jan Stomph Tjeerd, Paul Struik, Maarja Öpik

18:10 - 18:20 **ID 56** - The legacy effect of drought on fungal communities from agricultural land under contrasting management types. **Phillip Brailey**, Thorunn Helgason

18:20 - 18:30 **ID 302** - A participatory approach to harness native mycorrhizae. **Marie Chave**, Valérie Angeon, Anne-Charlotte Harter, Melina Goasduff, Geraldine Paul, Sophie Quinquenel, Helene Ster

Friday July 5, 2019

Oral Session 13 "New methods and innovative questions and approaches"

International Conference Center, room 26A, 10:30-12:30
Chairs: Annegret Kohler, Tatsuhiro Ezawa, Petr Baldrian and Leho Tedersoo

10:30 - 10:45 **ID 38** - Seasonality of ectomycorrhizal function at the spruce root-soil interface. **Petr Baldrian**

10:45 - 11:00 **ID 64** - Field transcriptomics: learning from gene-coexpression networks towards optimization and prediction of mycorrhizal functioning in the field. **Tatsuhiro Ezawa**, Yusaku Sugimura, Ai Kawahara, Hayato Maruyama

11:00 - 11:15 **ID 307** - Newest molecular methods for identification and quantification of fungi. **Leho Tedersoo**

11:15 - 11:30 **ID 30** - Using high-throughput shoot phenotyping to explore plant responses to arbuscular mycorrhizal fungi and nutrient availability over time. **Stephanie Watts-Williams**, Nathaniel Jewell, Binh Tran, Chris Brien, Bettina Berger, Trevor Garnett, Timothy Cavagnaro

11:30 - 11:40 **ID 35** - A method to quantify the contribution of arbuscular mycorrhizal fungi to plant phosphorus nutrition in situ in the field. **Feiyan Jiang**, Gu Feng

11:40 - 11:50 **ID 216** - Plants linked by a common arbuscular mycorrhizal fungal hyphal network: Zinc transfer and plant and fungal gene expression. **Alessio Cardini**, Elisa Pellegrino, A. Gamper Hannes, Maryline Calonne-Salmon, Stephan Declerck, Laura Ercoli

11:50 - 12:00 **ID 41** - Pyroloid *in vitro* germination. A novel method allowing to study these mixotrophic plants. **Tomáš Figura**, Edita Tylová, Jan Šoch, Marc-André Selosse, Jan Ponert

12:00 - 12:10 **ID 108** - PacBio genome sequencing decompress genomes and shows that genomes of ectomycorrhizal mushrooms are larger than we think. **Rodolfo Ángeles Argáiz**, Luis Lozano Aguirre Beltrán, Christian Armando Quintero Corrales, Roberto Garibay Orijel

12:10 - 12:20 **ID 79** - Cultural characteristics of ectomycorrhizal fungi. **Yeongseon Jang**, Rhim Ryoo, Sung-Min Jeon, Eun-Jin Wang, Kang-Hyeon Ka

Oral Session 14 "Models for mycorrhizal research and research for the future"

International Conference Center, room 26B, 10:30-12:30
Chairs: Jim Bever and Ignacio Querejeta

10:30 - 10:45 **ID 133** - Implications of intraspecific variation in ectomycorrhizal fungal communities for host plant response to climate change. **Catherine Gehring**, Adair Patterson, Amy Whipple, Lluvia Flores-Renteria, Thomas Whitham, Sanna Sevanto, Cheryl Kuske

10:45 - 11:00 **ID 177** - Models of mycorrhizae: from stability of the mycorrhizal mutualism to predictions of resource uptake across the landscape. **James D. Bever**

11:00 - 11:15 **ID 39** - An emerging model of an invasive species: Populations of the death cap *Amanita phalloides* are highly sexual but dispersal limited. **Anne Pringle**, Jacob Golan, Catharine Adams, Hugh Cross, Holly Elmore, Monique Gardes, Susana Gonçalves, Jaqueline Hesse, Franck Richard, Yen-Wen Wang, Benjamin Wolfe

11:15 - 11:30 **ID 172** - Genomics and evolutionary relationships of non-model arbuscular mycorrhizal fungi. **Mercè Montoliu Nerin**, Marisol Sánchez-García, Anna Rosling

11:30 - 11:40 **ID 36** - Hurricane disturbance affects the structure of rhizosphere fungal communities and mycorrhizal network in a Neotropical forest. **Julieta Álvarez-Manjarrez**, Mohammad Bahram, Sergei Polme, Roberto Garibay-Orijel

11:40 - 11:50 **ID 78** - Ecosystem consequences of shifts in arbuscular and ectomycorrhizas of a dual-colonized common tree species. **Justine Karst**, James Franklin, Andrea Simeon, Ashley Light, Nadir Erbilgin, Jon Bennett

11:50 - 12:00 **ID 169** - Root demographics: How root stage distributions alter plant growth. **Tyler Poppenwimer**, Lou Gross, Joe Bailey, Megan Rúa

12:00 - 12:10 **ID 18** - Identifying the variables that limit predictability in AM fungal-plant-herbivore interactions. **Alison Bennett**

12:10 - 12:20 **ID 284** - Rapid changes of ectomycorrhizal fungal communities under global warming: implications from *Pinus pumila* forests on nine mountains. **Takahiko Koizumi**, Kazuhide Nara

DETAILED PROGRAM POSTER SESSIONS

Monday July 1, 2019

International Conference Center, Foyer, 12:30-13:30

Posters to be presented on Monday 1 or Tuesday 2 must be displayed both days.

Board 1 **ID 7** Mucoromycotina fine root endophyte fungi form nutritional mutualisms with vascular plants. **Grace Anna Hoysted**, Alison S. Jacob, Jill Kowal, Philip Geisemann, I. Martin, G. Duckett Jeffrey, Gerhard Gebauer, William R. Rimington, Sebastian Schornack, Silvia Pressel, Katie J. Field

Board 2 **ID 208** Fern gametophytes of *Angiopteris lygodiifolia* and *Osmunda japonica* harbor diverse Mucoromycotina fungi. **Yuki Ogura-Tsujita**, Kohei Yamamoto, Yumiko Hirayama, Atsushi Ebihara, Nana Morita, Ryoko Imaichi

Board 3 **ID 147** An endophytic fungi from *Rododendron* sp. is able to form ericoid mycorrhiza in *Vaccinium* sp. roots *in vitro*. **Isaac Alejandro Salmerón-Santiago**, Angélica Cisneros-Zambrano, Martha Elena Pedraza-Santos, Ma. del Carmen Rocha-Granados, Ana Tztzqui Chávez-Bárcenas

Board 4 **ID 220** Fatty acids promote energy production of arbuscular mycorrhizal fungi under asymbiotic conditions. **Rei Akiyama**, Yuta Sugiura, Katsuharu Saito

Board 5 **ID 226** Acid phosphatase activity released from extraradical hyphae of arbuscular mycorrhizal fungi and fractions of phosphorus in soil. **Suzuki Yaya**, Takumi Sato, Tatsuhiro Ezawa, Soh Sugihara, Weiguo Cheng, Keitaro Tawaraya

Board 6 **ID 242** Gene co-expression analysis and modeling reveal distinct gene regulatory networks for phosphate acquisition in mycorrhizal plants. **Hayato Maruyama**, Yusaku Sugimura, Ayumi Tezuka, Atushi J. Nagano, Tatsuhiro Ezawa

Board 7 **ID 243** Iron reduction as a potential mechanism to improve phosphorus nutrition by EMF. **Juan Pablo Almeida**, Michele D'Amico, Luisella Celi, Sonia Barbieri, Fabio Castelli, Elena Segura, Giulia Sineo, Maria Martin, Eleonora Bonifacio, Anders Tunlid, Per Persson, Tomas Johansson, Håakan Wallander

Board 8 **ID 306** Systemin modulates defense responses in roots of tomato plants (*Solanum lycopersicum*) during the pre-colonization stage of the mycorrhizal symbiosis. **Blanca de la Noval**, Norma Martínez-Gallard, John P. Délano-Frier

Board 9 **ID 159** *Funneliformis mosseae* alters soil fungal community dynamics and composition during litter decomposition. **Heng Gui**, Witoon Purahong, Tesfaye Wubet, Kevin D. Hyde, Jianchu Xu, Peter E. Mortimer

Board 10 **ID 194** Reconstructing food webs involved in utilization of organic N by arbuscular mycorrhizal fungi. **Martin Rozmoš**, Petra Bukovská, David Püschel, Kateřina Gančarčíková,JanJansa

Board 11 **ID 202** Effect of native arbuscular mycorrhizal fungi on the initial growth of chili pepper *Capsicum* spp. and its potential to reduce the reproduction of *Meloidogyne incognita*. **Elizabeth Herrera Parra**, José Alberto Ramos Zapata, Víctor Parra Tabla, Laura Hernández Cuevas, Jairo Cristóbal Alejo

Board 12 **ID 228** Hyphosphere characterized by bacterial and fungal communities of *Gigaspora margarita* and *Rosellinia necatrix* from soil and host rhizosphere. **Nguyen Thi Thanh Huong**, Chie Katsuyama, Hitoshi Nakamura, Yukari Kuga

Board 13 **ID 251** Arbuscular mycorrhizal fungi compete with ammonia oxidising archaea and reduce nitrification in agriculture soil. Sophie Ravelli, W. Nicol Graeme, **Christina Hazard**

Board 14 **ID 69** Mycorrhizal fungi and zinc nutrition in pecan trees. **Socorro Héctor Tarango Rivero**

Board 15 **ID 70** Dynamics of phosphorus absorption in chile habanero (*Capsicum chinense* Jacq.) assisted with *Rizhophagus intraradices* in partially autotrophic culture *in vitro*. **Carlos Juan Alvarado López**

Board 16 **ID 100** Arbuscular mycorrhizal symbiosis: A new generation technology for sustainable agriculture. **Neera Garg**

Board 17 **ID 109** Ectomycorrhizal exoenzymatic activity is tightly coupled with host foliar nutrition. **Justin Meeds**, J. Marty Kranabetter, D. Melanie Jones

Board 18 **ID 134** Hyphosphere functional microbiome assemblage is affected by phosphorus forms. **Fei Wang**, Michael Kertesz, Gu Feng

Board 19 **ID 139** The phosphorus in the arbuscular mycorrhizal association and the growth of *Acaena elongata* L., in a temperate forest of Mexico City, Mexico. **Yasmin Vázquez Santos**, S. Castillo-Argüero, J. Álvarez-Sánchez, S.L. Camargo-Ricalde

Board 20 **ID 144** *Fusarium* spp. promotes the symbiotic germination of *Dendrobium wangliangii*. **Dake Zhao**, Wang Qiuxa, Shao Scheng, Shen Yong, Chen Suiyun

Board 21 **ID 188** Response of three cover crops to phosphate-solubilizing fungi and arbuscular mycorrhizal fungi inoculation. **Legnara Padrón Rodríguez**, Dora Trejo A., Rosa María Arias M., Rosario Medel O., Wendy Sangabriel, Yadeneyro de la Cruz E.

Board 22 **ID 193** Exploitation of different organic nitrogen sources in soil by the AM fungal networks. **Petra Bukovská**, Martin Rozmoš, Hana Hršelová, Jan Jansa

Board 23 **ID 195** Investigation of plant interactions across common mycorrhizal networks using rotated cores. **Joanna Weremijewicz**, David P. Janos

Board 24 **ID 205** Period of colonization of endomycorrhizas in tomato plants under greenhouse. Melchor Roa Huerta, **Griselda Madrid Delgado**

Board 25 **ID 206** Effect of radicular exudate on mycorrhizal infection. **Esmeralda Hidalgo Aguilar**, Melchor Roa Huerta

Board 26 **ID 211** First insights into stable isotope signatures of arbuscular mycorrhizal fungi. **Saskia Klink**, Philipp Giesemann, Timo Hubmann, Johanna Pausch

Board 27 **ID 218** Mycorrhizal colonization, growth and foliar concentration of nutrients in seedlings of pecan *Carya illinoensis* (Wang.) K. Koch and pistachio *Pistacia atlantica* Desf. inoculated with ecto- and endomycorrhizal fungi. **Socorro Héctor Tarango Rivero**

Board 28 **ID 225** Species difference of acid phosphatase activity in hyphal exudates of arbuscular mycorrhizal fungi. **Luthfiana Nuri**, Takumi Sato, Yaya Suzuki, Fikri Maulana Ahdiar, Tatsuhiro Ezawa, Weiguo Cheng, Keitaro Tawaraya

Board 29 **ID 236** Two arbuscular mycorrhizal plant species with different morphotypes (*Arum maculatum*, *Paris quadrifolia*) are distinguished in their stable isotope natural abundance. **Philipp Giesemann**, Hanne N. Rasmussen, Heiko T. Liebel, Gerhard Gebauer

Board 30 **ID 241** Phosphorus forms affect arbuscular mycorrhiza root colonization characteristics. **Michael Sakha**, Joseph P. Gweyi-Onyango, Joyce Jefwa

Board 31 **ID 248** Carbon to phosphorus exchange rate in relation to host-preference in AM fungi. **Fahad Alazzawi Zaenab**, Anna Rosling, Shadi E. Sahraeia

Board 32 **ID 265** Root colonization with arbuscular mycorrhizal fungi and supplementary P fertilization improve nutrient status, growth and physiological performance of *Anthurium pedato-radiatum* Schott. Araceae. **Andrés Adolfo Estrada-Luna**, Aurora Genoveva Palafox Arroyo, Victor Olalde-Portugal, Martha Elena Pedraza Santos, Feliza Ramón Farías, César Daniel Estrada-De La Rosa.

Board 34 **ID 298** Microbial dynamics and functionality influenced by phytate of soybean plants. **Bulbul Ahmed**, Zakaria Lahrach, Mohamed Hijri

Board 35 **ID 304** A semi-hydroponic cultivation system associating *Anchusa officinalis* with arbuscular mycorrhizal fungi for optimal production of plant secondary metabolites. **Annalisa Cartabia**, Ismahen Lalaymia, Maria Miguel, Evangelia Tsiokanou, Aikaterini Termentzi, Kyriaki Machera, Nikolas Fokialakis, Stéphane Declerck

Tuesday July 2, 2019

International Conference Center, Foyer, 12:30-13:30

Posters to be presented on Monday 1 or Tuesday 2 must be displayed both days.

Board 38 **ID 61** DSE colonization alleviated Cd toxicity of maize by remodeling host cell wall and Cd subcellular distribution pattern. **Tao Li**, Mi Shen, Zhiwei Zhao

Board 39 **ID 67** Do microbes support plant growth on natural bituminous soils? **James Franklin**, Pedro M. Antunes, Justine Karst

Board 40 **ID 221** Ectomycorrhizal community composition in Submediterranean oak secondary forest under changing environmental conditions. **Natasa Sibanc**, Tanja Mark, Ines Štraus, Jožica Gričar, Kraigher Hojka

Board 41 **ID 227** Microbial communities in potentially toxic metal contaminated soil before and after remediation. **Irena Maček**, Nataša Šibanc, Sara Pintarič, Domen Leštan, J. Alex Dumbrell, Marjetka Suhadolc

Board 42 **ID 229** Effect of inoculation with arbuscular mycorrhizal fungi and plant growth promoting bacteria on growth and development of *Theobroma cacao* L. affected by cadmium. **Bernabé Luis-Alaya**, Jesús Lirio-Paredes, Rocío Calsina, Wilson Castañeda, Katty Ogata-Gutiérrez, Marcia Toro, Esperanza Martínez, Doris Zúñiga

Board 43 **ID 230** The influence of wheat microbiomes on drought stress. **José Pineda De La O**, Thorunn Helgason, Andrea Harper

Board 44 **ID 239** Soil ectomycorrhizal fungal communities under chronic N deposition. **Lidia Trocha**

Board 45 **ID 259** Optimizing arbuscular mycorrhizal use in agriculture to reduce heavy metal uptake in crops. **Danielle Stevenson**

Board 46 **ID 260** Effect of inoculation with arbuscular mycorrhizae on the survival of *Araucaria araucana* subjected to drought. **Daniel Chávez**, Gustavo Rivas, Pablo Cornejo

Board 47 **ID 274** Disturbance and stability act as selection pressure for arbuscular mycorrhizal fungi in a volcanic ecosystem. **Atunnisa Rifa**, Tatsuhiro Ezawa

Board 48 **ID 315** Arbuscular mycorrhizal fungi (AMF) retain the photosynthesis efficiency and improve rice growth under drought stress. **Anupol Chareesri**, Thomas W. Kuyper, Gerlinde B. De Deyn

Board 50 **ID 33** Unipartite and bipartite mycorrhizal networks associated to *Abies religiosa*: understanding community structure to select facilitator plants and fungal links. **Andrés Argüelles-Moyao**, Roberto Garibay-Orijel, Mariana Benítez, Ana Escalante

Board 51 **ID 92** Do ectomycorrhizal fungi compensate for decreasing fine root area in old forests? **Josh Wasilyw**, Justine Karst

Board 52 **ID 141** Endo- and ectomycorrhizal fungi in an Amazonian rain forest soil of Colombia. Clara P. Peña-Venegas, **Aida M. Vasco-Palacios**

Board 53 **ID 152** Coninoculation of *Pinus greggii* Engelm. with arbuscular and ectomycorrhizal fungi. **Alicia Franco-Ramírez**, Jesús Pérez-Moreno, Gabriela Sánchez-Viveros, Carlos Roberto Cerdán-Cabrera, Víctor Manuel Cetina-Alcalá, Juan José Almaráz-Suárez, Magdalena Martínez-Reyes

Board 54 **ID 187** Shift on the arbuscular mycorrhizal communities with changes of land use. **Diana Carolina Londoño Gómez**, Martina Janouskova, Walter Osorio

Board 55 **ID 190** Arbuscular mycorrhizal diversity in soil, root and rhizosphere for coffee and its native forest relatives in Monteverde, Costa Rica. **Laura Aldrich-Wolfe**, Elizabeth Sternhagen, Stefanie Vink

Board 56 **ID 196** Response of pine root-associated fungi to the impact of nesting great cormorant colony. **Jurga Motiejunaite**, Reda Irsenaite, Audrius Kacergius, Jonas Kasparavicius, Ricardas Taraskevicius

Board 57 **ID 207** First identification assessment of macrofungi at pecan [*Carya illinoinensis* (Wangenh.) K. Koch] orchards in La Comarca Lagunera. **Judith Abigail Sánchez Ledesma**

Board 58 **ID 209** Arbuscular mycorrhizal communities at different root orders collected at Japanese cedar forests in the central Japan. **Yosuke Matsuda**, Kohei Kita, Yudai Kitagami, Toko Tanikawa

Board 59 **ID 212** Mycorrhizal mediation of invasive species soil legacy in a changing climate- **Julia Hull**, Catherine Gehring

Board 60 **ID 219** The response of native and invasive shrubs to a diverse soil fungal inoculum. **Louis Lamit**, Alex Ebert, Fang Bao, Douglas A. Frank, Jason D. Fridley

Board 61 **ID 234** Plant root-fungal interactions in a neotropical freshwater wetland. Jazmín Santillán-Manjarrez, A. Penélope Solís-Hernández, Patricia Castilla-Hernández, Ignacio E.

Maldonado-Mendoza, Gilberto Vela-Correa, Aurora Chimal-Hernández, Diederik van Tuinen, **Facundo Rivera-Becerril**

Board 62 **ID 240** Root mycobiome of different truffle producing forest in Serbian lowlands. Zaklina Marjanovic, **Ali Nawaz**, Tesfaye Wubet

Board 63 **ID 252** Initial tissue carbon fractions predict sporocarp necromass decomposition in mycorrhizal and saprotrophic fungi. **Craig See R**, Peter G. Kennedy

Board 64 **ID 253** Tree neighbor diversity and mycorrhizal trait affect the rhizosphere microbiome assemblages of tree species pairs. **Bala V.V.A. Singavarapu**, Ali Nawaz, Helge Bruelheide, Tesfaye Wubet

Board 65 **ID 256** Small scale spatial distribution of orchid mycorrhizal fungi in a tropical tree canopy. **Kel Cook**, Christoffer Harder, Jyotsna Sharma, Andrew Taylor, Lee Taylor

Board 66 **ID 263** Mycorrhizas and host tree mortality in the piñón-*Juniper* woodland. **Jessie Marlenee**, D. Lee Taylor, Marcy Litvak, William Pockman

Board 67 **ID 267** Functionality of arbuscular mycorrhizal fungi in the dry tropic: A landscape analysis. **Irene Sánchez-Gallen**, Karla E. Cortés-Tello, Eduardo León-Betancourt, J. Álvarez-Sánchez, J. Ramos-Zapata.

Board 68 **ID 280** Mediterranean woody plant species influence the phylogenetic structure of arbuscular mycorrhizal fungal communities. A. López-García, C. V. Ozuna, J. Prieto, J. M. Alcántara, J. L. Garrido, A. M. Rincón, **C. Azcón-Aguilar**

Thursday July 4, 2019

International Conference Center, Foyer, 12:30-13:30

Posters to be presented on Thursday 4 or Friday 5 must be displayed both days.

Board 1 **ID 9** The succession of arbuscular mycorrhizal community in the wheat cropping system. **Weige Huo**

Board 2 **ID 153** Effect of fairy ring bacteria on the growth of *Tricholoma matsutake in vitro* culture. **Young Woon Lim**, Ki Hyeong Park, Young Woon Lim

Board 3 **ID 197** A leafless epiphytic orchid, *Taeniophyllum glandulosum* Blume (Orchidaceae), is specifically associated with the Ceratobasidiaceae family of basidiomycetous fungi. **Kento Rammitsu**, Yumi Yamashita, Tomohisa Yukawa, Yuki Ogura-Tsujita

Board 4 **ID 222** Mycorrhizal symbiosis in plants of two temperate forest of Mexico. **Rosalva García Sánchez**, Eduardo Chimal Sánchez, Cecilia Gabriela Chávez Hernández, Claudia Janette de la Rosa Mera

Board 5 **ID 232** *Septoglomus mexicanum*, a new species of arbuscular mycorrhizal fungi (Glomeromycota) from semiarid regions in Mexico. Eduardo Chimal-Sánchez, Carolina Senés-Guerrero, **Lucía Varela**, Noé Manuel Montaño, Rosalva García-Sánchez, Adriana Pacheco, Susana Montaño-Arias, Sara Lucía Camargo-Ricalde

Board 6 **ID 233** Diversity of arbuscular mycorrhizal fungi in agricultural systems in acidic andisols. Yoselin Cerda, **Paula Aguilera**

Board 7 **ID 254** Relationship between 18S rRNA gene polymorphisms and endobacterial communities in a strain of *Gigaspora margarita*. **Chie Katsuyama**, Nguyen Thi Thanh Huong, Ryo Ohtomo, Yukari Kuga

Board 8 **ID 261** Checklist of the Glomeromycota in the Tehuacán-Cuicatlán Valley, Puebla Oaxaca, Mexico. **Sara Lucía Camargo-Ricalde**, Noé Manuel Montaño, Eduardo Chimal-Sánchez, Lucía Varela, Susana Montaño-Arias, Claudia Barbosa-Martínez, Blanca Larissa Salazar-Ortuño

Board 9 **ID 271** Phylogenetic diversity of the species of the Phalloideae section of the genus *Amanita* in the states with the highest incidence of fatal mycetisms in Mexico. **Amaranta Ramirez Terrazo**, Roberto Garibay Orijel

Board 10 **ID 275** Spatial and seasonal variation of ectomycorrhizae and sporocarps in mixed conifer/hardwood forests of southwest Oregon. **Daniel l. Luoma**, Joyce L. Eberhart, Michael P. Amaranthus

Board 11 **ID 278** Richness and diversity in aquatic environments: New records of arbuscular mycorrhizal fungi in Brazil. **Juliana Aparecida Souza Leroy**, Mariana Bessa de Queiroz, Stephania Ruth Silva Gomes, Bruno Tomio Goto

Board 12 **ID 281** Molecular diversity of arbuscular mycorrhizal fungi community associated with *Cocos nucifera* in southeastern Mexico. **Luis Alberto Lara-Pérez**, Iván Oros-Ortega, Othón P. Blanco, Ismael Pat Aké

Board 13 **ID 292** Richness and abundance of arbuscular mycorrhizal fungi from rhizosphere soils of mono-cropped maize. **Ma. Blanca Nieves Lara Chávez**, Lucia Varela Fregoso, Patricio Apáez Barrios, Eduardo Chimal Sánchez, Yurixhi Atenea Raya Montaño, Margarita Vargas Sandoval, Salvador Aguirre Paleo, Noe Manuel Montaño Arias

Board 14 **ID 293** Morphological and molecular characterization of ectomycorrhizae of *Phylloporus* (Boletales) and tropical *Quercus* species in Eastern Mexico. **Leticia Montoya**, David Ramos Antero, Victor M. Bandala

Board 15 **ID 305** Truffles diversity in alpine regions. **Tine Grebenc**, Jie Wei, Tina Unuk, Marcelo Sulzbacher, Sana Jabeen, Nasir Khalid Abdul, Mitko Karadelev

Board 16 **ID 310** Do native and invasive *Conyza canadensis* interact differently with AM fungi? **Min Sheng**, Christoph Rosche, Ylva Lekberg

Board 17 **ID 289** Effect of P fertilization level on arbuscular mycorrhizal communities and maize growth under a tilled and no-tilled system. **Yuya Tatewaki**, Masao Higo, Yoshihiro Kawamura, Koya Nakamura, Katsunori Isobe

Board 18 **ID 283** Impact of different cover cropping on the arbuscular mycorrhizal fungal communities colonizing maize roots. **Masao Higo**, Yuya Tatewaki, Koya Nakamura, Yoshihiro Kawamura, Katsunori Isobe.

Board 19 **ID 160** Non-target effects of pesticides on maize growth and mycorrhiza formation in different fertilization settings. **María Semiramis Gutiérrez Núñez**, Felipe García-Oliva, Alejandro Alarcón, John Larsen

Board 20 **ID 290** Effect of arbuscular mycorrhiza on the interaction of invasive and native European plants. **Tereza Konvalinková**, Veronika Řezáčová

Friday July 5, 2019

International Conference Center, Foyer, 12:30-13:30

Posters to be presented on Thursday 4 or Friday 5 must be displayed both days.

Board 21 **ID 122** The relationship between aboveground diversity and AMF on agroecosystems. **Aidee Guzmán**, Anne Kakouridis, Mary Firestone, Timothy Bowles, Claire Kremen

Board 22 **ID 199** Arbuscular mycorrhizal fungal diversity response to fertilizer and crop rotation in wheat rhizospheres over multiple years. **Yolanda Plowman**, Michael Kertesz, Feike Dijkstra, Paola Corneo, Chris Baldock

Board 23 **ID 224** Microbiome transplants: a dirt simple method to enable urban forestry. **Natalia Vargas Estipuñan**, Nora Duncritts, John Zuber, Anne Pringle

Board 24 **ID 231** Host identity rather than soil heterogeneity is the key determinant of the early ectomycorrhizal fungal community assembly for exotic and native pine seedlings. **Chen Ning**, Gregory Mueller

Board 25 **ID 270** Mycorrhizal colonization and Indole-3-butyric acid on the vegetative propagation of *Stevia rebaudiana*. Sergio David Valerio Anda, Evangelina Esmeralda Quiñones Aguilar, Jhony Navat Enríquez Vara, **Gabriel Rincón Enríquez**, Cecilia Guízar González, Luís Guillermo Hernández Montiel

Board 26 **ID 272** Arbuscular mycorrhizal fungi native from acid soils as growth promoters in hybrid mayze. Alejandro Huerta Ramírez, Jhony Navat Enríquez Vara, Gabriel Rincón Enríquez, Cecilia Guízar González, Philippe Lobit, Nuria Gómez Dorantes, Luis López Pérez, **Evangelina Esmeralda Quiñones Aguilar**

Board 27 **ID 276** Seed coating: a tool for delivering arbuscular mycorrhizal fungi to agricultural crops. **Rui S. Oliveira**, Inês Rocha, Ying Ma, Pablo Souza-Alonso, Aleš Látr, Miroslav Vosátka, Helena Freitas

Board 28 **ID 285** Variation of arbuscular mycorrhizal fungal communities along a chronosequence of *Betula alnoides* stands. **Yuebo Jing**, Zhiwei Zhao, Lingfei Li, Tao Li, Yongpeng Li.

Board 30 **ID 301** Effectiveness of native AMF from a Cuban agroecosystem vs. exogenous AMF on *Zea mays* L. **Yakelin Rodríguez-Yon**, Lianne Arias-Pérez, Kalyanne Fernández-Suárez, Kris Audenaert, Geert Haesaert

Board 32 **ID 51** Identification and *in vitro* selection of root-associated fungi for use in ecological engineering and ecosystem restoration of iron-ore tailings in subarctic tundra of Northern Quebec, Canada. **Léonie Côté**, Damase P. Khasa

Board 33 **ID 238** Moving together with flat-mates: Sympatric arbuscular mycorrhizal fungi after three seasons in allopatric conditions. **Alena Voříšková**, Michael Remke, Matthew A. Bowker, Nancy C. Johnson, Zuzana Kolaříková, Jana Rydlová, Martina Janoušková

Board 34 **ID 245** Revegetation technique changes root mycorrhizal communities: The advantage of direct seeding over transplanting tube-stock in riparian ecosystems. **Ana Isabel Bermudez Contreras**, Cristina Aponte, Fiona Ede, Vicky Waymouth, Rebecca Miller

Board 36 **ID 14** Arbuscular mycorrhizal fungi serve as keystone taxa for revegetation on Qinghai-Tibetan Plateau. **Huyuan Feng**, Shi Guoxi, Zhang Qi, Meng Yiming, Liu Yongjun, Pan Jianbin, Jiang Shengjing, Zhou Guoying

Board 37 **ID 175** Plant specific arbuscular mycorrhizal fungal species communities of important agricultural crops (pequin pepper, soybean and orange) in the northeast Mexico. **Carolina Senés-Guerrero**, Adriana Pacheco, Arthur Schüßler (Schüssler)

Board 38 **ID 215** Tight and flexible regulation of mycorrhizal formation and functioning through a gene-coexpression network module in diverse and fluctuating environments. **Yusaku Sugimura**, Ai Kawahara, Hayato Maruyama, Tatsuhiro Ezawa

Board 39 **ID 250** Concept of mycorrhizal potential applied to inoculants. C. Plenchette, **C. Hecker**

Board 40 **ID 266** Evaluation of the performance of MALDI-TOF-MS biotyping to identify Gigasporaceae. Thomas Crossay, **Franck Stefani**, Claudia Banchini, Sylvie Séguin, Dirk Redecker, Hamid Amir

Board 41 **ID 282** Simple and convenient observation methods of mycorrhizal fungi by a newly developed portable fluorescence microscope using mycorrhizal fungus-detection fluorescence reagent. **Takaaki Ishii**

Board 42 **ID 296** Web interface of arbuscular mycorrhizal fungal and bacterial classification pipeline. **Hideki Hirakawa**, Niwa Rieko, Shusei Sato, Tatsuhiro Ezawa

Board 43 **ID 258** Analysis of mycorrhizal associations of the invasive plant Brazilian pepper tree (*Schinus terebinthifolius*) in South Florida. **Karim Dawkins**, Nwadiuto Esiobu

REGISTRATION

Registration Booth and Conference Office

The Registration Booth is located at the foyer taking the stairs or the elevator to the first floor of the conference center. The Speakers' Ready room for any other matters than registration is located in Room 13 (see ICC map).

Registration Desk Opening Hours

The registration Desk will be open as follows:

Sunday, June 30 2019	15:30-18:30
Monday, July 1 2019	8:30-18:30
Tuesday, July 2 2019	8:30-18:30
Thursday, July 4 2019	8:30-18:30
Friday, July 5 2019	8:30-15:30

ABSTRACTS BOOK

The Abstracts Book is available in the ICOM10 website at:
http://www.icom10.org/index.php/abstracts

CERTIFICATE

Certificates of Attendance will be sent by e-mail to corresponding authors. Printed certificates can be requested at the Registration Booth from Tuesday, July 2.

SPEAKERS' READY ROOM AND CONFERENCE OFFICE

Please come to the Speakers' Ready Room (Mezzanine, room 13) to deliver and check your presentation at least 24 hours before the beginning of your session. Speakers presenting on Monday, July 1 are encouraged to send their presentations by email to icom10@ciencias.unam.mx before the conference starts.

Name your file as the following example: **S1_ID123_1030.pptx**
Were:
S= number of your session
ID= code of your work
1030= Time when your talk is scheduled

IMPORTANT: we will not receive presentations when the session has started.
15-minutes oral presentations include 3 minutes for questions; 10-minutes oral presentations include 2 minutes for questions. **Please respect the time allowed for questions from the audience**

Acceptable formats
MS Windows: Microsoft PowerPoint 2016 or earlier, Acrobat PDF X
Macintosh: Microsoft PowerPoint 16.25 or earlier, Acrobat PDF X
Macintosh users: When choosing fonts for your presentation, notice that the first item on the Font menu is Font Collections. In the Font Collections, please use the fonts you find on the Windows Office Compatible sub-menu and you'll have no trouble with PowerPoint 2016 for Windows.

Opening hours of the Speakers' Ready Room (Mezzanine, room 13)

Sunday, June 30	16:00-18:30
Monday, July 1	10:00-13:30; 16:00-19:00
Tuesday, July 2	10:00-13:30; 16:00-19:00
Thursday, July 4	10:00-13:30; 16:00-19:00
Friday, July 5	10:00-13:30

NAME BADGE

Delegates will receive a name badge and set of tickets for lunches and social events. Please wear this badge for all ICOM activities, including lunches, coffee breaks and social events. There will be a 500 Mexican pesos charge for replacement of lost badges.

Participant	Green
Accompanying Person	White
Local Organizing Committee	Pink
Exhibitor	Black

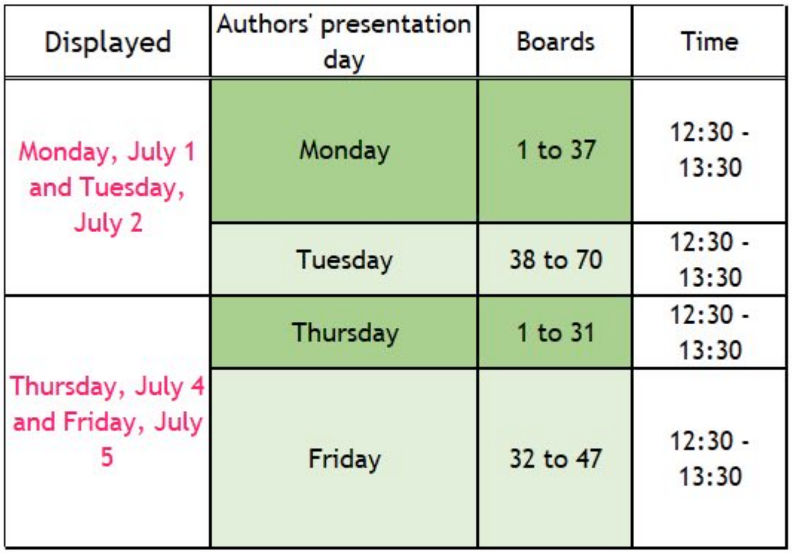
POSTER PRESENTATION AND EXHIBITION

Posters must be prepared in a standard portrait format. Allowed size: 90 cm width x 120 cm height. The typeface will be of at least 70 points size for the title and 30 points for main text, tables and figures. Fonts selected should have a clear appearance and be readable at 1 m distance. The organizers will provide materials to set up your poster.

The poster exhibition area will be located at the foyer of the conference floor (Level 1, ICC).

Attended Poster Sessions (Foyer)

According to the following table, the posters presenting on Monday and Tuesday will be displayed continuously both days, posters presenting on Thursday and Friday will be displayed continuously both days. Poster presenting authors will receive instructions indicating the day and hour when they should be by their posters, as their official time to present their work and interact with the audience.



Displayed	Authors' presentation day	Boards	Time
Monday, July 1 and Tuesday, July 2	Monday	1 to 37	12:30 - 13:30
	Tuesday	38 to 70	12:30 - 13:30
Thursday, July 4 and Friday, July 5	Thursday	1 to 31	12:30 - 13:30
	Friday	32 to 47	12:30 - 13:30

SOCIAL EVENTS

Welcome mixer

Date: Sunday, June 30 2019

Time: 18:30-20:30 after the lecture of the special guest speaker. It is included in the registration fee.

Location: terrace International Convention Center

Yucatan food and drinks will be served, and a classic Yucatan live music will accompany the evening.

Wines of the world

It will take place on Tuesday, July 2, from 20:00 to 23:00 at the Terrace of the Fiesta Americana Hotel.

This is a tradition in ICOM, please bring your bottle of wine or any other good beverage from your country you would like to share with us and participate in the competition. We have had great experiences tasting amazing beverages from all over the world.

We will have a traditional Yucatan Ballet (Filigrana de Oro Ballet; Prof. Rosa Ake Anguas).

Cost: $700.00 MXN per person

Tickets can be purchased at the Registration Booth until July 1, 12:00 am.

Conference Dinner

The place for the conference dinner is a huge, beautiful garden in an old hacienda in Mérida where we will have lots of space to eat, talk and dance. The buffet dinner will be followed by international music (perhaps a little biased to latin music). The place is so big that there will be room for partying people and quieter corners on the grass for non-dancers and talkers. Do not miss it!!!

It will take place on Thursday July 4, from 20:00 to Friday 5 at 1:00 at the Hacienda Chenkú (haciendasenyucatan.com/chenku/)

There will be no bus service. Taxis or Uber services are cheap in Mérida and are good options. If you wish to walk, Hacienda Chenkú is a 25 min walking distance from the Conference Center. Follow Avenida Cupules until you cross Colonias circuit. Continue straight ahead. The street name changes from Avenida Cupules to Calle (Street) 43) first and then to Calle 103. Keep going straight until it becomes Calle 19 and shortly after the Hacienda Chenku is on the right side between Calle 34 and Calle 30.

Cost: $1,200.00 MXN per person

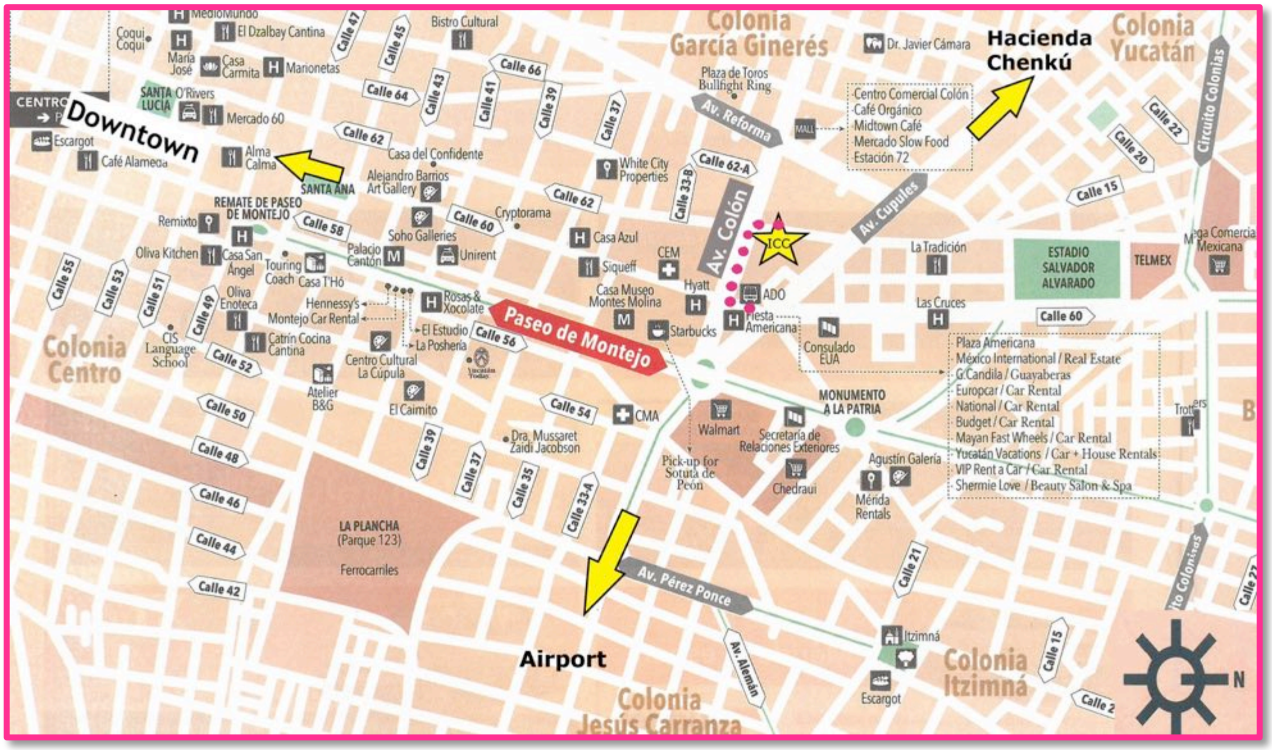
Tickets can be purchased at the Registration Booth until July 1, at 12:00 am.

TRIPS AND EXCURSIONS
Wednesday July 3, 2019

FIELD TRIP	MEETING POINT	DURATION	COST
Celestún, Flamingos & Beach	8:50 am at the Lobby of the Fiesta Americana Hotel	8 Hours	$1,300.00 MXN
Chichén Itzá Be Maya	8:20 am at the Lobby of the Fiesta Americana Hotel	9 Hours	$2,000.00 MXN
Progreso (Beach)	9:50 am at the Lobby of the Fiesta Americana Hotel	6 Hours	$800.00 MXN
Chichen Itza & Cenote Ikkil	8:20 am at the Lobby of the Fiesta Americana Hotel	9 Hours	$1,350.00 MXN
Uxmal & lunch at Lodge	8:50 am at the Lobby of the Fiesta Americana Hotel	7 Hours	$1,500.00 MXN
Hacienda & Cenote Experience	8:50 am at the Lobby of the Fiesta Americana Hotel	7 Hours	$1,400.00 MXN
Plant and fungi coastal communities at Hunucmá-Sisal	8:00 am at the Lobby of the Fiesta Americana Hotel	9 Hours	$1,100.00 MXN
Izamal Magic town of Mexico	9:20 am at the Lobby of the Fiesta Americana Hotel	6.30 Hours	$950.00 MXN

GENERAL INFORMATION

Mérida Conference venue and Hotels map



ICC = International Conference Center

Conference Venue

International Convention Center (ICC), (yucatancenter.com)
Street 62 No. 294, Between Av. Cupules and Av. Colon, Mérida, Yucatan.
Tel. (52) 999 920 1118

Language

The official language of the ICOM10 conference is English. Translation services are not provided.

Public transport

Public transportation rates:
Adults $7.50 MXN, children and students $ 2.50 MXN
Complaints: 01 800 890 91 92, 8:00 - 0:00 hours Monday to Friday, 8:0 - 20:00 hours on Saturdays and Sundays

Taxi services

-Taxi Santa Ana. Opens 24 hs
https://taxissantaanasitio14.com/
Address: Calle 64, 400/A, Centro, Mérida, Yucatan, C.P. 97000, México
Tel.: (999) 928-5600, 924-5918, 928-5316
e-mail: sitio142011@hotmail.com
-Taxi Mérida Airport. Ground transportation: Transfers Airport hotel / Hotel airport, To tourist destinations and archaeological zones (Chichen Itza, Chelem, etc.).
Tel.: (999) 946-15-29 ó (999) 946-23-14
https://taxiaeropuertomerida.com/
-There is also Uber service in Mérida

Currency

The official currency of Mexico is the Peso ($1 USD = approximately $19.60 MXN pesos). International credit cards are accepted for payment in most hotels, restaurants and shops. Exchange offices and ATM machines are easily available throughout the city and at the Mérida and Cancún International Airports. Small restaurants and shops may not have credit card options, participants are advised to withdraw a small amount of cash ($100 USD or $2000 MXN) upon arrival to a Mexican airport to pay in these places and for buses or taxis. US dollars and euros in cash are accepted sometimes but at a very bad exchange rate.

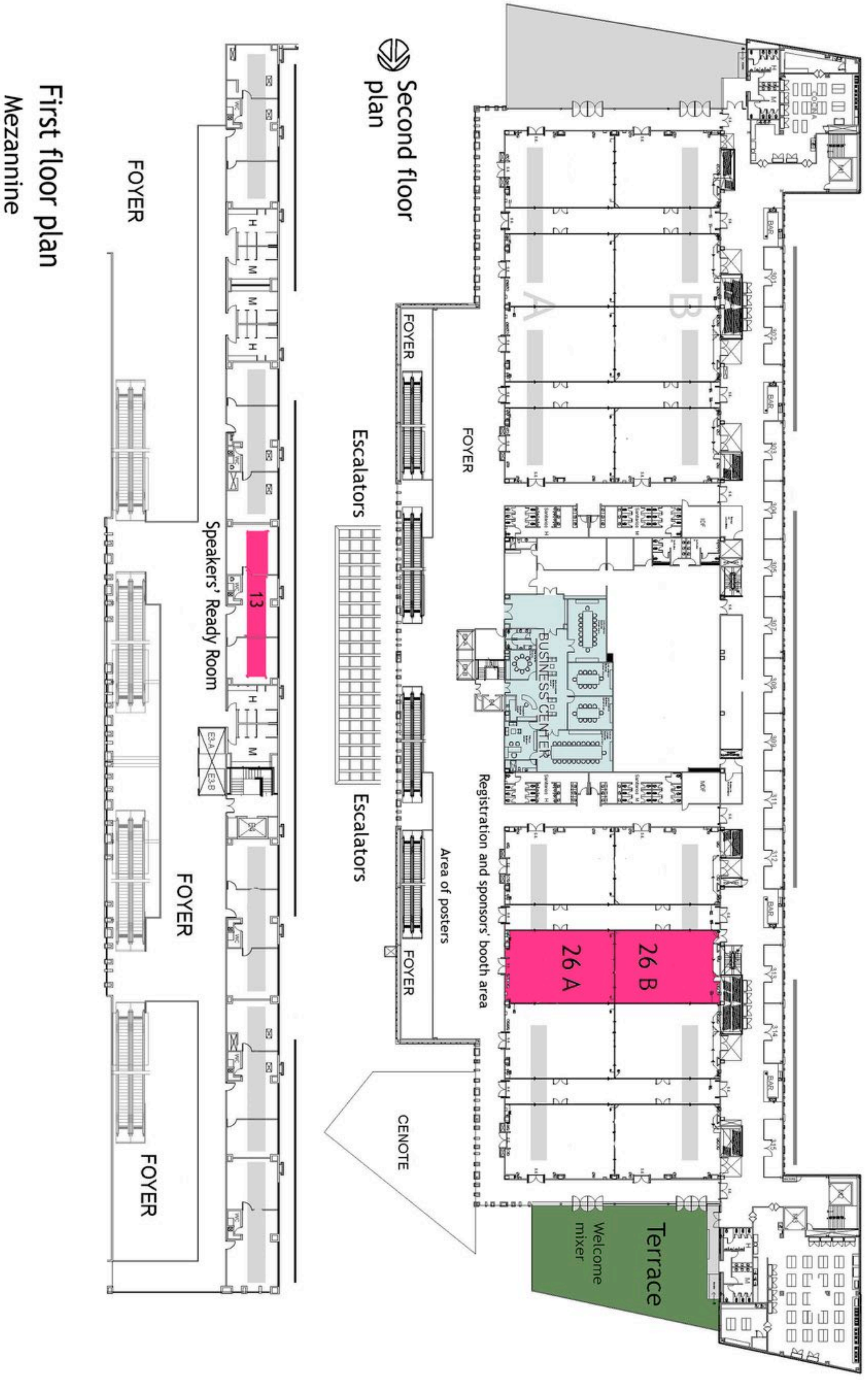
Important Telephone Numbers

911 General Emergency
116 Fire
942-00-60 Mérida Police
114 Red Cross

Insurance

The organizers can accept no liability for personal injuries or for loss or damage to property belonging to the conference participants, either during or as a result of the event. Participants are advised to take out proper care of their belongings and travel and health insurance before departing from their home country.

International Convention Center (ICC) map



INSTRUMENTS
REGENT

Image Analysis Tools for Roots and Seedlings

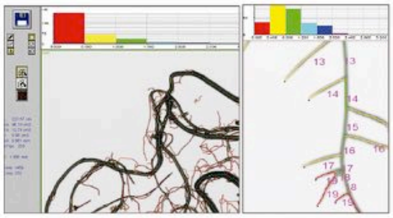
WinRHIZO™ 2019

Basic, Regular & Pro

Automatic Analysis Systems for Washed Roots

Scan washed roots with Regent's scanners and root positioning systems.

See analysis results summarized on screen after scanning.



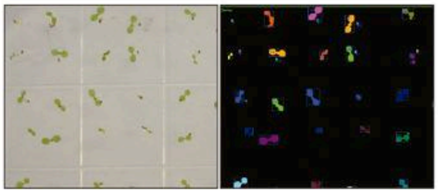
√ Root morphology in function of root diameter and color: length, area, volume and number of tips
√ Number of forks and crossings
√ Root overlap detection for accurate measurement
√ Topology, link and architecture with fractals
√ Developmental classification
*** Available measurements and features vary according to WinRHIZO's version. See our website for details.

Arabidopsis

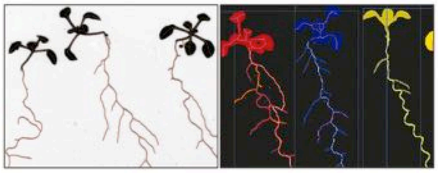
Automatic Analysis System for Washed Roots and Seedlings grown in Petri Dish

Analyse seedlings and leaves:

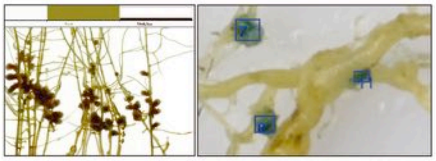
Globally	Individually
one analysis per image	multiple analyses per image



√ Leaf area of seedlings in Petri dish
√ Germination Count



√ Leaf area - leaf/hypocotyl distinction
√ Root morphology
√ Topology and developmental analysis



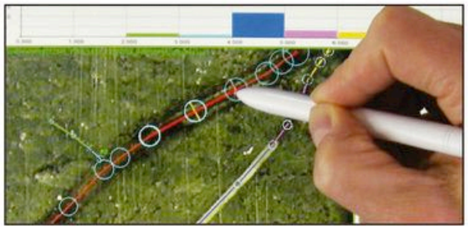
√ Surface area and automatic count of non-touching nodules
*** All measurements and features of the WinRHIZO Pro version are included.

WinRHIZO™ Tron 2019

Tron & Tron MF

Software Programs for Interactive Analysis of Images of Roots in Soil and Rhizotron

Trace roots manually with a mouse or by touching the screen of all-in-one or tablet computers.



Monitor root growth by analysing Multiple Frames (images) of a root system taken at different times.

√ Root morphology in function of root diameter and color: length, area, volume and number of tips
√ Topology and developmental analysis
√ Data retrievable from file names using the ICAP naming scheme
√ Previous analysis can be retrieved to resume analysis of the same location at a later time simply by adding new or dead roots since the last analysis.

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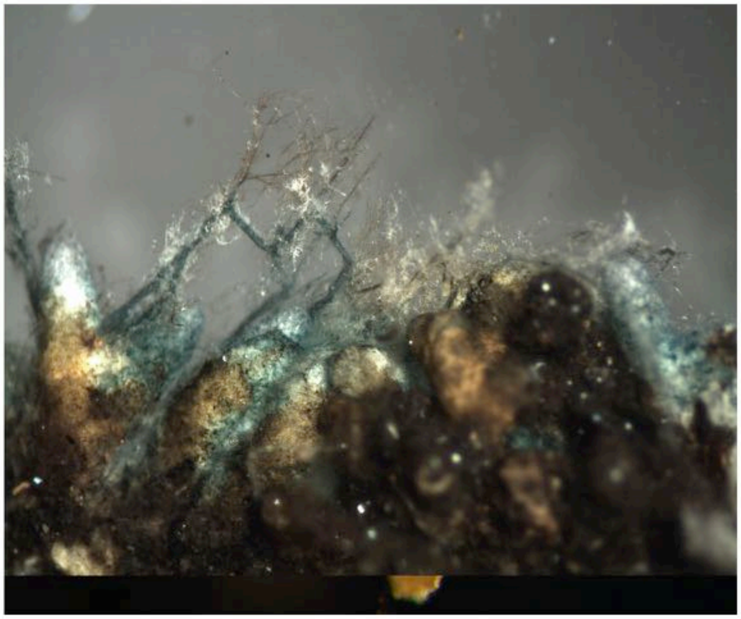
icom10

International Conference on Mycorrhiza
Merida, Mexico 2019.

Mycorrhizae for a Sustainable World



Abstracts Book

Acknowledgements

New Phytologist Trust

IMS

CIENCIAS

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Instituto de Biología UNAM

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CONACYT

INSTRUMENTS REGENT Image Analysis for Plant Science

Casa abierta al tiempo

Universidad Veracruzana

UNIVERSIDAD AVTÓNOMA D TLAXCALA · MCMLXXVI ·

UNIVERSIDAD MICHOACANA DE SAN NICOLÁS DE HIDALGO

WELCOME TO icom10!

We are very pleased to welcome you to the 10th International Conference on Mycorrhiza (ICOM 10) in Mérida, Mexico. We are very happy because it is the first time that this important conference takes place in Mexico.

ICOM 10 wishes to encourage innovation in the researchers, students, companies and organizations that study the mycorrhizal symbiosis in order to generate basic and applied knowledge in a way committed to sustainable development. We hope you will enjoy this week of scientific and social interactions and feel enriched by the presentations and conversations with colleagues and friends from almost 40 countries. We have made our best to provide an excellent scientific program and make you feel at home. We also encourage you to go out and experience the Mayan culture. We are confident that ICOM 10 will be very successful because you are coming to join us.

On behalf of the Local Organizing Committee
Dr. Javier Álvarez-Sánchez (Chair)
Dr. Mayra E. Gavito (Co-Chair)

INTERNATIONAL MYCORRHIZA SOCIETY
WELCOME MESSAGE

Dear Colleagues,

I am very pleased to welcome you to the 10th International Conference on Mycorrhiza in Mérida, Mexico.

Scientists working on mycorrhizal symbioses have known for more than a century that plant-associated microbes, such as mycorrhizal fungi, take center stage in terrestrial ecosystems. A century of research has clarified the nature of what is undoubtedly the commonest and most important symbiosis in terrestrial ecosystems. Simply stated, nearly all families of plants form root symbiotic associations, named mycorrhizas, with soil fungi. The importance of this symbiosis in promoting plant nutrient status and growth is now well established, and mycorrhizas are used worldwide to develop sustainable agriculture and forestry.

Primary research papers in the last few years since ICOM9 in Prague have broken the ground for new lines of research, from regulation of gene expression to the ecological relevance of mycorrhizal symbioses. They have provided detailed insights into the complexity of mycorrhizal fungal communities and populations, offering exciting prospects for elucidation of the processes that structure their communities and biogeography.

There is no doubt that ICOM10 sessions and workshops will be fertile ground for novel hypotheses that will advance our general perspective on plant and fungal ecology and evolution, and will provide new insights on the biological dynamics that mediate the flux of matter and energy in terrestrial ecosystems through mycorrhizal interfaces.

It is hoped that the ICOM10 will stimulate further research and will encourage younger scientists in our community to look to future challenges that lie ahead.

I would like to thank Professor Javier Álvarez Sánchez, the Local Organizing Committee and the International Scientific Committee for putting together very exciting scientific and social programs.

On behalf of the Board of Directors of the International Mycorrhiza Society

Dr. Francis M. Martin
President of the International Mycorrhiza Society

COMMITTEES

Local Organizing Committee

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International Scientific Committee

IMS scientific committee

Francis Martin (general coordinator), Marcel van der Heijden (scientific board coordinator)

Local committee

Mayra E. Gavito (scientific program coordinator), Ignacio Maldonado Mendoza, Roberto Garibay Orijel, Rosalva García Sánchez, Rocío Vega Frutis (session coordinators), Irene Sánchez Gallén, América Baleón-Sepúlveda, Isaac Acevedo Rojas (communication coordinators).

IMS Awards

John Klironomos (IMS awards coordinator)

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Jim Bever
Martin Bidartondo
Jan Colpaert
Tatsu Ezawa
Katie Field
Gu Feng
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www.intermeeting.com.mx
Tel. (52) 55 5661-7905
Nataly Juárez, Claudia García

TABLE OF CONTENTS

OPENING LECTURE

Mycorrhizas and environmental sustainability for development

Julia Carabias

Facultad de Ciencias, Universidad Nacional Autónoma de México/ El Colegio Nacional

Scientific evidence has shown that non-sustainable development processes which humankind has carried out have led the planet to an unprecedented environmental crisis, with significant adverse effects on social well-being. Society has interfered natural systems functions to the point of crossing several planetary boundaries. With the aim of stopping environmental degradation and socioeconomic crisis, countries agreed on the 2030 Agenda and its 17 Sustainable Development Goals (SDGs). Achieving the SDGs will require technological innovation and the use of scientific evidence on public policy design and implementation.

Especially, reaching both Goal 2 'Zero hunger' and Goal 15 'Life on Land' (Protect, restore, and promote sustainable use of terrestrial ecosystems) requires overhauling our currently inadequate food production and forest management systems, as well as our inefficient methods for ecosystem restoration.

Scientific research on mycorrhiza has demonstrated there is great potential for increasing and sustaining agricultural production, improving forest plantations successfully, and increasing efficiency in environmental restoration efforts. However, attention has not been drawn to this already generated and proven knowledge. Therefore, it has not been used on public policy design or implementation. This presentation analyzes the potential and obstacles for including mycorrhiza knowledge on environmental management and policies.

CONFERENCE KEYNOTE LECTURES

The evolution of mycorrhizal genomes and transcriptomes

Annegret Kohler, Eniko Kiss, Emmanuelle Morin, Shingo Miyauchi, Laszlo G Nagy, Igor Grigoriev, Francis Martin, Mycorrhizal Genome Initiative

Institut National de la Recherché Agronomique
annegret.kohler@inra.fr

Mycorrhizal fungi have coevolved with their hosts since the emergence of land plants and the combination of calibrated phylogenies with the growing number of fungal genomes, allows new insights into the evolutionary history of mycorrhizal symbiosis.

The comparison of 112 genomes from mycorrhizal fungi, wood decayers and litter decomposers revealed several independent lifestyle transitions from saprotrophism to mutualism. The general trend within ectomycorrhizal fungi (ECM) is the reduction of genes coding for plant cell wall degrading enzymes. However, ECM species seem to have retained diverse sets of enzymes depending on their ecological niches.

More genomes enable us as well to compare mycorrhizal transcriptomes and to identify symbiosis-induced genes. Do these symbiosis-related transcripts originate from conserved genes or are they species-specific? For *Laccaria bicolor* we could show, by comparison to other fungal genomes, that both conserved and clade-specific genes are used to establish symbiosis with the roots of the host tree *Populus*. Using a phylostratigraphy approach we compared the « symbiosis-toolbox » of 15 mycorrhizal interactions. Again, the age distribution of mycorrhiza-induced genes showed two peaks corresponding to ancestral genes made of conserved gene families and species-specific orphan genes. About 45% of the mycorrhiza-induced genes predate the origin of mycorrhiza, suggesting gene co-option as a major mode of recruiting genes for symbiosis. Conserved mycorrhiza-induced genes showed little overlaps across species, suggesting that independently evolved mycorrhizal lineages have co-opted different genes. Interestingly, induced genes are coding for the same functions but without orthology, like small-secreted proteins, transporters or carbohydrate active enzymes.

Key words: Ectomycorrhiza, evolution, genomics, transcriptomics.

Increased metabolic plasticity underlies enhanced stress resistance in mycorrhizal plants

María J. Pozo, Javier Rivero, Victor Flores, Concepción Azcón-Aguilar

Estación Experimental del Zaidín, CSIC
mjpozo@eez.csic.es

Phenotypic plasticity allows plant adaptation to the ever-changing environment and fuels their ability to cope with stress. Arbuscular mycorrhizas (AM) can improve plant stress tolerance, and we propose that such bioprotection is related to an enhanced phenotypic plasticity.

We have explored the potential of AM fungi (AMF) to protect plants against diverse stresses. Our results illustrate that AM have a strong impact on the root metabolic profile, with a set of AM-overaccumulated metabolites, but also with fungus-specific fingerprints, which may underlie functional diversity among different AMF. Moreover, we found differential reprograming when plants were challenged with different stress conditions (moderate and severe drought and salinity stress or leaf herbivory). Under osmotic stress, the beneficial effects of AM positively correlated with stress intensity. The strongest protection was achieved by a *C. etunicatum* isolated from a high-salinity environment. Untargeted metabolic profiling revealed stress specific changes: Mycorrhizal plants showed primed accumulation of a subset of salt-induced compounds including flavonols and B6 vitamers. Exogenous application of these compounds confirmed their anti-stress properties.

Moreover, a higher mortality and delayed development of the common pest *Spodoptera exigua* was observed when they fed on mycorrhizal plants. These plants showed a primed accumulation of defensive alkaloids, fatty acids derivatives and phenylpropanoid-polyamine conjugates in response to local damage. Such effect depends on jasmonic and abscisic acid signaling.

In summary, the potential of AMF as multifunctional bioprotectors in sustainable agriculture seems to rely on an enhanced plant metabolic plasticity, and stress-adapted strains should be explored for optimized plant protection.

Key words: Defense priming, functional diversity, metabolic profiling, phenotypic plasticity, stress tolerance.

Mycorrhizal benefits and costs - do we understand enough to design more sustainable agroecosystems?

Jan Jansa

Czech Academy of Sciences
jansa@biomed.cas.cz

Most plant species on Earth establish mycorrhizal symbiosis, which emerges as a pivotal ecosystem feature in cycling mineral nutrients and reduced carbon between the living soil and the plants. This symbiosis is also heavily implicated in buildup and stabilization of soil structure and soil organic matter stocks, modulates plant responses to multiple biotic and abiotic stresses including drought, and exerts significant feedbacks on diversity and resilience of natural ecosystems. Number of lessons have been learnt through decades of research on general principles of mycorrhizal functioning from long-term ecosystem observatories and successional gradients, and from model experiments conducted under more or less precisely controlled conditions. Resource stoichiometry has been recognized as unifying concept explaining mycorrhizal functioning across scales and mechanistically predicting the magnitude and direction of plant responses under different environmental contexts. Yet, most of this knowledge is (still) not widely used in production agriculture. This is surprising because most crops actually form arbuscular mycorrhizal symbiosis under field conditions – with well-recognized constraints imposed by certain management practices (e.g., use of mineral fertilizers, pesticides, and/or tillage). Current agricultural practices, literally feeding the humanity, continue relying on substantial inputs of non-renewables. The transition to more sustainable agroecosystems will require gradual replacement of those non-renewables with renewable resources, particularly organic wastes and clean energy. Future agriculture will be required to maintain or increase current production levels. To achieve this, it will depend on heathy soils including mycorrhizal fungi. To successfully manage such underground resources, more integrative knowledge and unorthodox thinking is required.

Key words: Agriculture, environmental context, functioning, resource stoichiometry, sustainability.

Mycorrhiza and global change

Matthias Rillig

Freie Universität Berlin
rillig@zedat.fu-berlin.de

Global change is inherently a multifactorial phenomenon affecting the Earth’s ecosystems, with soils occupying a key position. Many factors of global change also have the potential to affect soil biodiversity including mycorrhizal associations, with mostly unknown consequences for terrestrial ecosystems and sustainability. Our knowledge about effects on mycorrhiza remains quite fragmentary. This talk highlights some of the known and emerging effects of global change drivers on arbuscular mycorrhiza, discusses experimental approaches to study the multifactorial nature of anthropogenic change, and offers an outlook on the role of mycorrhiza in ecosystem sustainability.

Key words: Arbuscular mycorrhiza, global change, sustainability.

Seeing the forest beneath the trees: Mycorrhizal fungi as trait integrators of ecosystem services

Richard Phillips

Department of Biology, Indiana University
rpp6@indiana.edu

Global changes are shifting the distribution and abundances of species globally, yet the consequences are poorly understood. Here, I present a framework that seeks to unify the heterogeneity of plant-microbe-soil interactions, as a means for predicting the impacts of community change on ecosystem functioning. The Mycorrhizal-Associated Nutrient Economy (MANE) hypothesis predicts that species that associate with different types of mycorrhizal fungi possess an integrated suite of nutrient-use traits that lead to the maintenance of biogeochemical syndromes. I combined observations, experiments, syntheses and modeling to test the MANE hypothesis in forests dominated by tree species associating with arbuscular mycorrhizal (AM) fungi vs. ectomycorrhizal (ECM) fungi. I compared nutrient use traits between AM and ECM trees, examined the effects of plant-fungal trait variation on microbial communities and ecosystem processes, and investigated how plant-microbe-soil mineral interactions govern carbon (C) and nitrogen (N) retention and loss. AM trees possess nutrient acquisitive traits (e.g., fast-decaying litters and nutrient scavenging), such that soils dominated by AM trees contain greater abundances of N-cycling microbes, accelerated C and N losses via leaching and gaseous efflux, and enhanced C and N retention via mineral stabilization. ECM trees possess nutrient conservative traits (e.g., slow-decaying litters and nutrient mining), such that soils dominated by ECM trees are characterized by high fungal to bacterial ratios, slow C and N cycling, and limited C and N stabilization to minerals. Collectively, these results suggest that shifts in the relative abundance of AM and ECM trees may have profound implications for forest sensitivity to global change.

Key words: Carbon cycling, ecosystem processes, mycorrhizal associations, nutrient cycling.

Eminent Mycorrhiza Researcher Award

Ectomycorrhiza diversity and ecosystem function around the world: a tale of two hemispheres

James Trappe, Michael P. Amaranthus

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Ectomycorrhizal fungi and hosts differ strikingly between the northern and southern hemispheres. These differences are most pronounced for hypogeous fungi that normally don’t disperse spores aerially, but the ectomycorrhizal host species and the animals that disperse spores of hypogeous fungi also differ between those hemispheres. For example, the widespread ectomycorrhizal Pinaceae and its obligate ECM fungi *Suillus*, *Rhizopogon* and many *Tuber spp*. are endemic to the northern hemisphere as are their animal dispersers, including many rodents plus armadillos, badgers, bears, and mountain goats. The most striking ECM’s endemic to the southern hemisphere are in Australia, which began to separate completely from Gondwana some 320 million years ago to become the “Island Continent” about 60 million years ago. It’s endemic ECM host family, Myrtaceae, principally contains the genus *Eucalyptus* with ca 700+ species, with its endemic ECM fungi in the Mesophelliaceae, Bolbitiaceae, and Tuberaceae, and its many marsupial spore dispersers including bandicoots, bettongs, potoroos and wallabies. These hemisphere differences relate to evolutionary and ecological histories of continental drift and rotation over eons. Despite such strong differences between the hemispheres and their plant/fungus communities, they perform the same essential ecosystem functions such as nutrient and water uptake and conservation, plant establishment, soil improvement and stabilization. In both hemispheres crucial mycorrhizal populations persist similarly through a combination of aerial and animal mycophagy as dispersal agents for the fungi. In these northern and southern hemispheres, evolution's billions of genetic experiments have produced identical symbiotic systems around the world.

Key words: Ectomycorrhizal diversity, ecological y evolutional history and function, mycophagy.

DETAILED PROGRAM ORAL SESSIONS

Monday July 1, 2019

Oral Session 1 "Evolution"

ID 312 - Plant-Mucoromycotina mutualisms: a nitrogen affair?

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Introduction. In the last decade our understanding of the evolution and diversity of plant-fungus associations have been revolutionised by the discovery that early-divergent, non-vascular plant lineages form nutritional mutualisms not only with Glomeromycotina fungi but also with members of the subphylum Mucoromycotina, with both fungal groups sometimes co-colonising the same plant host in so called dual symbioses.

Results and discussion. We have shown that in liverworts these diverse symbiotic partnerships differ considerably cytologically and physiologically, varying in their responses to changes in atmospheric CO_2 concentration and in their ability to transfer soil nutrients to their host. Most recently we have shown that mutualisms with Mucoromycotina are also present in vascular plants and that the same Mucoromycotina fungi colonize a wide range of plant hosts including non-vascular and vascular spore-producing lineages and flowering plants, in line with the recently proposed reclassification of fine root endophytes, FRE, in the Mucoromycotina. Our latest results also reveal a potentially prominent role of Mucoromycotina FRE in plant host nitrogen nutrition, pointing to further important functional differences between Mucoromycotina and Glomeromycotina symbioses. I will discuss the implications of these latest findings for understanding the origin and evolution of mycorrhiza as well as the hitherto unappreciated significance of Mucoromycotina FRE in modern ecosystems

Key words: Mucoromycotina, nitrogen nutrition, plant-fungus associations.

ID 316 - Mycorrhiza-like symbioses and Earth's early climate

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Introduction. Fossil evidence from the Rhynie Chert indicates that the earliest land plants, which evolved in a high CO_2 atmosphere during the Paleozoic Era, hosted diverse fungal symbionts - including both Glomeromycotina-like and Mucoroycotina-like fungal endophytes. It is generally thought that the rise of early nonvascular land plants, and the later evolution of roots and vasculature, drove the long-term shift towards a high-oxygen, low-CO_2 climate that eventually permitted the evolution of mammals and, ultimately, humans. However, very little is known about the productivity of the early terrestrial biosphere, which depended on the acquisition of limiting nutrients, such as phosphorus, via fungal symbioses. Recent laboratory experiments have shown that plant-fungal symbiotic function is specific to fungal identity, with carbon-for-phosphorus exchange being either enhanced or supressed under superambient CO_2 depending on whether plants associate with Glomeromycotina arbuscular mycorrhizal fungi or with Mucoromycotina “fine root endophytes”.

Results and discussion. By incorporating our experimental findings into a biogeochemical model, we show that the differences in these symbiotic nutrient acquisition strategies could greatly alter the plant-driven changes to climate, allowing drawdown of CO_2 to glacial levels, and altering the timing of the rise of oxygen by up to 100 Myrs.

Conclusion. We conclude that an accurate depiction of plant-fungal symbiotic systems, informed by high-CO_2 experiments, is key to resolving the question of how the first terrestrial ecosystems altered our planet and the key role of mycorrhiza-like symbioses may have played.

Key words: Biogeochemistry, climate, evolution, Glomeromycotina, Mucoromycotina, Paleoclimate.

ID 132 - How are contemporary outcomes of mycorrhizal interactions shaped by early and ongoing evolution?

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Introduction. It is unclear how coevolution operates in diverse mutualisms, including mycorrhizas. Outcomes of mycorrhizal symbioses are highly variable, both among and within species, but to what degree is this variability shaped by early or ongoing coevolution, adaptation to the environment, or plasticity in response ecological context?

Methods. Meta-analysis was conducted across 646 combinations of arbuscular mycorrhizal (AM) and ectomycorrhizal (EM) plants and fungi in the MycoDB database to quantify the relative importance of early evolutionary history, recent diversification, and ecological context for plant growth benefits from mycorrhizal symbiosis. Results were also synthesized from a variety of laboratory and field experiments to estimate the nature of genetic variation in potentially coevolving traits of EM symbioses with pines.

Results and discussion. Meta-analysis demonstrated that evolutionary history had a different influence on outcomes of EM versus AM symbioses in meta-analyses; the former are best explained by the multiple evolutionary origins of ectomycorrhizal lifestyle in plants, while the latter are best explained by recent diversification in plants; both are also explained by evolution of specificity between plants and fungi. Experiments showed that substantial genetic variation for candidate coevolving traits is found within populations of EM plants and fungi, including genotype by genotype interactions consistent with ongoing coevolution and those trees can apparently evolve independently with different species of EM fungi.

Conclusions. Contemporary traits and outcomes of mycorrhizal symbioses are likely influenced both by evolutionary history and by contemporary coevolution. Diverse mycorrhizal symbioses may provide a model system for exploring how coevolution operates in multi-specific mutualisms.

Key words: Arbuscular mycorrhiza, coevolution, ectomycorrhizal, meta-analysis, *Pinus*.

ID 55 - Genomic differentiation of an ectomycorrhizal fungus (*Laccaria trichodermophora*) in Mexican sky-islands

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Introduction. Mycorrhizal fungi play fundamental roles in their hosts by increasing their fitness under abiotic and biotic stress. Under a sky-islands dynamic, pine populations tend to be isolated at mountaintops, but during the glacial-interglacial periods those populations can migrate to lowlands, facilitating connectivity with populations from other mountains, or can remain isolated in refugia, promoting differentiation. Considering the history of the Trans Mexican Volcanic Belt (TMBV) during the Pleistocene climate fluctuations, we hypothesized fungal symbionts reacted in accordance to their pine hosts

Methods. To better understand the patterns of genomic diversity associated with climatic fluctuations cycles, we conducted a population genomics study with the non-model ectomycorrhizal fungus *Laccaria trichodermophora* in three sky-islands pine forests of the TVMB. We generated 2,638 SNPs using Genotyping by Sequencing method at very low DNA concentration (5 ng/µl), and mapped using the *Laccaria bicolor* genome as reference. Then we inferred population structure, isolation by distance and populations connectivity. Finally, we searched for loci under divergent selection using FST outliers' approaches.

Results and discussion. We identified three differentiated genetic clusters that coincided with each mountain peak and fitted them to a model of isolation by distance. Outlier loci were identified at strict significant values ($q < 0.0005$). Both, the FST values and genetic clustering suggest recent vicariance events supporting the allopatric differentiation hypothesis as expected during a sky-island dynamic.

Conclusion. All our results suggests that *L. trichodermophora* populations began to diverge recently through a sky-island dynamic promoting isolation, and the assumption of "*almost nothing is everywhere*" is supported by our system.

Key words: Distribution, ectomycorrhiza, GBS, genomic structure, isolation by distance.

ID 112 - Population genomics of toxins genes in Amanita phalloides

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Introduction. Fungi produce a wide array of secondary compounds, often used for commercial and medical applications, but their function in natural contexts is poorly understood. Species in the genus *Amanita* (Agaricales, Basidiomycota) are responsible for a majority of mushroom related poisonings worldwide. The invasive death cap, *A. phalloides*, which produces among the most potent toxins known to science, was introduced into California in the mid-1900s. The subsequent spread of *A. phalloides* in California provides an ideal model to study how natural selection shapes fungal secondary chemistry.

Methods. Recently, our laboratory generated 68 genomes of *A. phalloides* from California and Portugal. We have developed a novel bioinformatic pipeline to compare MSDIN (toxin) gene composition across individuals and populations of *A. phalloides* in Californian versus European populations. Our pipeline combines multiple de novo assemblers and PacBio based scaffolding to generate high accuracy genomes. Next, we analyze MSDIN genes using BLAST and motif filtering, followed by alignment and phylogenetic comparisons of concatenated MSDIN exomes.

Results and discussion. MSDIN gene composition varies more among individuals from California than between Californian and Portuguese individuals, suggesting multiple introductions to California or rapid diversification within California. The composition of MSDIN genes in Californian individuals give them the ability to produce a greater number of different toxin products.

Conclusion. The dissimilarity of MSDIN repertoires among Californian individuals and their more diverse repertoire compared to Portuguese populations suggests that Californian populations are evolving differently from native populations.

Key words: Bioinformatics, evolution, fungi, genetics, toxins.

ID 65 - Variation in plant and fungal traits indicates mycorrhizal mediated selection for Pinus radiata

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Introduction. Much progress has been made in analyzing the dynamics and consequences of coevolution, but little is understood about how coevolutionary selection operates within multispecies interactions.

Methods. We investigated natural selection on pine and ectomycorrhizal fungi (ECM) fungal traits through a common garden experiment. We planted 1178 Monterey pine (*Pinus radiata*) seedlings from all five native populations of Monterey Pine, as well as crosses to represent intermediate phenotypes/genotypes, for a total of 47 unique genetic families. We then measured pine seedling traits, ECM fungal traits, and ECM species composition and related them to relativized measures of plant and fungal fitness using standard procedures for calculating selection gradients. Coevolutionary selection was assessed using interaction terms combining plant and fungal traits.

Results and discussion. We found evidence for natural selection on a variety of plant and ECM traits, including potential coevolutionary selection. For example, the fungal trait fungal hyphal biomass, which separated low biomass from high biomass fungi, played a significant role in coevolutionary selection for the plant traits relative growth rate (RGR) and specific root length (SRL). In fungal fitness models, selection was positive, experiencing peak selection across multiple combinations of RGR / SRL values but declining to a single value; in plant fitness models, selection was negative, stemming from a single peak fitness value and declining across multiple combinations of RGR / SRL.

Conclusion. This work represents the first field-based, community-level investigation of coevolutionary selection in a multispecies nutritional symbiosis, suggesting that ongoing coevolution and interspecific selection are important contemporary forces driving trait evolution in these interactions.

Key words: community ecology, ectomycorrhizal fungi, evolution, mutualism, soil micro-organisms, symbiosis.

ID 203 - Association with arbuscular mycorrhizal fungi modifies phenotypic natural selection of fruit production in Ruellia nudiflora (Acanthaceae)

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Introduction. The influence of multiple biotic interactions over the evolution of plant phenotypic traits has been widely recognized. However, little is known regarding the manner in which the phenotypic natural selection (PNS) of these characters is modified by the presence of more than one pair of interacting species, and even less is known regarding how the selective effects change and feedback among different trophic levels.

Methods. In this study, we evaluated whether the presence of arbuscular mycorrhizal fungi (AMF) and intra-specific variation among individuals of *Ruellia nudiflora* affect the intensity of the PNS exerted over fruit production by a specialized pre-dispersal seed predator. Manipulating the presence of AMF and the origin per cross type of the progeny (self-pollination vs. cross-pollination), we used a factorial design to generate four selective scenarios under which we estimated the gradients of selection over fruit production.

Results and discussion. Our results showed significant directional PNS events under all four scenarios. However, we found that the presence of AMF reduced the selective effect of the herbivores. In contrast, the origin per cross type of the plants did not alter the PNS. To our knowledge, this study is the first to demonstrate that the “bottom-up” effects of AMF have consequences for the intensity of the PNS exerted above ground level, establishing a link among trophic levels along the gradient from below- to above-ground.

Conclusion. We conclude that the presence of AMF can contribute to diffuse selection processes in *R. nudiflora*.

Key words: Arbuscular mycorrhizal, cross type, diffuse selection, fruit production, herbivores.

Oral Session 2 "Cellular and molecular studies on symbiosis development and functioning"

ID 83 - Nutrient availability and the impact on host receptivity to ectomycorrhizal fungi: separating host from fungal influences on symbiosis

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Introduction. Forest trees are able to thrive in nutrient poor soils in part because they obtain growth-limiting nutrients, especially nitrogen (N), through mutualistic symbiosis with ectomycorrhizal (ECM) fungi. Addition of inorganic N into these soils is known to disrupt this mutualism and reduce the diversity of ECM fungi. Despite its importance, relatively little is known about the mechanisms governing the flux of nutrients between partners and how this is affected by soil nutrient levels.

Methods. We addressed this by using a compartmentalized in vitro system to independently alter nutrients to each symbiont. Using stable isotopes, we traced the nutrient flux under different nutrient regimes between *Eucalyptus grandis* and its ectomycorrhizal symbiont, *Pisolithus albus*.

Results and discussion. We demonstrated that giving *E. grandis* independent access to N causes a significant reduction in root colonization by *P. albus*. Transcriptional analysis suggests that the observed reduction in colonization may be brought about, in part, by altered transcription of microbe perception and defence genes. We showed that delivery of N to the host is not influenced by host nutrient deficiency but by fungal nutrient status.

Conclusion. Overall, this advances our understanding of the factors governing nutrient transfer and gives mechanistic reasoning to some of the observations seen at ecosystem scales. Further, I would like to reflect upon some of the bigger-picture ramifications of these findings and highlight some avenues of research that may be attractive to pursue in the future.

Key words: Ectomycorrhizal fungi, nitrogen deposition, nutrient trading, stable isotope tracing, transcriptomic.

ID 189 - In silico analysis of fungal small RNA accumulation reveals putative plant mRNA targets in the symbiosis between an arbuscular mycorrhizal fungus and its host plant

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Introduction. Small RNAs (sRNAs) are short non-coding RNA molecules that regulate gene expression at transcriptional or post-transcriptional levels through a mechanism known as RNA interference (RNAi). Recent studies have highlighted that sRNAs are also involved in cross-kingdom communication: they can move across the contact surfaces from “donor” to “receiver” organisms where they can target specific mRNAs, leading to a modulation of host metabolic pathways and defense responses. Very little is known about RNAi mechanism and sRNAs occurrence in Arbuscular Mycorrhizal Fungi (AMF), an important component of the plant root microbiota.

Methods. We characterized the fungal sRNAs population, highlighting the occurrence of an active sRNA-generating pathway and the presence of microRNA-like sequences. In silico analyses revealed that several fungal sRNAs have the potential to target *M. truncatula* transcripts, including some specific mRNA already shown to be modulated in roots upon AMF colonization.

Results and discussion. Taking advantage of the available genomic resources for the AMF *Rhizophagus irregularis* we described its putative RNAi machinery, which is characterized by a single Dicer-like (DCL) gene and an unusual expansion of Argonaute-like (AGO-like) and RNA-dependent RNA polymerase (RdRp) gene families. Focusing on the symbiosis between *R. irregularis* and the model plant *Medicago truncatula*.

Conclusion. The identification of RNAi-related genes, together with the characterization of the sRNAs population, suggest that *R. irregularis* is equipped with a functional sRNA-generating pathway. Moreover, the in silico analysis predicted several plant transcripts as putative targets of specific fungal sRNAs suggesting that cross-kingdom post-transcriptional gene silencing may occur during AMF colonization.

Key words: Arbuscular mycorrhizal fungi, microRNA-like, *Rhizophagus*, RNA interference, small RNAs.

ID 105 - Tracing fungal nitrogen and host carbon in arbuscular mycorrhizal symbiosis by correlative ultrastructural TEM observation and high-resolution secondary ion mass spectrometry imaging

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Introduction. Arbuscular mycorrhizal plants benefit by obtaining elements, such as phosphorus, nitrogen, from the symbiotic fungi, at a cost of providing fixed carbon to the fungi. The objective of this study was to trace host C and fungal N in the mycorrhiza at the ultrastructural level.

Methods. Onions inoculated with *Gigaspora margarita* were labelled with 15NH$_4$ added to the extraradical hyphae and with 13CO$_2$ to the plants. Colonized roots were either chemically fixed or underwent high-pressure freezing. Resin-embedded sections were observed by TEM and then analyzed by nano-scale secondary ion mass spectrometry.

Results and discussion. In the host, spaces between root cells and intercellular hyphae contain 13C. Higher 13C accumulations were found in the plastid, lipid droplet (some were rich in P), nucleolus, and interface of arbuscule, and cell wall facing on the plasma membrane, especially at around penetrating hyphae. 15N accumulation of cytoplasm, nucleus, plastid and interface of arbuscule were noticeable in colonized host cells. Within the fungus, higher 13C was found in ER, glycogen, and lipid, and that of 15N were along with polyphosphate, cytoplasm, glycogen, and nucleus.

Conclusion. Results suggest that fungal N is necessary for glycogen synthesis using host C, probably sugar. These events, especially at fungal penetration points, trigger degradation of polyphosphate and the release of N and P from the vacuole, which are then transferred to the host. In response to fungal colonization and to receive N and P, the host allocates C and N to the cell. P may be involved in host lipid metabolism, proposed C transfer through arbuscules.

Key words: Arbuscular mycorrhiza, SIMS, ultrastructure, 13CO$_2$, 15NH$_4$.

ID 176 - Interactions between arbuscular mycorrhizal fungi and non-host plants

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Introduction. Arbuscular mycorrhizal (AM) fungi are unable to form symbiotic associations with approximately 29% of all vascular plant species, including important crops and model organisms, and often antagonize their growth. The underlying mechanism of this antagonism is still poorly understood.

Methods. We deployed the AM fungus *Rhizophagus irregularis* against the nonhost plant Arabidopsis to analyze transcriptional changes and monitor fungal colonization and plant growth depression in *Arabidopsis* lines altered in phytohormone or microbe-associated molecular pathways. We analyzed also de novo hyphal germination and fungal metabolism under the influence of *Arabidopsis* roots or exudates. *R. irregularis* activated

Results and discussion. *Arabidopsis* strigolactone biosynthesis genes, suggesting that early detection of AM fungi is not completely impaired in nonhost roots. However, in colonized *Arabidopsis* roots, fungal nutrient transporters were inactive. Although we observed defense-related GO term enrichment in *Arabidopsis*, associated with mycorrhizal-induced resistance, neither the compromised defense nor growth phytohormone pathways affected the AM fungal antagonism against *Arabidopsis*. Moreover, plant mutants susceptible to various pathogens were not susceptible to *R. irregularis*. Conversely, a coumarin exudation pathway stimulated colonization in *Arabidopsis* when *R. irregularis* was nursed by neighboring host plants. This was associated with activation of fungal metabolism and de novo hyphal germination.

Conclusion. *R. irregularis* did not act like a typical pathogen nor *Arabidopsis* autoregulated growth-defense tradeoffs, which suggests that fungal antagonism against nonhosts may entangle a more specialized mechanism yet uncharted. Furthermore, we uncover that coumarin exudation involved in plant responses to nutrient depletion can excite AM fungi during the prepenetration dialogue.

Key words: Arbuscular mycorrhiza, coumarins, nonhost plant defense, prepenetration dialogue, strigolactones.

ID 182 - Cellulose content increase as a possible mechanism of priming in shoots of mycorrhizal tomato

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Introduction. Interaction of plants with beneficial microorganisms such as PGPRs and arbuscular mycorrhizal fungi (AMF) have shown to induce defense priming, which is a condition that allows a stronger defense response, in colonized plant vs non-colonized, in a subsequent pathogen attack. Cell walls constitute the first protection barrier against pathogens, and it is known that biotic stress triggers the upregulation of genes involved in the synthesis or modification of cell walls as part of the immune defense response in plants.

Methods. Previously, a cellulose synthase gene was identified as upregulated in a differential transcriptomic analysis between shoots of mycorrhizal vs non-mycorrhiza control tomato plants. The aim of this work was to confirm by qPCR the differential expression pattern of this gene previously observed in the transcriptomic analysis, as well as to quantify the content of cellulose in these leaf tissues.

Results and discussion. Our results corroborate the upregulation at the transcriptional level of the cellulose synthase analyzed. Additionally, we found that cellulose content in leaves of mycorrhiza plants was higher than in non-mycorrhizal ones.

Conclusion. These results support the idea that the increasing of cellulose in leaves of mycorrhiza plants, might be due to the higher expression of cellulose synthase, in order to reinforce cell walls in leaves, as one of the possible mechanisms for mycorrhiza-induced priming.

Key words: Cell wall, cellulose, defense, priming shoot.

ID 21 - Structural variation in the genomes of AMF

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Introduction. Structural variation (SV) contributes to a large extent of genetic diversity of living organisms and is of high importance for comparative genomics and evolutionary genetics. Recent studies in humans and other model organisms have shown that SV can not only affect gene dosage, but also the basic mechanisms of gene regulation, in some cases causing important disfunction or disease.

Methods. In this study, through the analysis of novel sequencing data, we present a first insight on SV existing among six isolates of the model species of AMF *R. irregularis*.

Results and discussion. Few comparative genomics studies have been carried out on arbuscular mycorrhizal fungi. Understanding its complex genetic organization is of high evolutionary and agronomic importance, both. These studies showed that there is indeed a high degree of genome diversity among different AMF isolates and also, suggested that this feature might play a crucial role in AMF adaptation to many different environments. However, even though these previous studies have certainly shed light on the complexity of AMF genome organization, there is still an important piece of information missing.

Conclusion. The lack of a gold standard for SV detection and other technical limitations has obstructed its in-depth assessment in these fungi. In addition, we were able to get an insight into the structural variation occurring between the two different nucleus genotypes of a dikaryotic isolate of *R. irregularis*.

Key words: Diversity, genomics, structural, variation.

ID 22 - *Tricholoma*-spruce ectomycorrhiza: phytohormones and volatiles

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Introduction. The ectomycorrhizospheric habitat contains a diverse pool of organisms, including the host plant, mycorrhizal fungi, and other rhizospheric microorganisms. Different signaling molecules may influence the ectomycorrhizal symbiosis. Here, we investigated the potential of the basidiomycete *Tricholoma vaccinum* to produce communication molecules for the interaction with its coniferous host, Norway spruce (*Picea abies*).

Methods. We focused on the production of volatile organic compounds and phytohormones in axenic *T. vaccinum* cultures and identified the potential biosynthesis genes.

Results and discussion. *T. vaccinum* released volatiles not usually associated with fungi, like the plant defense compounds limonene and ß-barbatene, and geosmin. Using stable isotope labeling the biosynthesis of geosmin was elucidated. In addition, the fungus released the volatile phytohormone ethylene and excreted salicylic and abscisic acid as well as jasmonates into the medium. The tree also excreted the auxin, indole-3-acetic acid, and its biosynthesis intermediate, indole-3-acetamide, as well as salicylic acid with its root exudates. These compounds could be shown for the first time in exudates as well as in soil of a natural ectomycorrhizospheric habitat. The effects of phytohormones present in the mycorrhizosphere on hyphal branching of *T. vaccinum* were assessed and salicylic and abscisic acid shown to decrease and increase branching.

Conclusion. Since extensive branching is, an important factor in mycorrhiza establishment, mycorrhizospheric phytohormones can be seen to be well balanced during mycorrhization where they form an “interkingdom language”

Key words: Geosmin, phytohormones, *Picea abies*, *Tricholoma vaccinum*, volatiles.

ID 235 - Phosphate acquisition through the mycorrhizal pathway upregulates the genes involved in arbuscule development and Pi homeostasis

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Introduction. Arbuscular mycorrhizal (AM) fungi associate with 80% of land plants. The fungi promote growth of the host plants through enhanced uptake of phosphate (Pi), and in return, the host supplies organic carbon (C) to the fungi. The molecular mechanism underlying the C-Pi exchange has not been well understood.

Methods. Here we employed comparative transcriptome analysis toward a comprehensive understanding of the mechanism at the molecular level. *Rhizophagus clarus* HR1 was grown in association with *Nicotiana benthamiana* in the mesh-bag separated two-compartment culture system for 9 weeks, and then extraradical mycelia and mycorrhizal roots were collected 0 - 36 h after 1mM Pi application to the hyphal compartment. mRNA was purified from the roots for 75-bp single-end sequencing, and the sequence reads were mapped on the genome/transcripts. Polyphosphate translocation to intraradical mycelia upregulated RcSYG1-1 that is a Pi exporter and expressed exclusively in arbuscules.

Results and discussion. Gene ontology analysis indicated significant enrichment of the genes involved in lipid/fatty acid biosynthesis and metabolism in those that were coexpressed with RcSYG1-1. It is noteworthy that most of the genes involved in arbuscule development and nutrient exchange, including those encoding the transcription factors, lipid biosynthetic enzymes/exporters, Pi transporters, ammonium transporters, SPX-domain containing proteins/transporter, and gibberellin metabolic enzymes, were coexpressed.

Conclusion. These results suggest that Pi delivery through the mycorrhizal pathway (i.e. through SYG1-1) activates the plant lipid biosynthetic pathway and gibberellin metabolism for arbuscule development and also the Pi homeostasis regulatory system through the inositol polyphosphate-mediated Pi signaling pathway via the SPX-domain.

Key words: Arbuscule development, nutrient exchange, phosphate delivery, transcriptome.

Oral Session 3 "Interactions with other biota"

ID 8 - Ectomycorrhizal symbiosis buffers responses to above/belowground biotrophic interactions governed by endogenous rhythmic growth in trees

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Introduction. Episodic growth in trees is linked to fluctuations in resource allocation between below- and aboveground plant parts that affect the formation of ectomycorrhiza. Here we use *Quercus robur* L., a foundation tree species displaying endogenous rhythmic growth (ERG) with alternating shoot (SF) and root (RF) flushes, to disentangle the interplay between tree growth and beneficial or detrimental biotrophic interactions, and reveal the modulation of this interplay by ectomycorrhiza.

Methods. In an interdisciplinary project (www.TrophinOak.de), micro-propagated oaks inoculated with the EMF *Piloderma croceum* and interacting with further biotrophic partners (microorganisms and animals) were analysed at the levels of gene expression profiling, biomass, carbon and nitrogen allocations.

Results and discussion. The EMF enhanced plant growth and resource availability without modifying the ERG, although extensive changes in gene expression along the ERG were largely reduced or even suppressed by EMF inoculation. In the absence of the EMF, interactions with the other biota triggered differential gene expression patterns, which were specific to the targeted plant part, related to the flushing stage, but also leveled by EMF inoculation. For instance, increased differential expression and defense responses induced by leaf herbivores and a pathogenic fungus during RF and by root feeding nematodes and mycorrhization helper bacteria during SF were attenuated in the presence of the EMF.

Conclusion. The presented data suggests that ERG in trees allows sequential defense responses to diverse biotrophic interactors, during which the EMF plays a determinant tuning role.

Key words: Allocation, biotic interactions, EMF, rhythmic growth, transcript.

ID 26 - Cooperation with hyphosphere microbiome helps arbuscular mycorrhizal community assembling in the root system

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Introduction. One plant root is always colonized by dozens of arbuscular mycorrhizal (AM) fungi which are morphological, physiological, genetic and functional diversity. In this study, we examined whether their hyphae associated microbes (hyphosphere microbiome) played important role when different AM fungi co-colonizing in the same root system.

Methods. A root divided cultural system was conducted and three AM fungi species *Rhizophagus intraradices* (R.i), *Gigaspora margarita* (Gig.m) and *Funneliformis mosseae* (F.m) were inoculated to different root compartments respectively. Combined with 13C-DNA-SIP and high throughput sequencing, we investigated the interspecies interaction between different AM fungi and their hyphosphere microbiome on organic phosphorus mineralization.

Results and discussion. Different AM fungi co-colonizing in the same root system cooperated with distinct structure of microbiome harboring alp gene through hyphal exudates. Inoculation with AM fungi improved soil organic P mineralization through stimulating bacterial alp gene copy number. R.i and F.m stimulated bacterial alp gene copy number through improving the whole hyphosphere microbiome amount, while Gig.m could recruit more alp gene harboring microbes. Comparatively, Gig.m contained higher soil organic P utilization efficiency. Closely related AM fungi contained similar cooperation strategy with their hyphosphere microbiome and organic P mineralization efficiency.

Conclusion. Our results suggested that the AM fungi associated microbes reduced the competition between different AM fungi and contributed to the co-existence of different AM fungi in the same root system.

Key words: Arbuscular mycorrhizal fungi, community assembly, cooperation, function, hyphosphere microbiome.

ID 31 - Signal beyond nutrient – Fructose exuded by an arbuscular mycorrhizal fungus triggers phytate mineralization by a phosphate solubilizing bacterium

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Introduction. The extraradical hyphae of arbuscular mycorrhizal (AM) fungi harbor and interact with a microbial community, e.g., phosphorus solubilizing bacteria, which perform important roles in phosphorus mobilization. However, the mechanisms by which hyphal exudates may stimulate phosphorus mineralization by bacteria are still unknown as well as the potential candidate signaling compounds.

Methods. We collected the hyphal exudates in the Petri dish and determined the components and concentrations of sugars by Ion Chromatography System. Then the phosphatase genes expression influenced by hyphal exudates and different sugars were analyzed by real-time qPCR under strict in vitro culture conditions.

Results and discussion. We observed that AM fungus exuded fructose, glucose and trehalose at different concentrations. Fructose stimulated the expression of phosphatases genes in the phosphate solubilizing bacterium as well as the rate of phosphatases release into the growth medium by regulating its protein secretory system. The phosphatase activity was subsequently increased, promoting the mineralization of organic phosphorus (i.e. phytate) into inorganic phosphorus, stimulating simultaneously the processes involved in phosphorus uptake by the AM fungus.

Conclusion. Our results demonstrated for the first time that fructose not only is a carbon source, but also plays a role as a signal molecule triggering bacteria-mediated organic phosphorus mineralization processes. These results highlighted the molecular mechanisms by which the hyphal exudates play a role in maintaining the cooperation between AM fungi and bacteria.

Key words: Fructose, hyphosphere, interaction, organic phosphorus, phosphatase genes.

ID 63 - Aphid herbivory decouples of carbon-for-nutrient exchange in the AM symbiosis

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Introduction. Encouraging the formation of arbuscular mycorrhizal (AM) associations in crops has been proposed as a means of reducing inputs within sustainable agro-ecosystems. AM can enhance plant-nutrient uptake in exchange for photosynthetic carbon, although the mechanisms controlling resource exchange between mutualists are undetermined. The degree to which AM promote plant growth is governed by numerous abiotic factors, including atmospheric CO_2 concentrations (a[CO_2]). How biotic interactions with insect herbivores impact crop-AM functioning is unclear; defoliation can suppress root-internal colonisation, but whether this equates to a loss of symbiotic function is equivocal.

Methods. By supplying an isotopically-labelled nutrient solution (33P and 15N) to fungal symbionts within mesh-walled cores and 14CO_2 to winter wheat, we present the first quantification of how a specialist phloem-feeding herbivore of cereals - the bird cherry-oat aphid (*Rhopalosiphum padi*) - influences carbon-for-nutrient exchange between crops and AM, and how this might be affected by rising a[CO_2].

Results and discussion. AM-distributions of recently-fixed C decreased following aphid exposure, with elevations in a[CO_2] only partially buffering this decline in fungal-allocated photosynthate. AM uptake of 33P and 15N was maintained in the presence of herbivores - and increased at elevated a[CO_2] - representing a decoupling in the bidirectional exchange of nutrients between symbionts.

Conclusion. Here, we show that insect herbivory modifies resource exchange dynamics between crops and mycorrhizal fungi under present-day and projected-future a[CO_2], representing the first complex systems test of biomarkets in the AM symbiosis. Given the ubiquity of insect defoliators, further investigation is encouraged to ascertain the efficacy of AM within complex agricultural systems.

Key words: Arbuscular mycorrhizal fungi, climate change, multi-trophic interactions, *Rhopalosiphum padi*, Tritic.

ID 25 - The adversaries of arbuscular mycorrhizal fungi

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Introduction. The activity of AMF may be suppressed in un-sterile soils. The causes are not completely resolved although it is clear that both abiotic and biotic factors are involved. This study aimed to assess whether suppression of AMF activity by un-sterile soil is common, and if specific groups of soil microorganisms are responsible.

Methods. We investigated suppression of AMF activity in model systems with 33P-labeled patches of soil, where hyphae but not roots access the patches. We used 33P uptake from labeled soil patches into shoots of *Medicago truncatula* as a proxy for AMF activity. Additionally, we evaluated the effects of sterilization for selected soils. We compared data for 33P uptake to microbiome profiles obtained by 16S rRNA gene or ITS amplicon sequencing. Furthermore, we inoculated sterilized soil with potential AMF-suppressors.

Results and discussion. We found that AMF suppression was relatively common in both cultivated and non-cultivated soils, with large variation between soils. Multivariate analysis of amplicon sequencing data revealed a clear separation between AMF suppressive and non-suppressive soils. Several bacterial and fungal groups were more abundant in suppressive than in non-suppressive soils and their concerted actions may lead to AMF-suppression. For selected soils, pasteurization and irradiation mitigated suppression. By adding fungal strains isolated from suppressive soil to irradiated soil, we found reduction on the AMF activity. However, we were not able to achieve complete suppression of AMF activity by introduction of individual strains.

Conclusion. We conclude that the biotic component of AMF suppression is probably due to synergistic effects of bacterial and fungal soil microbiota.

Key words: Arbuscular mycorrhizal fungi, interactions, microbiome, suppression, 33P radioisotope.

ID 45 - Characterization of mycorrhizal seed treatments on rice growth, yield, and tolerance to rice water weevil injury

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Introduction. Associations with AMF have been shown to both increase or decrease resistance to herbivores in different crop systems. However, the impact of AMF on the tolerance of rice to belowground root-feeding herbivores remains unknown. In crop protection, tolerance is a type of plant defense that plants employ to reduce the impact of damage (yield loss) from herbivore attack. The rice water weevil (RWW, *Lissorhoptrus oryzophilus*) is the most important early-season pest of rice in the USA. Because tolerance may be positively affected by growth rate, as plants with high growth rate can often regrow faster following herbivore damage, we suspect that rice growth would not be smaller and yield losses following RWW root injury would be smaller in the presence of AM fungi.

Methods. We used factorial combinations of two levels of AMF seed treatment (+AMF, -AMF) and two levels of insecticide (+NipsIt, -NipsIt) with 10 replications each in four field experiments over three years.

Results and discussion. Our results showed that AMF positively influenced plant growth in the rice fields. Additionally, AMF reduced resistance to weevils relative to plots not treated with AM fungi. However, root injury suggests that RWW larvae do not limit the plant's ability to benefit from AM fungi. Also, RWW densities were dependent on insecticidal seed treatments. AM fungi increased rice yields despite the positive effects on RWW densities. However, yield losses of AM fungi treated plants trend higher than plants protected from injury.

Conclusion. Therefore, rice inoculated with AMF may provide an effective method for weevil control and for increasing rice yields.

Key words: AMF, rice, rice water weevil, tolerance, yield.

ID 74 - The enemy of my enemy is my friend: using dual inoculation of beneficial above- and belowground fungal symbionts to save the endangered Hawaiian mint *Phyllostegia kaalaensis* from a foliar fungal pathogen

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Introduction. There is increasing recognition of the importance of the microbiome in plant health, but few studies have examined its role in plant defense. Hawaii is known as the extinction capital of the world where native species face threats from non-native pests. One such species is the endemic mint, *Phyllostegia kaalaensis*, which is currently extirpated from the wild. While this species is maintained in greenhouses, all attempts at reintroduction to the wild have failed. These failures are at least in part owed to a non-native mildew, *Neoerysiphe galeopsidis*. Here we set out to test whether inoculation with a foliar mycoparastic yeast, *Moeziomyces aphidis* that feeds upon *N. galeopsidis* as well as belowground colonization by arbuscular mycorrhizal fungi (AMF) that aid in plant fitness, could provide additive and increased disease resistance in *P. kaalaensis*.

Methods. In a full-factorial greenhouse experiment we inoculated axenic *P. kaalaensis* clones with either AMF, the foliar yeast, both AMF and the foliar yeast, or nothing (control). Replicates from each treatment were then exposed to the pathogen *N. galeopsidis*. After 2.5 months of exposure we measured pathogen incidence across treatments.

Results and discussion. We found that all treatments significantly decreased disease incidence relative to the controls, but none of the treatments were significantly more effective than another.

Conclusion. Our study shows that the plant microbiome can play a critical role in plant defense, and that native plant restoration should incorporate considerations of the holobiont into their practices.

Key words: Arbuscular mycorrhizal fungi, biotic interactions, foliar fungi, microbiome, plant disease.

ID 124 - Plant-fungus-animal-virus interactions: Arbuscular mycorrhiza affects Grapevine fanleaf virus transmission by the nematode vector *Xiphinema index*

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Introduction. The soil-borne nepovirus Grapevine fanleaf virus (GFLV) spreads mainly via the nematode vector *Xiphinema index*. Since the arbuscular mycorrhizal (AM) fungus *Rhizophagus intraradices* can induce local and systemic protection against *X. index*. Therefore, the objective of the present study was to investigate if AM may represent a means for limiting GFLV infection by reducing nematode attack.

Methods. Mycorrhizal or nonmycorrhizal grapevine rootstock SO4 (*Vitis berlandieri* x *V. riparia*) plants were inoculated with 10 or 100 viruliferous nematodes per plant under glasshouse conditions. Plants were harvested 35 and 90 days after inoculation with *X. index* (DAIN), prior to and after the appearance of fanleaf degeneration symptoms, respectively.

Results and discussion. Both levels of viruliferous *X. index* inhibited root growth of nonmycorrhizal plants at 90 DAIN, while the presence of mycorrhizal colonization significantly decreased gall formation on roots and reduced nematode reproduction in soil. GFLV was not detected by one-step reverse transcription PCR in the roots of any plant at 35 DAIN after viruliferous *X. index* inoculation. At 90 DAIN with 10 viruliferous nematodes per plant, the virus was present in nonmycorrhizal roots but absent from mycorrhizal grapevine. However, mycorrhizal colonization did not exclude root GFLV infection at the higher nematode pressure and the virus was detected in both mycorrhizal and nonmycorrhizal plants 90 DAIN.

Conclusion. Inhibition of *X. index* proliferation and penetration by AM may protect grapevine against GFLV at a low abundance of the viruliferous nematode in soils and so contribute to virus control under these conditions.

Key words: Biological protection, gall formation, Grapevine fanleaf degenerate, *Rhizophagus intraradices*, *Vitis*.

ID 174 - Interaction between arbuscular mycorrhizae, plant growth promoting bacteria and bacterial metabolites in growth and development of *Phaseolus vulgaris* var *Canario Centenario*

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Introduction. *Canario centenario* bean is a variety of *Phaseolus vulgaris*, with high nutritional value and consumption in Peru; it is intended to improve its production and yield with beneficial microorganisms, such as arbuscular mycorrhizae and plant growth promoting bacteria (PGPR). PGPR´s metabolites may biocontrol phytopathogens and can favor the performance of beneficial microorganisms.

Methods. To study the effect of the interaction of the AM fungus *Rhizophagus intraradices* with PGPR strains E-10 (rhizobia), *Bacillus* TruBac2. 32, *Bacillus* IcBac2.1 and its metabolites on growth and development of bean, a greenhouse experiment was set for 75 days. Controls were established only with bacterial and metabolite inoculation without mycorrhiza, and without microorganisms. At sowing, 2 pregerminated seedlings/pot were inoculated with 20 g / pot of Glomeromycota inoculum with 800 spores / 100 g soil, 1 mL of strains E-10, *Bacillus* TruBac2.32 and *Bacillus* IcBac2.1 (108 cfu / mL) and 1 mL of bacterial metabolite, according to each treatment.

Results and discussion. At harvest, it was determined that the interaction of *Bacillus* IcBac2.1 and metabolite with *R. intraradices* favored the production of shoot and root dry biomass of bean, with maximum values of 2.25 g and 7.95 g respectively; *Bacillus* IcBac2.1 and metabolite also favored the production of total glomalin (2.24 mg / gdws) by the fungus. In the tripartite symbiosis *Phaseolus*- mycorrhiza-rhizobia with strain E-10, nitrogen biological fixation was favored compared with non-mycorrhized, with a maximum ARA of 1.99 µmol C2H2 h-1.g (NDW). h-1.

Conclusion. Microbial interactions were specifc for each combination, favoring growth of *P. vulgaris*, constituting potential biofertilizers. Founded by Magnet Project 009-2016-Fondecyt-Peru.

Key words: Glomalin, PGPR, *Phaseolus vulgaris*, *Rhizophagus intraradices*, tripartite simbiosis.

Oral Session 4 "Biogeography"

ID 47 - Environment and host as large-scale controls of ectomycorrhizal fungi

Martin Bidartondo, Laura Martinez Suz, David L. Orme, Filipa Cox, Henning Andreae, Endla Asi, Bonnie Atkinson, Sue Benham, Christopher Carroll, Nathalie Cools, Bruno De Vos, Hans-Peter Dietrich, Johannes Eichhorn, Joachim Germann, Tine Grebenc, Hyun S. Gweon, Karin Hansen, Frank Jacob, Ferdinand Kristöfel, Paweł Lech, Miklós Manninger, Jan Martin, Henning Meesenburg, Päivi Merilä, Manuel Nicolas, Pavel Pavlenda, Pasi Rautio, Marcus Schaub, Hans-Werner Schröck, Walter Seidling, Vít Šrámek, Anne Thimonier, Iben Margrete Thomsen, Hugues Titeux, Elena Vanguelova, Arne Verstraeten, Lars Vesterdal, Peter Waldner, Sture Wijk, Yuxin Zhang, Daniel Žlindra, Sietse van der Linde

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Introduction. Explaining the large-scale diversity of soil organisms that drive biogeochemical processes—and their responses to environmental change—is critical in our rapidly changing planet. However, identifying consistent drivers of belowground diversity and abundance for functionally key soil organisms at large spatial scales has remained problematic.

Methods. We investigated a major guild, the ectomycorrhizal fungi, across European forests at unprecedented spatial scale and resolution with *in situ* data, to determine key biotic and abiotic predictors of ectomycorrhizal diversity and to identify dominant responses and thresholds for change across complex environmental gradients.

Results and discussion. We showed the effect of host, environment, climate and geographical variables on ectomycorrhizal diversity, and defined thresholds of community change for key variables. We quantified specificity to tree hosts and revealed plasticity in functional traits involved in soil foraging across gradients.

Conclusion. We conclude that environmental and host factors explain most of the variation in ectomycorrhizal diversity, that the environmental thresholds used as major ecosystem assessment tools (*i.e.* critical loads) need strong adjustment and that the importance of belowground specificity and plasticity has previously been underappreciated. This research is a fundamental methodological platform to achieve large-scale long-term biological monitoring of forest soils by providing a first robust benchmark.

Key words: Community, diversity, ectomycorrhizal, indicator, nitrogen.

82 - Does the biogeographic origin of ectomycorrhizal fungi differ among non-native woody plants species?

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Introduction. Woody plants are of principal significance as drivers of fundamental ecosystem processes and autogenic engineers in many ecosystems. Both historically and presently, they have been globally moved by humans for centuries outside of their native ranges for economic and cultural purposes for example due to introduction to the parks. Fitness of most of introduced EcM plants depend on successful establishment of mycorrhizal symbiosis upon their arrival. Absence of co-evolved mutualists can thus potentially limit their successful establishment and serve as a barrier to their naturalization or even invasion.

Methods. In this metastudy, we investigated how biogeographic origin of ectomycorrhizal fungi differ among non-native woody plants species. In accordance with previous studies, we recognize three broad categories of (a) co-introduction of mycorrhizal symbionts from native area, (b) association with cosmopolitan or already known mycobionts from native area and (c) novel association with indigenous species. We collected 57 datasets of EcM fungal communities associated with introduced EcM plants, covering all continents (except Antarctica). We used UNITE and other global database for identification of putative native ranges of EcM fungi.

Results and discussion. Introduced species of *Pinus* and *Eucalyptus* genera were over-represented compare to other plant taxa in the dataset. Our results shows that non-native woody plants predominantly associate with co-introduced EcM fungi in the introduced range, which indicates that the this strategy enables establishment of woody plant species on novel sites.

Conclusion. Future conservation efforts should therefore encompass management of impacts of non-native EcM mycobionts. The authors acknowledge support of the project (NAKI II) Ministry of Culture CR (DG16P02M041).

Key words: Biogeography of ectomycorrhizal fungi.

ID 145 - Does plant mycorrhizal trait assignment method matters for biogeographic analyses?

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Introduction. Two main methods are used to assign plant mycorrhizal types (i.e. AM, ECM, ERM or NM) and statuses (facultatively –FM- or obligately - OM –mycorrhizal plants) to plant species list. These methods are either based on exhaustive collections of empirical evidences at species level ("empirical"), or on expert assignation ("taxonomic"), extrapolating background knowledge to whole plant genera or families. Our aim is to compare them empirically, in order to understand their optimal use in biogeographic studies.

Methods. We estimated the percentage of mismatch of plant mycorrhizal trait assignments and illustrated its consequences to the biogeographical analyses between the two main methods for more than 1300 species of the European flora.

Results and discussion. The biogeographic patterns were different particularly for FM (91% of mismatch), NM (45 %) and AM (16 %), while comparable results were found for OM, ECM and ERM plant species. The differences on FM, NM and AM were also related to the use of different conceptual definitions and diagnosis criteria.

Conclusion. The "empirical" approach represents a more stable and sound approach when the plant mycorrhizal information covers a representative proportion of the flora under study. In contrast, the "taxonomic" approach is useful in exploratory scenarios, when the availability of plant mycorrhizal trait information is scarce. Overall, this study highlights the need to discuss central concepts in mycorrhizal ecology, such as mycorrhizal vs non-mycorrhizal and facultatively vs obligately mycorrhizal plant species.

Key words: Arbuscular mycorrhizal plants, biogeography, facultative mycorrhizal plants, non-mycorrhizal plants.

ID 192 - Biogeography of plant mycorrhizal traits along a latitudinal gradient in the Southern Hemisphere

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Introduction. Plant mycorrhizal type (MT) and mycorrhizal status (MS) are two plant mycorrhizal traits related to nutrient cycling, plant interactions and ecosystem processes. Despite its relevance, there are no studies about plant mycorrhizal traits along large gradients in the southern hemisphere. Therefore, studying their large-scale patterns can provide independent insights on ecological processes within and across biomes. Thus, the aim of this study is to analyze the patterns of distribution of plant MT and MS in the Southern Hemisphere, specifically along a large continental gradient in Chile.

Methods. For this study we have considered all plants species in the region, across most prominent biome types (Desert, Mediterranean and Temperate) and in relation to plant species distribution (native or endemic) and plant life forms (tree, shrub, sub-shrub, and annual, biennial or perennial herb).

Results and Discussion. Our results showed that arbuscular mycorrhizal (AM) type was more frequent, in all latitudes, biomes and among plant distributions and life forms. The proportion of AM plant species decreases towards higher latitudes, while the other plant mycorrhizal types increase. Very few non-mycorrhizal plant species were found, with highest proportions within biennial herbs. Regarding the plant distribution, endemic plants showed higher proportion of mycorrhizal symbiosis association than native ones.

Conclusion. Finally, the relative proportion of Ectomycorrhizal plants was highest within trees, with most trees showing obligate status. Despite the patterns found, more empirical data are needed in order to confirm and expand those patterns, and to understand their ecological role within the biomes and ecosystems of the Southern hemisphere.

Key words: Chile, distribution, mycorrhizal status, mycorrhizal type, South America.

ID 183 - Biogeography of ectomycorrhizal fungi associated with Nothofagaceae in the Southern Hemisphere

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Introduction. Current understanding of fungal biodiversity is particularly limited in the southern hemisphere, and global studies have identified many fungal lineages unique to this region. The ectomycorrhizal tree family Nothofagaceae is one striking example of vicariance associated with the final breakup of Southern Gondwana (the supercontinent that included South America–Antarctica–Australia–New Zealand) and the onset of Antarctic glaciation at the Eocene/Oligocene boundary ca. 35 mya. However, conflicting evidence suggests that long-distance dispersal has continued long after the fragmentation of Southern Gondwana.

Methods. Based on our large biodiversity assessment of ectomycorrhizal fungi in the Patagonian region (Chile and Argentina), we detected strong biogeographic patterns connecting South America with Australasia in many groups. We traced the most recent common ancestors of several southern temperate lineages of Basidiomycota and Ascomycota using nuclear ribosomal regions ITS and LSU as well as RPB2 and EF1-alpha. We tested alternative hypotheses of vicariance or long distance-dispersal, in relation with spore dispersal abilities, or if the taxa are early or late successional in Nothofagaceae associations.

Results and discussion. We found strong evidence for a Southern Gondwanan origin in most clades. Recent long-distance dispersal events were also detected, but not necessarily in correlation with spore dispersal abilities or successional stage.

Conclusions. Biogeography of Southern hemisphere ectomycorrhizal fungi was strongly impacted by the break-up of Southern Gondwana, while events of long-distance dispersal occurred rarely. Continued efforts are necessary to further understand the diversity of ectomycorrhizal fungi in the Southern Hemisphere.

Key words: Biogeography, fungal diversity, Nothofagaceae, Southern Hemisphere.

ID 12 - Ectomycorrhizal fungal communities associated with Betulaceae in Chinese secondary forest ecosystems

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Introduction. Environmental filtering and dispersal limitation are two of the primary drivers of community assembly in ecosystems, but their effects on ectomycorrhizal (EM) fungal communities associated with wide ranges of Betulaceae taxa at a large scale are poorly documented.

Methods. We examined the EM fungal communities associated with 23 species from four genera (*Alnus*, *Betula*, *Carpinus* and *Corylus*) of Betulaceae in Chinese secondary forest ecosystems covering an area of approximately 2.3 million km^2, using Illumina MiSeq sequencing of the ITS2 region. Effects of factors linked to environmental filtering (host plant phylogeny, soil and climate) and dispersal limitation (geographic distance) on the EM fungal community were explored.

Results and discussion. In total, we distinguished 1 738 EM fungal operational taxonomic units (OTUs) at a 97% sequence similarity level. The EM fungal communities of *Alnus* had significantly lower OTU richness than those associated with the other three plant genera. The EM fungal OTU richness was significantly affected by geographic distance, host plant phylogeny, soil and climate. The EM fungal community composition was significantly influenced by host plant phylogeny (12.1% of variation explained in EM fungal community), geographic distance (7.7%), edaphic factors (4.6%) and climatic factors (1.1%).

Conclusion. This finding highlights that environmental filtering linked to host plant phylogeny and dispersal limitation strongly influence EM fungal communities associated with Betulaceae plants in Chinese secondary forest ecosystems.

Key words: Betulaceae, dispersal limitation, ectomycorrhizal fungal community, environmental filtering, Illumina.

ID 257 - Patterns of global distribution of families in Glomeromycota related to soil properties and biomes

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Introduction. Biodiversity patterns for arbuscular mycorrhizal fungal species have emerged recently based on molecular and morphological approaches. However, patterns of distribution of families in Glomeromycota as related with soil properties and vegetation still remains to be elucidated.

Methods. Based on an extensive biogeography database of glomeromycotan fungi, we used contigency tables followed by chi-square analysis and the Freeman-Tukey deviation test to determine whether the frequency of families in Glomeromycota were represented differently among classes of soil pH, phosphorus and organic matter. BrayCurtis' similarity was utilized to calculate similarity of family composition between the main biomes.

Results and discussion. Based on the frequency of occurrence, the distribution of Glomeromycota families was significantly different among classes of soil pH, soil P, and organic matter. Freeman-Tukey analysis evidenced that Acaulosporaceae was overrepresented in soil with > 10% of organic matter and in acid to medium soil pH. Gigasporaceae was overrepresented in soils with < 1% of organic matter and in soil pH from 4.1 to 6.2. Both families were underrepresented in neutral to basic soils. Claroideoglomeraceae and Glomeraceae was overrepresented in soil pH > 6.3. Acaulosporaceae was overrepresented in soil P of 11-30 mg/kg while Paraglomeraceae was overrepresented in soil P of 51-100 and > 100 mg/kg. On average, biomes shared 52%, 52% and 64% of species in Acaulosporaceae, Gigasporaceae, and Glomeraceae.

Conclusions. Distribution of families of Glomeromycota are affected mainly by soil pH and organic matter and families are equally distributed among the main terrestrial biomes.

Key words: Acaulosporaceae, biogeography, gigasporaceae, glomeraceae, soil factors.

Tuesday July 2, 2019

Oral Session 5 "Nutrition and resource allocation"

ID 173 - Friend or foe: how does a host plant distinguish among high and low benefit AM fungi?

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Introduction. Arbuscular mycorrhizal (AM) fungi form symbiotic associations with the majority of land plants, and increase the uptake of nutrients, and improve the resistance of plants against many abiotic (e.g. drought, salinity, heavy metals) and biotic (root pathogens) stresses. However, AM fungi differ greatly in the benefit that they provide for their host plant, but it is currently unknown what mechanisms control the AM community composition of plants.

Methods. We studied the nutritional benefits from two AM fungi, one low benefit and one high benefit fungus, examined by Q-PCR whether the plant nutrient demand or the fungal access to nutrients affects the AM community composition, and studied the transcriptome of the plants in response to the colonization with these different root symbionts.

Results and discussion. Our results demonstrate the role that the plant nutrient demand plays in the AM fungal community composition, and AM fungi that are less beneficial for the host can gain a competitive advantage in AM fungal communities over more beneficial AM fungi. The plant transcriptome responds with distinct changes to the colonization with AM fungi differing in plant benefit. While the colonization with the high benefit fungus induced the expression of lipid transfer proteins, and of a bidirectional sugar transporter, stress response genes are highly expressed after colonization with the low benefit fungus.

Conclusion. We correlate these findings to changes in the plant's gene expression and the processes that could allow host plants to control their AM community composition in the rhizosphere.

Key words: Arbuscular mycorrhizal communities, gene expression, fungal diversity, *Medicago truncatula*.

ID 80 - Exploring the secrets of hyphosphere processes

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Introduction. A mycorrhizal plant acquires nutrient from soil through two pathways, root direct pathway and mycorrhizal pathway (Bucher, 2007; Smith et al., 2011). To a certain extent, the mycorrhizal pathway contribution to total P uptake are greater than root pathway (Nagy et al., 2009), even replace root direct pathway (Smith et al., 2008). The root and the hyphae form two interfaces with soil, which are called rhizosphere and hyphosphere. Driven by root or hyphal exudates, some unique chemical, physical and biological reactions are happening which are involved in biological interactions, soil mineral nutrients turnover, transformation and bioavailability processes are intensified.

Methods. The processes and ecological functions of rhizosphere have been found and investigated for more than a hundred of years, while the hyphosphere, a narrow and specific zone influenced by only extraradical hyphae of arbuscular mycorrhizal (AM) fungi, was identified about thirty years ago. Exploring the nature of hyphosphere interactions has received more and more attention in recent years.

Results and discussion. Many advances in uncovering the ecological process and functioning in hyphosphere have been achieved, including the innovation of research methodologies, quantitative measurement of mineral nutrients mobilization, identifying the biodiversity of microbes and biological interactions, etc.

Conclusion. In this review paper, we are going to summarize following points of research advances. First, the structure of hyphosphere; second, the natures of physical and chemical and biological processes in hyphosphere soil; third, the methodology of hyphosphere research. This study was supported by the National Key Research and Development Program of China (2017YFD0200200/2017YFD0200203), the National Natural Science Foundation of China (U1703232, 31501831).

Key words: Ecological process, hyphosphere, mycorrhizal pathway.

ID 129 - Polyphosphate metabolism in arbuscular mycorrhizal fungi in relation to phosphate transfer to their host

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Introduction. Plant phosphorus nutrition is improved through the formation of arbuscular mycorrhiza (AM). AM fungi take up phosphate (Pi) from the soil and then store it in the form of polyphosphate (polyP) in their vacuoles. PolyP is then translocated to the arbuscules where it is metabolized, resulting in the release of Pi and its subsequent transfer to the host.

Methods. Here, we investigated the Pi transfer mechanism from the perspective of polyP metabolism in AM fungi. Some proteins involved in Pi homeostasis have an SPX domain that can interact with inositol polyphosphates. This interaction modulates their enzymatic activity.

Results and discussion. *Rhizophagus irregularis* has 10 SPX domain-containing proteins, including vacuolar transporter chaperons (VTCs) that function as polyP synthases. VTC genes were expressed in extraradical and intraradical hyphae. There may be a continuous turnover of polyP in AM fungi because endopolyphosphatase genes are also expressed in these hyphae. We investigated the biochemical properties of VTC4, a catalytic subunit. VTC4 catalyzed the synthesis of polyP using ATP as a substrate. Interestingly, VTC4 was also capable of catalyzing the reverse reaction, i.e., using polyP for generating ATP when there is excess ADP. We further examined polyP localization in AM fungi colonizing the plant ha1 mutant, defective in transferring Pi via mycorrhiza due to a mutation in a symbiotic H+-ATPase gene. There was increased polyP accumulation in the arbuscular branches in the mutant, while less polyP was detected in those of the wild-type.

Conclusion. These results indicate that polyP metabolism in AM fungi is related to the Pi transfer process.

Key words: H+-ATPase, phosphate, polyphosphate, vacuolar transporter chaperon.

ID 42 - Are ectomycorrhizal networks associated with greater growth of adult interior Douglas-fir?

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Introduction. Ectomycorrhizal fungal networks can serve as conduits to transfer carbon and water along source-sink gradients between trees. How networks may mediate growth in adult trees, however, has been difficult to study due to the logistics of mapping network topology. Here, we leveraged a previously mapped ectomycorrhizal network formed by two species of *Rhizopogon* and mature Interior Douglas-fir (*Pseudotsuga menziesii* var *glauca*) to test if network connectivity was associated with differential growth in mature trees.

Methods. We assessed annual ring growth of trees as a function of network connectivity, connections to unique fungal genets, tree DBH, and tree age. We compared results for the year the networks were mapped (i.e., 2008) to eight years previous and eight years post-mapping.

Results and discussion. Greater ring growth was associated with 1) the number of connections to other trees via *Rhizopogon vinicolor*, and 2) the number of genets of *Rhizopogon vesiculosis* to which a tree was connected. Additionally, resistance and resilience of trees to drought was positively associated with network connectivity via *Rhizopogon vinicolor*.

Conclusion. This is the first study to identify a significant association between fungal networks and mature tree growth. The positive association with *Rhizopogon vinicolor* network connectivity and *Rhizopogon vesiculosis* genet number with mature tree growth may indicate the benefits to mature trees from participating in ectomycorrhizal networks. The results suggest that network-associated growth additions are not dependent on tree size and thus resource benefits are not strongly allocated along a source-sink gradient.

Key words: Douglas-fir, ectomycorrhizal networks, growth response, *Rhizopogon*, tree resistance.

ID 34 - Field evidence for higher specific contribution of AMF to oats P uptake under long-term conservation agriculture than under conventional tillage

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Introduction. Besides high fertilization, tillage affects arbuscular mycorrhizal fungi (AMF) development and function by the continuous disruption of extraradical mycelium in most agricultural fields. We compared the development and specific contribution of AMF to early P uptake of oats in a field with long-term conservation agriculture (CA) and conventional tillage (CT) treatments in Zealand, Denmark. We expected higher early 33P transfer in the CA than in the CT treatment due to faster reactivation of the preserved mycelium network in the CA treatment.

Methods. Soil labeled with 33P was buried between two rows of plants in nylon mesh bags that allowed access only to mycorrhizal hyphae or to roots and mycorrhizal hyphae. Some mesh bags contained Carbendazim fungicide to impair AMF development. We sampled periodically mesh bags and shoots to follow plant and AMF development and 33P transfer to shoots.

Results and discussion. AMF development was low in general, due to heavy fertilization, but AMF development and total 33P transferred to vegetative and reproductive shoot tissue were significantly higher in the CA than in the CT treatment. Moreover, specific root 33P uptake capacity was 3 times higher in CA roots than in CT roots, and the latter was similar to the uptake capacity of nonmycorrhizal roots in the Carbendazim treatment. Plant development did not differ.

Conclusion. We show the high capacity of AMF for P transfer to plants, even under high fertilization, when mycelium networks are preserved. This is one of the few studies demonstrating under realistic conditions the hidden contribution of AMF to crop P uptake.

Key words: Crop, network, plowing, uptake, 33P.

ID 66 - Changes in atmospheric CO_2 induce cultivar-specific carbon-for-nutrient exchange responses in wheat-arbuscular mycorrhizal fungal symbioses

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Introduction. Arbuscular mycorrhizal fungi (AMF) form symbioses with most crops, potentially improving their nutrient assimilation and growth. However, AMF sometimes act as parasites instead of mutualists, with their function being influenced by both biotic (e.g. genotype) and abiotic (e.g. CO_2) factors. The effects of climate change-relevant variation in atmospheric CO_2 concentrations (a[CO_2]) on wheat-AMF carbon-for-nutrient exchange and how this is influenced by cultivar remain critical knowledge gaps in exploitation of AMF in agriculture.

Methods. We used stable and radio-isotope tracers (15N, 33P, 14C) to quantify AMF-mediated nutrient uptake and fungal acquisition of plant carbon in 3 cultivars of wheat (*Triticum aestivum* L.). To investigate the effects of projected climate change on the symbiosis, we grew plants at current ambient (440ppm) and future projected atmospheric CO_2 concentrations (800ppm).

Results and discussion. We found significant 15N transfer from fungus to plant in all cultivars of wheat, and cultivar-specific differences in total N content. There was also a trend for reduced N uptake under elevated a[CO_2]. Similarly, 33P uptake via AMF was affected by cultivar and a[CO_2]. Total P uptake varied significantly between wheat cultivars and was greater at future than current a[CO_2]. We found limited evidence of cultivar or a[CO_2] effects on plant-fixed carbon transfer to the fungus.

Conclusion. Our results suggest that AMF will continue to provide a route of nutrient uptake to crops in the future, but that consideration must be paid to cultivar-specific AMF receptivity and function.

Key words: Arbuscular mycorrhiza, CO_2, nutrient exchange, wheat.

ID 171 - Ericaceous root enzymes are more sensitive than ectomycorrhizal to nutrient addition in Arctic tundra

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Introduction. Changes in nutrient availability can alter the dynamics of mycorrhizal relationships. While large increases in nutrient availability reduce allocation to mycorrhizae, small increases may alleviate, but not fully relieve nutrient limitations, tightening the plant-fungal relationship. In Arctic tundra, warming is stimulating nutrient release. Based on high-dose fertilization experiments, increased nutrient availability is thought to favor ectomycorrhizal, rather than ericaceous, shrubs. However, these experiments simulate a higher nutrient release than what is projected. How these shrubs' ectomycorrhizal (EcM) or ericoid mycorrhizal (ErM) fungi respond to a range of nutrient increases is critical in predicting their future role in the tundra.

Methods. To understand how nutrient availability affects EcM and ErM function, we measured root tip enzyme activity of the dominant shrubs and soil properties across a 12-year experimental nitrogen and phosphorous fertilization gradient near Toolik Lake, Alaska.

Results and discussion. Surprisingly, activities of only two of the five enzymes on EcM and ericaceous root tips decreased with increased inorganic nitrogen, but none correlated with soil carbon:nitrogen or moisture. Ericaceous root enzymes responded more strongly to fertilization than nutrient availability, decreasing at both low and high levels of fertilization. Generally, enzyme activities were higher on ectomycorrhizal root tips than ericaceous root tips.

Conclusion. The decrease in ericaceous enzyme activity with fertilization suggests a higher sensitivity to nutrient release than EcM roots as well as a reduction in allocation towards mycorrhizal acquisition of organically-sourced nutrients. Consequently, the relatively non-responsive ectomycorrhizae may play a larger role in liberating soil organic nutrients as both their host plant expands and ErM reduce in activity.

Key words: Arctic, ectomycorrhiza, ericoid mycorrhiza, nutrient availability.

ID 44 - Arbuscular mycorrhiza reduces rhizosphere priming effects on the decomposition of soil organic matter

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Introduction. Arbuscular mycorrhizal fungi (AMF) represent an important route for plant carbon (C) input into the soil. However, the C input via AMF as well as its impact on C sequestration and soil organic matter (SOM) stabilization remains largely unknown.

Methods. A mycorrhizal wild type progenitor (MYC) and its mycorrhiza defective mutant (reduced mycorrhizal colonization: rmc) of tomato were continuously labeled with ^{13}C-enriched CO_2 to trace root C input and rhizosphere priming effects (RPE) as affected by AMF symbiosis at two N fertilization levels. Mycorrhizal colonization and the ^{13}C incorporation into shoots, roots, soil and in CO_2 released from rooted soil were measured 8, 12, and 16 weeks after planting.

Results and discussion. AMF symbiosis decreased relative C allocation (% of total assimilated C) to roots but increased the net rhizodeposition. Increased SOM decomposition (compared to an unplanted control), i.e. positive RPE, were observed for both MYC and rmc plants, ranging from 16-71% and 25-101% of the unplanted control, respectively. The positive RPE induced by AMF decreased with plant age, likely due to the increased competition for nutrients between AMF and free-living decomposers. At the end of the experiment, net rhizodeposition was higher, whereas RPE was lower for MYC than rmc plants, indicating a higher potential for C sequestration by MYC plants.

Conclusion. We conclude that AMF symbiosis may facilitate C sequestration in soil not only by higher root C input, but also by lowering native SOM decomposition and RPE.

Key words: Carbon, isotopes, mycorrhiza, nitrogen, priming, rhizodeposition.

ID 106 - How arbuscular mycorrhizal fungi and rhizobia compete for host carbon resources in tripartite interactions of *Medicago truncatula*?

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Introduction. Legumes form tripartite interactions with arbuscular mycorrhizal (AM) fungi and nitrogen-fixing rhizobia bacteria. Both root symbionts transfer nutrients to their host, and in return, the host plant shares a significant proportion of its photosynthetically fixed carbon with these root symbionts. The carbon costs play a key role in symbiotic nutrient uptake and transport but our current understanding of the mechanisms that control the carbon allocation to different root symbionts is limited.

Methods. We performed split-root experiments with the model plant *Medicago truncatula* after colonization with the AM fungus *Rhizophagus irregularis* and the *rhizobium* model *Ensifer meliloti*. We examined how plant nutrient demand, fungal access to nutrients, and the nitrogen-fixing ability of rhizobia affected carbon allocation, and the gene expression of various plant carbon transporters from the Sucrose Uptake Transporter (SUT) and Sugar Will be Eventually Exported Transporter (SWEET) families.

Results and discussion. Tripartite interactions lead to synergistic growth responses and enhance phosphate and nitrogen uptake of the host plant. The carbon allocation to different root symbionts is controlled by the nutrient demand of the host plant and fungal access to nitrogen. When the plant is under nitrogen demand, more carbon is allocated to rhizobia bacteria, while the fungus becomes a stronger competitor for carbon resources, when the plant or the fungus has access to nitrogen. These shifts in carbon allocation are correlated to changes in SUT and SWEET transporter expression.

Conclusion. Understanding these mechanisms is critical to maximize nutritional benefits for leguminous plants in agricultural systems.

Key words: Carbon allocation, rhizobia, *Rhizophagus irregularis*, SUT, SWEET transporter.

ID 110 - Can we increase wheat growth and nutrient uptake using AMF inoculum?

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Introduction. With a continuously increasing human population alongside exhaustion of global rock phosphorus reserves; it is becoming imperative to reduce our reliance on nutrient inputs, while simultaneously maintaining food security. Arbuscular mycorrhizal fungi (AMF) associations have been found in many important crop species, leading to questions concerning AMF's role in sustainable agriculture, including whether the application of AMF inoculants could provide an alternative to large nutrient inputs. However, nutritional benefit from the symbiosis can vary significantly between crop species and cultivars; bringing into question the advantage of widespread inoculant applications.

Methods. This study assessed physiological responses of three wheat cultivars to inoculation with *Rhizophagus irregularis* in an agricultural soil with low nutrient inputs. The crops were grown in greenhouse conditions, and plant growth and nutrient concentrations were assessed. Radio/stable isotopes of carbon, phosphorus and nitrogen were used to quantify carbon-for-nutrient exchanges between wheat and AMF.

Results and discussion. Root colonisation and phosphorus concentrations increased in wheat when inoculated with *R. irregularis*. The extent of increases in colonisation and phosphorus differed between wheat cultivars. Despite the gains in root colonisation and phosphorus, carbon allocation to the fungus did not rise. AMF could pass nitrogen to the host plants; however, overall nitrogen concentrations were not affected by *R. irregularis* inoculation. Furthermore, above ground biomass did not increase with *R. irregularis* inoculation despite improvements in plant phosphorus nutrition, potentially due to the plant nitrogen limitations.

Conclusion. *R. irregularis* inoculants have the potential for improving wheat phosphorus nutrition, and possibly growth where nitrogen is not limiting.

Key words: 14C, 15N, 33P, *Rhizophagus irregularis*, wheat.

Oral Session 6 "Environmental stress"

ID 49 - Arbuscular mycorrhiza and altered plant drought responses – soil water flow resistances are mitigated beyond the ambit of roots

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Introduction. Arbuscular mycorrhizal fungi (AMF) influence soil properties and confer plant drought tolerance. We hypothesized that extraradical substrate colonization affects substrate water retention and hydraulic conductivity which leads to a shifted physiological drought response of plants.

Methods. We grew potted tomatoes colonized or not with *Rhizophagus irregularis* hydroponically on a substrate mix for 6 weeks under ample irrigation followed by a drying phase of 9 days with three sampling time points. Substrate water retention and hydraulic conductivity were measured in introduced sampling cores that allowed root and fungal ingrowth. A comprehensive dataset comprising plant morphology, gas exchange, and their physiological/hydraulic state served as an input for root water uptake modeling to compute substrate water fluxes from the periphery to root surfaces.

Results and discussion. Plant available water contents and substrate hydraulic conductivity increased in mycorrhizal pots with equal rooting densities. These effects scaled with colonization intensity. Water flows from the periphery to root surfaces necessary to realize particular whole-plant transpiration rates were sustained at lower substrate moisture in mycorrhizal substrates. Consistently, physiological plant drought responses also shifted to lower soil moisture. Finally, we show AMF influences on soil hydraulic properties to be soil specific and apparent under root growth exclusion.

Conclusion. Mycorrhizal plants experience/sense different degrees of drought at equal soil moisture than non-mycorrhizal plants because AMF alters water transport capacities of soils/substrates. These soil specific mycorrhizal effects can promote resource acquisition of plants but also exhaustive behavior. This also merits attention when irrigation treatments are used to study plant stress responses in mycorrhizal systems.

Key words: Drought, photosynthesis, soil colonization, soil hydraulic properties, water uptake.

ID 136 - Drought stress leads to differential gene expression in both plant and fungus in arbuscular mycorrhizal symbiosis

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Introduction. Arbuscular mycorrhizal fungi play an important role in natural and agronomic settings, offering host plants increased uptake of mineral nutrients, pathogen resistance, and abiotic stress tolerance. Improved tolerance to drought stress of colonized plants is well-documented, but the molecular underpinnings of this benefit are poorly understood.

Methods. To evaluate the impacts of drought on host and fungus, we inoculated carrots (*Daucus carota* cv. 'Napoli') with spores of *Rhizophagus irregularis* DAOM 197198. Carrots grew in a greenhouse. After carrots established, we imposed water restriction for ten days. Plants were flash frozen, and the fine roots of carrots were used for RNAseq. Root staining revealed an average colonization percentage of 35% for inoculated plants and no evidence of fungi was found in mock-inoculated controls.

Results and discussion. Well-watered carrots had significantly higher rates of photosynthetic assimilation, transpiration, and stomatal conductance than those in the drought group, regardless of the inoculation status. Well-watered carrots grew taller shoots and outweighed their drought counterparts (p-value < 0.001). Within the drought treatment, mycorrhizal carrots grew 15% longer shoots than mock-inoculated carrots (p-value < 0.05). There were 1,555 differentially expressed transcripts of carrot and 3,224 for fungus (p-value < 0.05) between well-watered and drought treatments. Preliminary analyses revealed that transcripts associated with fungal aquaporins differed in their response to drought, with AQPF2 upregulated and AQP1 downregulated under drought conditions (p-values < 0.001 and < 0.01, respectively). Fungal nutrient transporters also differed in response to drought.

Conclusion. Transcriptomic differences occurred in fungi and in mycorrhized plants subjected to drought.

Key words: Arbuscular mycorrhiza, drought, stress, transcriptomics.

ID 103 - Above the tree line: Drivers of ectomycorrhizal fungal communities in the European Alps

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Introduction. Studying distribution patterns of ectomycorrhizal (EcM) communities along environmental gradients is frequently used to identify the primary factors that determine their structure and composition. Little is still known, however, about their distribution patterns in harsh environments, such as alpine ecosystems above the tree line. In this study, we aim to identify the biotic and abiotic factors that shape EcM fungal communities across the European Alps. We hypothesise that i) EcM community richness will be negatively affected by elevation; ii) dominant EcM fungi will vary across environmental gradients; and iii) plant host population dynamics will be reflected in their associated EcM communities.

Methods. We sampled twenty-eight sites across five countries representing different environmental and climatic gradients within the distribution range of *Dryas octopetala*, *Bistorta vivipara* and *Salix herbacea* at different elevations from the tree line up to the nival zone. To assess the EcM communities associated with these hosts, we combined molecular identification of *ca* 9,000 individual ectomycorrhizas with high throughput DNA sequencing of bulk soil.

Results and discussion. Results indicate that elevation and soil pH are among the main drivers of EcM fungal communities in the European Alps. Above the tree line, plants harbour diverse EcM communities, with significant differences in richness and composition among the three plant hosts.

Conclusion. We generated the first baseline data for EcM fungi that can provide insights into the complexity of plant-fungal interactions in alpine ecosystems and help to better understand the resilience of these ecosystems to environmental shifts driven by climate change.

Key words: Alpine ecosystems, ectomycorrhiza, environmental drivers, soil, tree line.

ID 62 - Zn tolerance in *Suillus luteus* is linked to a high transcription of a CDF transporter gene through extensive gene multiplication and differences in cis-regulation

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Introduction. Heavy metal pollution affects selection regimes for soil micro-organisms. Metabolic and genetic adaptations in both trees and their ectomycorrhizal symbionts are of great interest for establishment of forests on metalliferous soils. With a global distribution and multiple adaptive phenotypes available, *Suillus luteus* is an excellent ectomycorrhizal model to study evolutionary dynamics of local adaptation.

Methods. We assessed pathways of detoxification and homeostasis in a subset of *S. luteus* isolates, displaying a strong contrast in Zn tolerance in order to identify mechanisms underlying adaptive Zn tolerance. A larger subset of 30 randomly selected isolates, collected from metal-contaminated and control sites, was used to subsequently document Zn tolerance phenotypes, assess the link among identified candidate genes and explore its genetic basis through targeted amplicon sequencing and qPCR.

Results and discussion. Phenotypes covering the continuum from Zn-sensitive to Zn-tolerant were identified. Zn tolerance was inversely correlated to cellular Zn accumulation. Gene expression of a putative Zn transporter, SlZnT2, explained 72% of the observed variation in Zn tolerance. SlZnT2 copy number varied among isolates and different promotor genotypes were identified.

Conclusion. Rapid Zn adaptation in *S. luteus* is reinforced by the cumulative effect of gene copy number variation and alterations in cis-regulation of the SlZnT2 genes and might be induced by environmental stress rather than being the result of standing variation.

Key words: Ectomycorrhiza, heavy metals.

ID 86 - Mycorrhizal symbiosis induces divergent patterns of uptake, transport and partitioning of Cd and Zn in *Populus trichocarpa*

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Introduction. Plants have several mechanisms to tolerate Cd and Zn toxicity, these being affected by symbiotic associations, such as with arbuscular mycorrhiza (AM). Here we hypothesised that AM alters Cd and Zn uptake and partitioning in *Populus trichocarpa*, modulating the expression of metal transporters and chelator genes in the host plant.

Methods. *P. trichocarpa* was grown under Cd and Zn contamination with and without AM inoculation (*Rhizophagus irregularis*). Metal accumulation and partitioning were assessed. Expression of genes involved in trace element transport and chelation were determined in roots and leaves. The function of metallothionein PtMT2b was verified by heterologous expression in yeast under Cd contamination.

Results and discussion. *P. trichocarpa* was highly tolerant to both metals. AM increased Zn accumulation (mg plant-1) but kept its partitioning pattern. AM did not affect Cd accumulation but restricted its translocation to shoots. High Zn and Cd down-regulated PtHMA4 in roots and up-regulated PtZIP1 in leaves, suggesting that these are involved in transporting both metals in poplar. PtMT2b was highly up-regulated in mycorrhizal roots (except under high Zn) and could be linked to high Cd immobilisation. PtMT2b enhanced Cd tolerance in yeast.

Conclusion. *R. irregularis* increased Cd retention in poplar roots but did not alter Zn partitioning – maintaining its high Zn concentration in leaves. The gene expression patterns observed offer a glimpse into the mechanisms behind trace element uptake and translocation dynamics in poplar, as affected by AM symbiosis. This system, along with the genes presented here, are candidates for future biotechnological applications, such as phytoremediation.

Key words: Arbuscular mycorrhizal fungi, heavy metal transporters, heterologous expression, metallothionein, pH.

ID 107 - Kin recognition in Douglas-fir through mycorrhizal networks in response to neighbor plant stress

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Introduction. Mycorrhizal networks create pathways for movement of molecules belowground. Previous research has shown that ectomycorrhizas appear to act as a conduit for the transfer of defense chemicals in response to herbivory or pathogen attack. Recent evidence that Douglas-fir seedlings respond differently, in terms of root colonization and uptake of root exudates, depending on their relatedness. Here we examined the potential for preferential transfer of information chemicals between Douglas-fir kin under herbivory stress.

Methods. In a greenhouse experiment, three seedlings (two kin, one unrelated) were grown together in pots. Ectomycorrhizal network formation was controlled using one of three mesh treatments: i) hyphae blocking, ii) hyphae permitting, or iii) a no mesh control. All seedlings were placed in gas labelling bags before the application of an herbivory treatment to one kin seedling “donor”: i) spruce budworm herbivory, ii) manual defoliation, or iii) no defoliation (control). The donor was pulse labeled with 99%-13C-CO_2 immediately after treatment. The concentration of 13C in needles, roots, and stems of receiver seedlings was quantified following a 24 hour chase period.

Results and discussion. Regardless of treatment we found elevated levels of 13C label in all plant tissues of kin receivers compared to unrelated receivers. Herbivory effects were somewhat significant, and transfer of 13C label occurred regardless of the mesh treatment.

Conclusion. The detection of 13C label in receivers regardless of treatment is indicative of a general stress response to the experimental conditions. Our work suggests that Douglas-fir seedlings preferentially transfer stress response chemicals belowground to kin.

Key words: Communication, Douglas-fir, ectomycorrhizal networks, herbivory, kin recognition.

ID 93 - Characterisation of soil-fungus-plant transfer of 238U and 232Th in a natural contaminated environment

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Introduction. Transfer of long-lived radionuclides (238U and 232Th) to plants in terrestrial environments is of major interest because of their potential accumulation into the trophic chain. The role of microbes in the rhizosphere is crucial to characterise the mechanisms behind the mobilisation of these elements. We studied the role of arbuscular mycorrhizal (AM) fungi on the elemental transfer to *Plantago lanceolata*, using a compartmentalised experimental system and soil with increased background levels of naturally occurring radionuclides.

Methods. Soil from abandoned South Terras mine, Cornwall (UK) was collected as a source of 238U and 232Th. *P. lanceolata* was inoculated with four different AM fungal cultures (Symplanta and International Bank for the Glomeromycota) to compare the uptake and transfer from root to shoot. ICP-MS and ICP-AES analyses were carried out to obtain total elemental concentration in soil and plant tissue. Soil pH, anions concentration and total organic and inorganic carbon were measured. Root AMF percentage colonisation and hyphal density were measured.

Results and discussion. The compartmentalised system used proved to be efficient to test the contribution of roots and hyphae to the transfer of elements to plants roots and shoots. Differences in elemental concentrations in roots and shoots as well as in plant growth were found. The presence of other non-essential elements (As and Pb) was also found to differ among treatments.

Conclusion. Compartmentalised systems are a good way to approach a complex interaction such as the AM fungus-plant symbiosis and are to be used for further experimental procedures.

Key words: Arbuscular mycorrhizal fungi, radionuclide transport, TENORM sites, thorium, uranium.

Oral Session 7 "Ecology"

ID 20 - Fungal biofertilizers - establishment and spread

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Introduction. Mycorrhizal fungi are vulnerable to human interference. In particular, introduction of fungal inoculants may represent a threat to the soil fungal metagenome. The use of fungal biofertilizers is common place, yet there is little data surrounding the spread of biofertilizers into the natural environment. Commercial inoculants may pose a threat to local fungal communities, which may not be resistant to alien introductions. Unfortunately, long term data on the fate and effects of commercial fungal inoculant use are lacking.

Methods. We evaluated the establishment and spread of a commercial AMF inoculant in a variety of agricultural and natural settings to evaluate its value as a biofertilizer and its threat to indigenous fungal communities, including: vineyards, grain cropping systems and natural grasslands. We also looked at corresponding changes in plant performance and community.

Results and discussion. Our results show that while inoculant establishment occurs in some cases, it is not easily predictable. Inoculant spread beyond point of introduction was also difficult to predict and was influenced by both indigenous soil and plant communities. In all cases, there was inconsistent evidence for crop benefit.

Conclusion. Given the ubiquity of commercial inoculant use, and its ability to establish and spread from point of introduction, the use of fungal inoculants should be carefully evaluated.

Key words: Arbuscular mycorrhiza, establishment, inoculant, invasion, spread.

ID 87 - Relationship of plant mycorrhizal benefits and the quantitative composition of arbuscular mycorrhizal fungal communities

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Introduction. The identity and diversity of root-colonizing arbuscular mycorrhizal fungal (AMF) symbionts may importantly influence the mycorrhizal benefits of the host plant. However, little attention has been paid to the relationship of plant mycorrhizal benefits and the abundances of particular AMF species within the community, i.e. the quantitative AMF community composition.

Methods. In order to address this topic, we conducted complementary greenhouse experiments with a synthetic community of five functionally different AMF species and *Medicago sativa* as host plant. Either the species abundances within the root colonizing AMF community were manipulated via the composition of the inoculum pool or the degree of mutualism of mycorrhiza was influenced by the abiotic context, and the relationship between the quantitative AMF community composition and the mutualistic functioning of the mycorrhizas was followed.

Results and discussion. The composition of the synthetic AMF community was determined largely by the growth rates of the species, and only to a minor degree influenced by the inoculum pool composition or related to the mutualistic functioning of the mycorrhizas. However, initially different abundances of the fungal species after the manipulation of the inoculum pool affected the host plant's mycorrhizal benefits, depending on the fungal species' traits.

Conclusion. We conclude that the system with a ruderal annual neither benefited from nor supported diversity of fungal functional traits. However, the results encourage further research with systems of increasing complexity and indicate an important role of plant life strategy in shaping or responding to quantitative AMF community composition.

Key words: Community composition, competition, fungal traits, mycorrhizal benefits.

ID 10 - Mycorrhizal fungi influence global plant biogeography

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Introduction. Island biogeography has traditionally focused primarily on abiotic drivers of colonization, extinction, and speciation. Establishment on islands, however, could also be limited by biotic drivers, such as the absence of symbionts. Most plants, for example, form symbioses with mycorrhizal fungi, whose limited dispersal to islands could act as a colonization filter for plants.

Methods. We tested this hypothesis using global-scale analyses of ~1.4 million plant occurrences including ~200,000 plant species across ~1100 regions.

Results and discussion. We find evidence for a mycorrhizal filter (i.e. the filtering out of mycorrhizal plants on islands), with mycorrhizal associations less common among native island plants than native mainland plants. Furthermore, the proportion of native mycorrhizal plants in island floras decreased with isolation, possibly as a consequence of a decline in symbiont establishment. We also show that mycorrhizal plants contribute disproportionately to the classic latitudinal gradient of plant species diversity, with the proportion of mycorrhizal plants being highest near the equator and decreasing towards the poles. Anthropogenic pressure and land use alter these plant biogeographic patterns. Naturalized floras show a greater proportion of mycorrhizal plant species on islands than in mainland regions, as expected from anthropogenic co-introduction of plants with their symbionts to islands and anthropogenic disturbance of symbionts in mainland regions.

Conclusion. We identify the mycorrhizal association as an overlooked driver of global plant biogeographic patterns with implications for contemporary island biogeography and our understanding of plant invasions.

Key words: Island biogeography, plant invasions.

ID 29 - Taxonomic variation in aerial dispersal of AM fungi – testing trait-based predictions

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Introduction. Dispersal is a fundamental process influencing both large-scale biogeographical patterns and local community assembly. For Glomeromycotinan fungi, examination of dispersal mechanisms is lacking, owing predominantly to their hypogeous lifestyle. A handful of studies to date have shown that arbuscular mycorrhizal (AM) fungal spores travel via wind, but little is known about taxonomic variation in AM fungal dispersal. Variation in dispersal is predicted across taxonomic groups due to marked variation in spore traits, but these predictions have yet to be empirically tested.

Methods. Using passive dust collectors, we made month-long collections of aerial AM fungi for 12 consecutive months (Jan-Dec) in a mesic urban environment. Collected spores were categorized to species morphologically, enumerated, and measured for functional traits (e.g. size). Aerial AM fungal community structure was also characterized using DNA extraction and high throughput Illumina sequencing of dust.

Results and discussion. Aerial AM fungal spore abundance was much higher Aug-Nov compared to other months of the year. Community structure of aerial AM fungi shifted between all four seasons. *Archeospora trappei* and *Glomus fasciculatum* were the most commonly observed taxa, though 18 other unique morphospecies were also observed. Aerial spores ranged in size from 25-400µm and weighted average spore diameter was 48.9µm.

Conclusions. Aerial dispersal of AM fungi differs among taxa and is associated with variation in spore size. Variation in dispersal capabilities among taxa could contribute to species-specific biogeographical patterns. Future trait-based approaches will be used to develop predictions for long-distance dispersal capabilities across taxonomic groups of AM fungi.

Key words: Aerobiology biogeography, community assembly, neutral processes.

ID 77 - Arbuscular mycorrhizal fungi colonize leaf litter in ectomycorrhizal forests

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Introduction. Early researchers of arbuscular mycorrhizas (AM) believed AM fungi accessed and transferred organically-bound nutrients from leaf litter directly to host plants, thereby creating a closed nutrient cycle. However, subsequent research found AM fungi are limited to assimilating inorganic nutrients and thus theoretically restricted to mineral soils. Observations of AM fungi in tropical forest litter cast doubt on this theory. We conducted a study in ectomycorrhizal Douglas fir forests near Bellingham, Washington, USA to determine if AM fungal colonization of leaf litter extends beyond the tropics.

Methods. Air-dried leaves placed in 30 μm nylon mesh litter bags were deployed for 2.5-5 months during the wet season (winter). AM hyphal densities were assessed via light microscopy and AM fungi were molecularly identified in the leaves and underlying soil.

Results and discussion. AM fungi were found in dried leaves at all sites and their abundance was correlated with AM fungal sequence abundance in underlying soil. Despite large community variation from site to site, dominant AM fungi virtual taxa (VT) assemblages in litter were distinct from those in soil. Yet, VT detected only in leaf litter were phylogenetically similar to VT detected only in soil, suggesting niche differentiation within phylogenetic groups.

Conclusion. We corroborate and extend findings of AM fungi colonizing leaf litter across climatic regions. In addition, we find AM fungal taxa may differ in their tendency to colonize leaf litter, which could result in niche differentiation between substrates. These results change our understanding of the potential role of AM fungi in nutrient cycles.

Key words: Arbuscular mycorrhizal fungi, forest ecology, litter, nutrient cycling.

ID 163 - Primary succession of AM fungal communities on newly formed islands

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Introduction. Newly emerged islands provide a unique temporal and distance gradient to explore dispersal and community assembly of arbuscular mycorrhizal fungi.

Methods. Change in community structure during the early phases of colonization was followed for 6 years on an artificial island to test the hypothesis that the community will undergo a transition from stochastic to deterministic assembly. Using a combined molecular and trait-based characterization of AM fungal communities, we have quantified the relative role of stochastic and deterministic ecological processes in driving fungal community assembly during dispersal and subsequent succession.

Results and discussion. We found a deterministic community structure where age of the island explains most variation in community composition over time. The parallel increase in beta diversity in the island indicates a higher importance of deterministic factors in time. Although we did not find changes in average spore sizes or differences in spore sizes between species in communities, the relative abundance of sporulating species clearly decreased in time.

Conclusion. The study shows that dispersal of AMF seems to be limited at the beginning of the succession, favoring sporulating species. Indeed, importance of deterministic factors with time is congruent with the hypothesis that the effect of the stochastic input of propagules is relaxed, when more dispersal limited species reach the island.

Key words: Community structure, dispersal, islands, sporulation, succession.

ID 43 - Mycobiomes of boreal forest soils: Unraveling patterns in fungal communities following natural and anthropogenic disturbances

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Introduction. Novel disturbance regimes may transform boreal forests with uncertain consequences for soil fungal communities. With an expected increase in the frequency and severity of disturbances, pronounced shifts in the composition of fungal communities may occur. Here, we profiled fungal communities in soils of lodgepole pine (*Pinus contorta*) forests following disturbances including mountain pine beetle (*Dendroctonus ponderosae*) outbreak, wildfire, clear-cut harvesting, and salvage-logging after beetle attack. In particular, insect outbreaks and wildfire are disturbances expected to increase in the future.

Methods. Using DNA sequencing, we characterized soil fungal communities in replicated sites representing each disturbance paired with an intact forest. We focused on capturing the structure and diversity of ectomycorrhizal, arbuscular mycorrhizal, saprophytic, and pathogenic fungi. We also quantified fungal biomass by ergosterol concentration across all sites.

Results and discussion. Dominance shifted from ectomycorrhizal to saprophytic fungi across all disturbances compared to intact forests. However, in sites disturbed by beetle outbreak, the shift in dominance was less pronounced. Ectomycorrhizal diversity tended to decrease while arbuscular mycorrhizas increased relative to controls for most disturbances. The abundance of saprophytic fungi increased with salvage-logging and declined with wildfire. However, community structure and diversity of pathogenic fungi remained constant across the disturbances. In disturbances where tree biomass was removed (i.e., wildfire, clear-cut harvesting, and salvage-logging), fungal biomass declined.

Conclusion. Disturbances that impact the forest floor cause pronounced losses in fungal biomass and diversity. Shifts in fungal community composition may impact multiple ecosystem functions including nutrient/carbon dynamics and forest regeneration, effects that could be exacerbated under increased disturbance regimes.

Key words: DNA-metabarcoding, ergosterol, forest disturbances, fungal diversity, soil fungi.

ID 166 - Changes in plant community mycorrhization along a productivity gradient in temperate grasslands in Estonia

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Introduction. The prevalence of mycorrhizal symbiosis in plant communities (community mycorrhization), can help to understand the role of mycorrhizal symbiosis in ecosystem function. Here we analyzed (1) how the soil fertility (soil total N, P & K) affects community mycorrhization, and (2) how plant biomass and plant richness are related with community mycorrhization along a productivity gradient.

Methods. We estimated plant diversity, soil fertility and the proportion of plant biomass associated with mycorrhizal symbiosis (arbuscular mycorrhization index, AMI), in 29 secondary grasslands on abandoned arable fields in the South of Estonia, representing a steep productivity gradient (80.3 – 500.4 g/m^2). The relationships of those factors with AMI were analyzed using generalized linear and additive models.

Results and discussion. We found a positive linear correlation between soil N and AMI index, however soil P and K showed more complex nonlinear relationships. Plant biomass and richness showed a positive and negative linear relationship with AMI index, respectively.

Conclusion. In our study, AMI responses to soil fertility were complex, with higher values at higher soil N concentrations, and trends to non-linear decreases with increasing soil P and K values. We found that richer grassland communities had lower degree of mycorrhization, while plant productivity showed a positive relationship with community mycorrhization, suggesting that AM symbiosis enhanced few productive and competitive plant species along the productivity gradient.

Key words: Arbuscular mycorrhization index (AMI), grassland, plant diversity, soil fertility, soil nitrogen.

ID 186 - Functional traits of arbuscular mycorrhizal fungal communities along succession in a tropical dry forest

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Introduction. Functional traits in natural communities of arbuscular mycorrhizal fungi (AMF) has been little studied. Tropical dry forests (TDF) are highly dynamic ecosystems due to land-use change. The environmental heterogeneity generated by land conversion produces changes in the composition of AMF communities and in their response and effect traits.

Methods. To prove this, we have a field soil sampling to analyze the composition of AMF spores in sites with different successional stages, primary forest, pasture management, and land abandonment succession. We also take soil inoculum from each site to establish two experiments in divided pots: 1) to explore response traits of extraradical mycelium to water stress, and 2) to study effect traits (soil aggregation and enzymatic activity) of AMF communities. The response traits were measured after four months by microscopy and image analysis and the effect traits were analyzed during three years by aggregate fractions, enzymes, and fatty acid test.

Results and discussion. Contrary to our hypothesis, AMF communities were resistant and similar (62 – 89%) between successional age, soil properties were important only for *Gigaspora* species. Extraradical mycelium traits were also highly stable in their response to the humidity in all the communities. However, some effect traits as phosphatase activity and macroaggregates formation are recovered along successional age.

Conclusion. This work shows that AMF community composition and mycelium traits are highly stable within this environmental heterogeneity. Though, its functions are recovered through succession. This evidence suggests that AMF communities of TDF in Chamela, Jalisco are resilient to land-use change.

Key words: Arbuscular mycorrhizal fungi, diversity, ecological succession, extraradical mycelium, functional traits.

Oral Session 8 "Diversity"

ID 151 - Benefits of native mycorrhizal amendments to grassland restoration increases with field inoculation density

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Introduction. There have been frequent calls to include microbes within ecological restorations. Our past work identified that native arbuscular mycorrhizal (AM) fungi benefit restored prairie plant establishment better than fungi from disturbed soils or commercial products. Additionally, we have found that late successional plants are sensitive to specific species of mycorrhizae in their microbiome and that specific mycorrhizae can facilitate restoration succession. However, methods used to distribute native inoculum into restorations remains to be optimized.

Methods. In a grassland restoration, we applied eight different densities of native AM fungal amendment, ranging from 0 to 8192 kg/hectare, representing conventional restoration practices (no AM fungi addition), commercial product density recommendations, and higher densities more typically applied in scientific investigation.

Results and discussion. We found seeded richness and abundance increased with inoculation density. We found that lower inoculation densities (those recommended by commercial mycorrhizal products) tended not to be significantly different from the controls whereas we found significantly greater richness and abundance of seeded prairie species with the higher inoculation densities of AM fungi (densities more typical of scientific studies).

Conclusion. Providing grassland restorations with native mycorrhizae improved restoration success. Because inoculation densities recommended on commercial mycorrhizal products did not consistently benefit restoration, we conclude that greater inoculum application densities or alternative methods of introducing native mycorrhizal fungi into restorations are needed. These data emphasize the importance of conserving endangered plant and mycorrhizal communities. By identifying the key microbiome components of native systems, we can apply more holistic approaches to restoration that improve restoration success.

Key words: Field inoculation, grasslands, native mycorrhizae, plant diversity, restoration.

ID 89 - Fungal competition and host quality two underappreciated factors driving AMF diversity

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Introduction. AMF richness and diversity can be important determinants of plant community productivity and diversity, but factors that drive AMF richness and diversity are poorly understood. Plant richness may be important, but high AMF richness sometimes observed in mycotrophic monocultures suggests that host quality could also play a role. We quantified the relative importance of plant richness and host quality for AMF richness and diversity and predicted that they would be greatest in high-quality, mixed plant communities.

Methods. We selected five high-quality and five low-quality plant species based on the fungal biomass they support and grew them in monoculture or mixed communities together with eight AMF species. After three months, we harvested all plants and counted spores and estimated spore volume of individual species to quantify AMF abundance, richness, and diversity (Shannon's H).

Results and discussion. AMF spore numbers and volumes were greater in high-quality and mixed plant communities, indicative of more resources being allocated to AMF in those treatments. Contrary to our predictions, this corresponded with lower AMF diversity and no difference in richness. Host quality also affected AMF community composition; small-spored species did particularly well on high-quality hosts, which may have restricted less competitive species and reduced AMF evenness.

Conclusion. Host quality was a stronger driver than host richness for AMF diversity, but responses were opposite those predicted. This illustrates that while resources are important, outcomes may depend on the competitive ability of co-occurring AMF species. Additional work is required to determine if and to what extent AMF compete.

Key words: AMF diversity, fungal competition, host quality, plant richness.

ID 40 - The ecology and diversity of the genus *Clavulina* (Cantharellales, Basidiomycota) across tropical and temperate forests in Mexico

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Introduction. The macroscopic diagnosis and richness of *Clavulina* have been increased during the last 15 years, involving the description of new species mainly from tropical regions in South America. In contrast, in temperate ecosystems, this genus has been considered as relatively species-poor.

Methods. We synthesize the knowledge on the diversity and ecology of the genus, including molecular systematics (Maximum Likelihood and Bayesian Inference analyses of the ITS region), morphological taxonomy, community ecology (from ectomycorrhizae and basidiome sampling), and stable isotopes analyses (∂15N and ∂13C) through mass spectrometry.

Results and discussion. We have described nine new species for the genus from Mexico, which differ from the South American species in their relatively homogeneous clavarioid forms, and some of which resemble previously described species from Europe. Some of these species may contribute to the decomposition of soil organic matter, as we have seen through ∂ 15N and ∂ 13C results. The new species included are *Clavulina arboreoparva*, *C. flavopusillis*, *C. mahiscolorata*, *C. oreomunensis*, *C. parvispora*, *C. sphaeropedunculata*, *C. stipestrigosa*, *C. subtilis*, and *C. tuxtlasana*. Furthermore, we present the description of another new species (*Clavulina* sp. nov. 1) included in the "*cristata* complex", collected from Mexican subtropical forests.

Conclusion. Our results highlight the ecological relevance and taxonomic richness of this ectomycorrhizal genus, which is likely more diverse in North America than previously thought.

Key words: Clavulinaceae, ECM-SAP divide, species complex, taxonomy.

ID 137 - *Rhizoscyphus ericae* = *Hyaloscypha hepaticicola*: consequences for taxonomy, ecology and evolution of the youngest mycorrhizal symbiosis

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Introduction. Data mining for a phylogenetic study including the prominent ericoid mycorrhizal fungus *Rhizoscyphus ericae* revealed nearly identical ITS sequences of the bryophilous *Hyaloscypha hepaticicola* suggesting they are conspecific. Additional genetic markers and a broader taxonomic sampling furthermore suggested that the sexual *Hyaloscypha* and the asexual *Meliniomyces* may be congeneric.

Methods. In order to further elucidate these issues, type strains of all species traditionally treated as members of the *Rhizoscyphus ericae* aggregate (REA) and related taxa were subjected to phylogenetic analyses based on ITS, nrLSU, mtSSU, and rpb2 markers to produce comparable datasets while an *in vitro* re-synthesis experiment was conducted to examine the root-symbiotic potential of *Hyaloscypha* in the Ericaceae.

Results and discussion. Phylogenetic evidence demonstrates that sterile root-associated *Meliniomyces*, sexual *Hyaloscypha* and *Rhizoscyphus*, based on *R. ericae*, are indeed congeneric. To this monophylum also belongs the phialidic dematiaceous hyphomycetes *Cadophora finlandica* and *Chloridium paucisporum*, which are confirmed conspecific. We provide a taxonomic revision of the REA; most importantly, *Meliniomyces* and *Rhizoscyphus* are reduced to synonymy under *Hyaloscypha*. Surprisingly, the mycological and mycorrhizal sides of the same coin have never been formally associated, mainly because the sexual and asexual morphs of these fungi have been studied in isolation by different research communities.

Conclusion. Evaluating all these aspects allowed us to stabilize the taxonomy of a widespread and ecologically well-studied group of root-associated fungi and to link their various life-styles including saprobes, bryophilous fungi, root endophytes as well as fungi forming ericoid mycorrhizae and ectomycorrhizae.

Key words: Ecology, ectomycorrhizal, ericoid, evolution, mycorrhiza, *Rhizoscyphus ericae*.

ID 46 - Diversity of *Rhizopogon* in the Madrean Sky Islands, Southwestern United States and Northwestern Mexico

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Introduction. The Madrean Sky Islands (MSI) comprise mountain “islands” whose pine-oak forests appear in stark contrast to the surrounding “sea” of Sonoran Desert vegetation. *Rhizopogon* (Boletales, Basidiomycota) consists of obligate ectomycorrhizal (EcM) symbionts that associate exclusively with members of the family Pinaceae. This project seeks to describe the diversity of *Rhizopogon* across the sky islands and to characterize the impact of sky island geography on *Rhizopogon* biodiversity, population structure, and genetic diversity.

Methods. Nine islands across the MSI were selected and two sites were sampled per island. At each site three transects were established, and six stops were made per transect (18 sample points per site). At each stop we searched for sporocarps and collected a soil sample. Sporocarps were processed and used in DNA extractions. Soil samples were used in bioassay-based sampling with *P. muricata*, *Ps. menziesii* var. *menziesii* and *Ps. menziesii* var. *glauca* as host trees. Six months post-inoculation, EcM root tips were dissected for tissue culture and DNA extraction. The ITS rDNA fungal barcode was amplified and sequenced for all sporocarp collections and EcM root tips. ITS sequences were appended to a reference dataset and analyzed phylogenetically.

Results and discussion. Based on sporocarp data, eleven species of *Rhizopogon* are reported for the nine sky islands with one being found on all nine islands, five found on two to eight islands, and five restricted to a single island. ITS data from root tips bioassays are currently being sampled and will be presented alongside sporocarp data for a more complete assessment of *Rhizopogon* diversity.

Key words: Biodiversity, ectomycorrhizal fungi, island biogeography, truffles.

ID 90 - Assessing inter and intraspecific diversity of AM fungi in association with maize in Mexico and France

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Introduction. Arbuscular Mycorrhizal Fungi (AMF) diversity is a good soil fertility marker. The higher the number of taxa is the more beneficial for crop plants it is supposed to be. Impact of different cultural practices on AMF diversity was extensively reported in literature at the genera and species level. Nowadays, Illumina Miseq sequencing technologies, reference AMF genomes and the exponential increase of ITS sequences in databases allow addressing the question of diversity at the strain level. In order to test agricultural practices and geography on AMF diversity in maize roots and soils.

Methods. We carried out a new pipeline named EGRETTA. This pipeline was designed to analyse AMF diversity at the genus/species level by OTU assignment on a personal ITS2 database, and at the strain level with ITS2 haplotyping. We tested haplotypes with monosporal sequencing. We sampled 50 crop plots from Mexico and France.

Results and discussion. Our results show that ploughing reduces diversity in french plots. Diversity in soils is much higher than in maize roots with geographic specificities. However, AMF species found in maize roots are the same in all Mexican and French plots. At the strain level, we found distinct haplotypes in the various samples according to geography and maize genotypes.

Conclusion. Our EGRETTA pipeline will now allow measurement of very precise modifications in AMF community structures and identification of AMF strains.

Key words: Agroecology, AM fungi, diversity, EGRETTA, haplotyping.

ID 104 - Rescuing the ectomycorrhizal diversity from south American Nothofagaceae forest and unraveling confusing identities: the case of *Cortinarius magellanicus* complex

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Introduction. Native Patagonian forests are dominated by 11 species of Nothofagaceae and their establishment depend on ectomycorrhizae (EM). It is well known that *Cortinarius* is the most diverse genus, but our knowledge on Patagonian *Cortinarius* diversity is still poor and mainly based on Moser & Horak´s work from the early 1960ties.

Methods. We compiled and analysed 87 articles from peer-reviewed journal over the past 62 yr about EM fungal taxa from Nothofagaceae forests, both from fruiting bodies records or molecularly identified EM root tips. On the other hand, we performed an extensive sampling of 254 *Cortinarius* vouchers growing in Argentinian Nothofagaceae forests during March-May of 2017-2018. Morphological-anatomical analysis and Barcoding sequences from *Cortinarius* vouchers including Typus material and closely related sequences from GenBank were analysed.

Results and discussion. The overall analysis renders 479 taxa, included in 45 genera, 34 of them Basidiomycetes and 11 Ascomycetes. *Cortinarius* species resented 65% of total reported taxa. *Cortinarius* analysis revealed that 29% of the sequenced vouchers are 45 new taxa. Morphological variability within species were solved differently. For example, *Cortinarius magellanicus* represents a complex of species with different morphological-anatomical-ecological features, while *C. xiphidipus* variability remain within a single species with wide range sizes and habitus. Variables as layer of context, spore size, light properties and lamella colour seem to be the best taxonomic features.

Conclusion. Considering the gaps of reference molecular data about EM taxa from Patagonia, the assessment of the real EM diversity and host specificity deserves further studies combining phylogenetic analysis based on wide ecological surveys.

Key words: *Cortinarius*, diversity, ectomycorrhizal fungi, *Nothofagus*.

Thursday July 4, 2019

Oral Session 9 "Global worries"

ID 161 - The effect of land use change on the arbuscular mycorrhizal fungi community in a tropical rainforest, Los Tuxtlas, Veracruz, Mexico

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Introduction. Land-use change constitutes one of the primary explanations of ecosystem loss. Tropical rainforest (TRF) has been severely affected by the establishment of agropecuary systems, which cause the alteration of soil properties and organisms, such as the arbuscular mycorrhizal fungi (AMF). The aim of this study was to determine the effect of land use change on AMF through different functional variables.

Methods. We selected four land uses (TRF, secondary vegetation -SV-, livestock pasture, and crop fields). Our AMF response variables were species diversity and composition, fatty acid concentration, fungal respiration, extraradical mycelium, intraradical colonization, and inoculum potential; also we determined some physical and chemical soil properties. We performed a canonical correspondence analysis (CCA).

Results and discussion. We found 45 species (14 genera). Crops had the lowest diversity (0.49), while SV the highest (1.2). Abundance and composition depended on land use. *Claroideoglomus etunicatum* was the most abundant in TRF, while *Acaulospora scrobiculata* predominated in the TRF and SV. Moreover, *Funneliformis geosporum* was mainly found in agropecuary systems. The two first axes of the CCA explained 46% of the variance. Crops had the lowest values for almost all response variables, and TRF had low fatty acids and mycelia biomass but high fungal respiration, pH, C, P, NO_3 and silt content. Also, pastures had the highest number of estimated propagules while crops the lowest (46 435 and 95 per 50 g soil, respectively).

Conclusion. Land-use change represents the major negative driver of soil ecosystem functionality in TRF, especially the establishment of crop fields.

Key words: CCA, diversity, fatty acids, land-use change, tropical rainforest.

ID 121 - Restoration of arbuscular mycorrhizal fungal communities in response to conversion from arable cultivation to grass/clover leys

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Introduction. It is widely recognized that arable agriculture changes microbial diversity, and that use of uncultivated leys/fallows in a rotation is one method of re-introducing soil fertility and function. We address the question: how do microbes respond to cessation of disturbance: do existing, but disturbance sensitive, taxa increase in abundance, or do taxa migrate into the ley from undisturbed field boundaries, e.g. hedgerows?

Methods. A field experiment was set up at the University of Leeds Farm Research Unit (FRU) Wise Warren Farm. In 4 fields, grass/clover ley transects into the field from the hedgerow, were planted into the arable field. Root samples were taken at 5 times and distances, over 2 cropping cycles between April 2016 and July 2017 and the AM fungal communities assessed using MiSeq amplicon sequencing.

Results and discussion. The AM fungal community in the ley diverges from the arable within a single season. Detailed analysis of this pattern will be presented, showing whether this pattern represents recovery of a community already present in the field or if there is evidence for migration of taxa into the field from the hedgerow refuge.

Conclusion. Disturbance is known to affect arbuscular mycorrhizal (AM) fungal communities, selecting for taxa resilient to disruption of the mycelial network, and periodic removal of an available root niche. We conclude that in this system, over a 2-3 year cropping cycle, the annual cycle and field effects are more pronounced than succession, and we discuss the implications of this work for efforts to improve soil health.

Key words: Arbuscular mycorrhizas, communities, disturbance, migration, restoration.

ID 60 - Arbuscular mycorrhizal fungi in agriculture and restoration: consider the species pool

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Introduction. The roles of soil biota, including arbuscular mycorrhizal (AM) fungi, in agricultural and restoration systems are increasingly appreciated. However, understanding of impact of management practices on AM fungi, as well as potential of AM fungi to contribute to crop production or vegetation restoration is still fragmentary.

Methods. I will present results from experiments exploring dynamics of AM fungal diversity and abundance under the conditions of conventional and organic farming practices and vegetation restoration settings.

Results and discussion. Farming practices showed a consistent effect on richness and community composition of AM fungi in six European countries studied. Notably, AM fungal communities differed among countries (sites), but within each country, communities shifted depending on farming practices. In restoration systems, inoculation with regional-origin AM fungal mix was successful and effective, bringing about considerable increase in plant cover and diversity.
I will discuss the results in the context of species pool concept, which indicates important regional and biome-wise differences in the availability of AM fungal species diversity.

Conclusion. In conclusion, regional diversity and availability of AM fungi needs to be considered for efficient choice of management in both conventional and organic farming systems as well as in vegetation restoration.

Key words: Agriculture, inoculation, land use, restoration, species pool concept.

ID 223 - Mechanisms of local adaptation in mycorrhizal systems

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Introduction. Cooperative systems like mycorrhizas become locally adapted because they evolve in response to particular environmental conditions. What happens to locally adapted mycorrhizas when the environment changes? How do species invasions, extinctions, agricultural intensification, land-cover change, and climate change impact mycorrhizal function? Do mycorrhizas ameliorate or exacerbate these anthropogenic changes?

Methods. This talk will 1) describe how mycorrhizal function is an emergent property of complex systems of interacting organisms and environmental conditions, 2) examine two examples of mycorrhizal responses to changes in biotic and abiotic conditions, and 3) hypothesize the mechanisms by which these changes may uncouple locally adapted mycorrhizal systems and influence mycorrhizal function. Arbuscular mycorrhizal (AM) fungi in the Serengeti are predicted to be adapted to herbivory by large mammals; and the AM fungi in restored prairie at the Fermi National Laboratory are predicted to be adapted to nitrogen limited soil.

Results and discussion. We discovered that experimental removal of large herbivores in the Serengeti, and nitrogen fertilization of the Fermi prairie changed the biomass and species composition of AM fungi in the soil and inside roots of native grasses. These findings support the prediction that the structure of locally adapted AM fungal communities change in response to changes in biotic and abiotic conditions. Subsequent experiments are necessary to link the structure of AM fungal communities with their function in the context of a changing environment.

Conclusion. In the temperate forests of Mexico coexist of the arbuscular mycorrhizal and ectomycorrhizal symbiosis; they also harbored a great diversity of AMF and ectomycorrhizal fungi.

Key words: Anthropogenic change, emergent properties, evolution, local adaptation, Serengeti.

ID 113 - Diversity indices using arbuscular mycorrhizal fungi to evaluate the soil state in banana and coffee crops in Colombia and Mexico

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Introduction. Banana and coffee are widely and intensively cultivated in the tropics. Traditional production employs a high input of industrial supplements, the excess of which contaminates the environment, altering existing edaphic populations and their functions. Some producers have incorporated other plant species in polycultures to reduce costs and achieve an alternative production without the high consumption of chemical supplements.

Methods. With the aim of evaluating the effect of management system (Banana), the intensity of management (Coffee) and determining the edaphic factors that influence the richness and diversity of arbuscular mycorrhizal fungi (AMF), 17 banana and 4 coffee plantations in Colombia, and 4 coffee plantations in Mexico with different contents of edaphic phosphorous were sampled.

Results and discussion. Between 11-18 and 36-58 AMF species were found on average per plantation in banana and coffee crops respectively, indistinct of intensive agricultural systems or management, the dominant species in communities did appear to be influenced by the cultivation or management system. In banana crops pH was the only factor that correlated positively with richness and the Margalef index; in a larger spatial scale (Coffee crops) were the organic carbon and humidity who highly correlated positively with species richness.

Conclusion. It is concluded that soils of banana crops with high phosphorus content, pH shows a direct relationship with species richness and the Margalef index; in soils of coffee crops with variable phosphorus content are the organic carbon and humidity who show a direct relationship with species richness. Generalization in the use of ecological indices with AMF in crops is questioned.

Key words: Crop management, ecological indices, richness indicator.

ID 111 - Effect of drought and season on arbuscular mycorrhizal fungi in a subtropical secondary forest

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Introduction. Arbuscular mycorrhizal (AM) fungi can greatly affect plant productivity, diversity, and ecosystem processes. AM fungal responses to water availability may mediate shifts in ecosystem functioning to global climate changes. However, the impacts of drought on AM fungi in subtropical forest remains largely unknown.

Methods. Here based on a 4-year drought experiment in a Chinese subtropical secondary forest, AM fungi in both soil and roots of *Schima superba* collected from two seasons of May (summer) and December (winter) were examined using the 18S rDNA high-throughput sequencing and morphological methods.

Results and discussion. Drought significantly decreased AM fungal extraradical hyphal (ERH) density, spore density, and root colonization rate in both seasons. These AM parameters were significantly higher in summer than in winter in the control treatment, but only ERH density exhibited the same seasonal trend in the drought treatment. Totally, 45 AM fungal operational taxonomic units (OTUs) were obtained at a 97% sequence similarity level. Drought and season had no significant effects on AM fungal OTU richness in soil and roots. AM fungal community composition in soil and roots was significantly affected by season but not by drought.

Conclusion. AM fungal ERH density, spore density, and root colonization rate responded strongly to drought and seasonal changes. In contrast, the AM fungal community composition responded more to seasonal changes than to drought. These findings enhance our understanding of functional microbial responses to drought in subtropical forest ecosystem under global change scenarios.

Key words: Arbuscular mycorrhizal fungi, drought, illumina Miseq sequencing, season, subtropical forest.

ID 71 - Mycorrhizas shape plant communities: lessons from cross-continental grassland studies

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Introduction. Grasslands cover 35% of the earth's land surface, provide essential ecosystem services, and play an important role in global biogeochemical cycles. Understanding the role of AM fungi as drivers of grassland plant communities and ecosystem functions are critical for conserving, rehabilitating, and managing these imperiled landscapes. Our research assesses AM symbioses in North America and China to improve restoration and management of highly diverse and productive grasslands.

Methods. We characterized edaphic conditions at multiple research sites in NA and China. Mycorrhizal communities were assessed combining microscopic, chemical, and molecular techniques in semi-arid and mesic grasslands. Corresponding assessments of plant communities included species composition and diversity indexes across selected management and restoration practices. Our long-term and mechanistic studies link mycorrhizal ecology with grassland productivity and functionality.

Results and discussion. Our findings suggest AM symbioses have a significant and substantial role in shaping grassland plant communities in both semi-arid and mesic systems, with cascading benefits for soil aggregation, carbon storage, plant productivity, and ecosystem multi-functionality. Specific rehabilitation strategies, such as reseeding native plants, are highly successful when locally-adapted, diverse, and abundant AM fungi are present.

Conclusion. Overall, our results indicate AM fungi shape grassland plant communities while improving grassland ecosystems and subsequent societal benefits. Furthermore, mycorrhizas are critical for repairing degraded grasslands and conserving diverse plant communities. These observed trends are consistent across continental scales and wide-ranging circumstances including different edaphic, climatic, and land use histories. Mycorrhizas can be managed to regenerate landscapes, enhance environmental quality, and sustainably provide human needs.

Key words: China, grasslands, North America, restoration.

ID 19 - Rooting for the home team: belowground allocation and root traits in native and nonnative woody species

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Introduction. Invasive woody shrubs often exhibit higher assimilation rates and faster growth compared to native shrubs. One underexplored explanation for this difference in growth strategy involves belowground interactions with microorganisms such as arbuscular mycorrhizal fungi (AMF) in the invaded range. The objective of this study was to determine the extent to which AMF influence above and belowground production and root functional traits differently in invasive compared to native shrub species.

Methods. Using softwood cuttings from a common garden in Syracuse, NY, we grew 20 species of native and nonnative shrubs and lianas in mycorrhizal and nonmycorrhizal conditions under high and low nutrient regimes. Plants were harvested and measured after 4 months, and the intact root systems were analyzed for differences in root functional traits.

Results and discussion. Nonnative shrubs had greater biomass overall, and AMF increased both above and belowground biomass more for nonnatives than natives. Mycorrhizal plants had a smaller root mass fraction compared to nonmycorrhizal plants, which was again more pronounced in nonnative species. AMF significantly influenced a host of root functional traits, especially in nonnative shrubs.

Conclusions. Our results indicate that nonnative, invasive shrubs respond more positively than native congeners to colonization by AMF. The invasive shrubs also exhibited a greater plasticity in the majority of measured root functional traits in response to colonization compared to native species. Understanding these different growth and allocation patterns may help us better understand how invasive plant resource strategy translates to belowground microbial contexts.

Key words: Arbuscular mycorrhizae, invasion ecology, root functional traits, temperate forests, woody shrubs.

ID 37 - Networking South American mycorrhizal research

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Introduction. The South American Mycorrhizal Research Network (https://southmycorrhizas.org/) that originated in Chile in 2017, is a horizontal scientific community directed towards the progress of mycorrhizal applications, research, and outreach in South America.

Methods. The main activities of this network include: events organization, outreach, diffusion of career opportunities, and connecting local laboratories/teams with the hopes of establishing join research at the regional scale.

Results and discussion. Currently, the network has 176 members from 30 countries. We have organized two South American symposiums in Valdivia, Chile (2019), and in Bariloche, Argentina (2019), that included regional and international well-established mycorrhizologists. Several workshops, courses, student exchanges, and international collaborations (within and outside South America) have been achieved because of our network. We also have published some indexed articles as well as a recent Springer book on Mycorrhizal fungi in South America. We are forming a much-needed plant mycorrhizal traits database for our continent, and we are also integrated on global-scale monitoring projects aimed to jointly study soil ecosystem functions/services and biodiversity -an approach barely implemented so far.

Conclusion. Over the last four decades, mycorrhizal research in South America has been 2.5 times smaller than that of Europe (based on number of indexed articles), despite having a bigger area. European mycorrhizal research has mostly focused on anthropogenic effects on the symbiosis, while the research in South America is mostly focused on community structure, as there are still entire countries and biomes very underrepresented. Our regional networking effort hopefully would help to overcome all these knowledge gaps.

Key words: Biodiversity-ecosystem functioning, community structure, knowledge gaps, networking, South America.

ID 277 - Unexpectedly deep mycorrhizal fungi may mediate plant acquisition of permafrost nitrogen

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Introduction. As arctic tundra soils warm, thawed permafrost releases nitrogen that could stimulate plant productivity and offset soil carbon losses. The roles of mycorrhizal fungi in providing access to N from newly thawed permafrost is unknown.

Methods. We characterized depth profiles of roots and fungi of ecto- and ericoid mycorrhizal hosts and soil fungal communities at the thaw front in tundra at EML, Alaska. We tested the relationships between root and deep soil fungal composition and plant uptake of a 15N tracer applied at the permafrost boundary. Fungal composition was characterized by DNA and RNA sequencing of the ITS.

Results and discussion. Fungal DNA and RNA profiles from soil at the thaw front were very similar. Of 709 deep soil fungi, 142 were mycorrhizal. Of the 194 mycorrhizal taxa observed on roots, 72 were observed at the thaw front, suggesting mycelial connectivity between shallow roots and deep soil. Although isotope acquisition by roots was not related to the overall fungal connectivity with the thaw front, individual OTUs were significantly correlated with root 15N signatures. The occurrence of EMF and ERM fungi in RNA profiles of deep soil demonstrates the potential for mycobionts to access permafrost-derived N. Tracer was gradually assimilated by EMF and ERM hosts the year after addition. This may be due to rapid fungal immobilization of tracer and subsequent transfer to host plants over the growing season.

Conclusions. The mycorrhizal symbiosis may provide a mechanism for the vertical redistribution of deep, permafrost-derived nutrients with the potential to fertilize tundra as it warms.

Key words: Arctic tundra, global carbon cycle, global warming feedbacks, nitrogen uptake, permafrost.

Oral Session 10 "Sustainable management I"

ID 313 - Seed coating of mycorrhiza: A technique to a technology

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Introduction. During ICOM7 a major progress was presented. The same was pursued for many years to test the protocols and attenuate according to the seed type, Agro-climatic conditions globally.

Results and discussion. Multiple trials with diverse cropping systems and crop cultivars have shown results confirming successful viability of mycorrhizal propagules on seeds after coating for longer storage time besides compatibility with various synthetic polymers and filler materials. Extraction of coated propagules was also optimized besides testing them with other fungicides and bioinoculants and fertilizers on seeds.

Conclusion. It is now concluded that seed coating is a viable alternative for mycorrhiza application in agriculture with cereals, oilseeds and vegetables

Key words: Cropping systems, propagules, seeds.

ID 11 - Towards the effective breeding and development of improved microbial inocula for better cassava yields in Africa

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Introduction. There is currently much focus on using beneficial soil microbes to improve crop yields or protect crops against biotic and abiotic stresses. But very few, if any, of these have proven effective for globally important crops such as cassava at large scale. Plant breeders, and before that farmers themselves, have used naturally occurring genetic variation in crop ancestors to successfully breed greatly improved crop varieties – one of the main technological drivers of the green revolution. In contrast, proponents of microbial inoculants typically isolate one particular microbe individual, show that it improves plant growth in “lab” conditions and then expect this inoculant to be effective in real conditions. It is unsurprising that there have been so many disappointments.

Methods. In a joint Swiss, African and Colombian investigation in Tanzania and Kenya we have been using genetic variation in arbuscular mycorrhizal fungi (AMF) to improve cassava production.

Results and discussion. In a series of field trials we demonstrate that: 1. Inoculation of cassava with generically variable lines of the fungus can lead to extremely large differences in cassava yield in field conditions; 2. That variation in growth response could be the result of multiple factors of fungus and host plant genetics, and the environmental conditions of the planting sites.

Conclusion. Our work shows that there is a huge potential to use mycorrhizal fungi to greatly improve cassava production, but that this still requires a large-scale set of trials to test which are the most responsive cassava varieties and in which soils they will be most effective.

Key words: Africa, breeding, cassava, genetic variation, inoculation.

ID 48 - Arbuscular mycorrhizal fungal communities of 31 durum wheat cultivars (*Triticum turgidum* L. var. *durum*) under field conditions in Eastern Canada

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Introduction. Symbiotic relationships between crops and arbuscular mycorrhizal (AM) fungi are being explored to help reduce agriculture's ecological footprint. Available information indicates wheat may sometimes show poor response to AM symbiosis. This study aimed to investigate whether genetic variation among durum wheat genotypes (*Triticum turgidum* L. var. *durum*) might lead to shifts in AM fungal community structure.

Methods. An historical set of 31 durum wheat cultivars were grown in field under phosphorus limiting conditions. At the harvest, mycorrhizal colonization was measured, and AM fungal community was determined using Illumina MiSeq and 18S rRNA gene on DNAs extracted from roots, rhizospheres and bulk soils.

Results and discussion. AM fungal community in durum wheat roots was dominated by *Rhizophagus irregularis* and *R. intraradices*, while rhizosphere and soil communities were dominated by *Glomus* spp., *Claroideoglomus* spp. and *Rhizophagus* spp. However, the AM fungal community associated with wheat roots was not significantly different between genotypes (p-value> 0.05). Mean colonization percentages in the roots varied between 57.8% (Arnautka) and 84.0% (AC Navigator), although, these differences were not statistically significant. Results suggest all cultivars select similar AM fungal communities.

Conclusion. We conclude that the genetic variation in durum wheat doesn't influence the composition of AM fungal communities in their roots. Our study solved a controversy over the variation of wheat mycorrhization response at least in durum wheat.

Key words: AM fungi, amplicon sequencing, community structure, durum wheat, field condition.

ID 180 - Importance of arbuscular mycorrhizas in a maize-green manure rotation

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Introduction. Leguminous green manure like vetch (*Vicia sativa L.*) offer an important organic N and P source in agroecosystems and may also promote the performance of arbuscular mycorrhizal fungi (AMF). Here we investigated the importance of native populations of AMF in a maize-V. sativa rotation.

Methods. A greenhouse pot experiment was performed with low P soil in a fully factorial design with three factors: i) Green manure with vetch (without, incorporated or cut and left undisturbed), ii) Mineral fertilization (with and without NPK); iii) Fungicide (with and without Carbendazim). Carbendazim was applied to provide a non-mycorrhizal control. Each of the 12 treatments had four replicates resulting in 48 experimental units. The experiment had three growth phases: First vetch grew for 10 weeks, then was left to decompose for 10 weeks and finally maize was grown for 10 weeks.

Results and discussion. Incorporating green manure into the soil reduced the AMF soil inoculum potential in terms of the AMF biomarker fatty acid 161ω5, compared to green manure cut and left on the top of the soil. Green manure both incorporated and left on top of the soil increased maize plant growth though less than NPK. Highest maize growth was obtained with NPK and green manure left on top of the soil. Green manure had no effect of AMF root colonization. In general, mycorrhiza growth response was negative, but growth suppression was lower with both green manures.

Conclusions. Vetch as green manure improves maize growth and mitigates mycorrhiza growth suppression from native populations of AMF.

Key words: Cover crops, mineral fertilization, nutrient flow, phosphorus acquisition, tillage.

ID 123 - Interactive effects of mycorrhization, daytime and/or nighttime eCO_2 on plant performance are host-species (N_2-fixing vs. non-N_2-fixing) or cropping pattern (mono-culture vs. intercropping) dependent

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Introduction. Almost all elevated atmospheric CO_2 (eCO_2) studies have focused on plant aboveground characteristics under mono-cultures, whereas limited considerations of interactions with arbuscular mycorrhizal fungi (AMF) under intercropping, let alone under the same, yet unrealistic, daytime/nighttime CO_2 concentrations. We thus addressed how auto-simulated field daytime and/or nighttime eCO_2, AMF and N_2-fixing/non-N_2-fixing intercropping could interactively affect plant biomass production and major physiological characteristics.

Methods. Non-N_2-fixing winter wheat (*Triticum aestivum* cv. Yunmai) and N_2-fixing fababean (*Vicia faba* cv. 89-147) inoculated with AM fungus (*Funneliformis mosseae*) were grown in mono-cultures and intercropping in soil (Eutric Regosol) filled pots inside environmentally controlled glass-made chambers. Those chambers had the same growth conditions (nitrogen-fertilization, AMF inoculation, etc.), except CO_2 concentrations: ambient CO_2 (ACO_2, 400ppm daytime/450ppm nighttime), daytime elevated ($DeCO_2$, 550ppm/450ppm), nighttime elevated ($NeCO_2$, 400ppm/600ppm), and daytime/nighttime elevated ($D+NeCO_2$, 550ppm/600ppm). Plant physiological parameters were examined.

Results and discussion. Regardless AM-mycorrhization, root and shoot biomass and total soluble sugar were significantly increased, but tissue NPK, leaf gas exchange, total chlorophyll, soluble protein and free amino acids were significantly decreased under eCO_2 in mono-wheat, mono-fababean or wheat/fababean intercropping. Significantly different responses of plant growth parameters (tissue N, total chlorophyll, soluble protein and free amino acid) to eCO_2 patterned as: $DeCO_2 > D+NeCO_2 > NeCO_2 > ACO_2$, while to AM-mycorrhization as $D+NeCO_2 > DeCO_2 > NeCO_{2.}$

Conclusion. Mycorrhization and/or eCO_2 have varied interactive effects on plant biomass production and physiological characteristics, no matter whether plants were grown in mono-cultures or intercropping. Such interactive effects are probably plant host-species or cropping pattern dependent.

Key words: Elevated CO_2, fababean, intercropping, N_2-fixation, winter wheat.

ID 120 - Artificial cultivation of *Tricholoma matsutake* using the matsutake-infected pine seedlings

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Introduction. *Tricholoma matsutake* is known as pine mushroom through a symbiotic relationship with *Pinus densiflora* in Korea. This mycorrhizal mushroom is commercially expensive in Asia, specially, China, Japan and Korea. Even this mushroom was used as the important present of inter-Korean Submits.

Methods. So, we try to study a various method for successful artificial cultivation of pine mushroom. Among them, our institute succeeded artificial producing of fruit-body using matsutake-infected pine seedlings. Since these infected trees were transplanted from 2001 to 2004, the fruit-body has produced continuously in 2010, 2017 and 2018 at the field experiment forest for matsutake artificial cultivation.

Results and discussion. The first time, just only one fruit body occurred in 6 months 6 years after the transplantation of infected seedlings, and then second time five mushrooms and third time one mushroom occurred in 5 months 13 years and 5 months 15 years at the same experiment site. The distances were these artificial produced mushroom and matsutake-infected pine seedlings from 12 cm to 115 cm. Theses fruiting bodies occurred 13-16 days after the underground temperature below 19.

Conclusion. In this research, we suggest the standardization artificial matsutake cultivation using matsutake-infected pine seedlings. We will study the artificial cultivation research of other commercial mycorrhizal mushrooms, *Sarcodon aspratus*, *Mattirolomyces terfezioides*, *Ramaria* spp., using this method and new technology in the further.

Key words: Artificial cultivation, Matsutake-infected pine seedling, mycorrhizal mushroom, *Tricholoma matsutake*.

ID 95 - Tracking introduced arbuscular mycorrhizal fungus in root of *Allium fistulosum* and its effect on phosphorus uptake and growth under field with or without indigenous fungi

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Introduction. Increased phosphorus uptake and growth of host plant by arbuscular mycorrhizal fungi (AMF) are less observed in field condition than in pot culture condition. Interaction between introduced and indigenous AMF can affect growth response under field condition. The aim of this study was to dissect dynamics of introduced AMF in root of *Allium fistulosum* and to determine its effect on phosphorus uptake and growth with or without indigenous AMF.

Methods. The field soil was applied with (+D) or without (-D) fumigant dazomet at the rate of 2000 kg ha1. Superphosphate was applied at the rate of 0 (P0) and 500 (P500) kg ha^{-1}. A. fistulosum inoculated with (+M) or without (-M) Glomus R-10 were transplanted to fumigated and non-fumigated field. AMF colonization, sequence read abundance of the inoculum fungus, shoot P concentration, and shoot growth were measured 31, 60, 90 and 131 days after transplanting (DAT).

Results and discussion. AMF colonization at +D-M plant was lower than 10% and higher than 40% at +D+M plant 31 DAT. Sequence read abundance of the inoculum fungus was lower than 50% at -D-M and -D+M plants and higher than 90% at +D+M plant. Shoot fresh weight and P uptake was not different between -D-M and -D+M plants. Shoot fresh weight and P uptake of +D+M plant was higher than that of +D-M plant.

Conclusion. These results indicate that colonization of introduced AMF in root is affected by abundance of indigenous AMF and this interaction determine growth response of host plant under field condition.

Key words: Colonization, dazomet, field, inoculum, sequence read abundance.

ID 27 - Methodology and efficacy of the *Zea mays* seed coating (Maize) with the arbuscular mycorrhizal fungus, *Glomus iranicum* var. *tenuihypharum*

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Introduction. Arbuscular mycorrhizal (AM) fungi promote plant growth through the nutrient supply, improving crop yields and physicochemical properties of soils. The seed coating with bioproducts constitutes a technological challenge to maintain stable the seed viability. The objective of the present study was to know the industrial viability of seeds treated with bioproduct Resid HC, based in the AM fungus *Glomus iranicum* var. *tenuihypharum*, as well as to evaluate the physiological and productive effects of the treated maize crop.

Methods. Germination tests on seeds, mycorrhizal colonization capacity on root, growth and development parameters on plants and crop yield were analysed. It was studied seeds treated with this AM fungus and stored at 24ºC. An optimal mycorrhizal viability was detected on seeds treated and stored during 6 months. Also, non-adverse effects on the seed germination capacity were observed in treated seeds.

Results and discussion. After seed germination, *Glomus iranicum* var. *tenuihypharum* produced an increase both root branching (+ 40%) as the fresh weight of shoot (+ 42%) of the treated plants. This improvement in the growth and development of the treated plants induced a greater photosynthetic capacity (+ 9%). Finally, these results were translated into 9% more of grain production in the treated maize crop compared to non-treated.

Conclusion. Therefore, it can be affirmed that Resid HC is an effective product in the seed coating able to improve the physiological state of the plant and the yield of the maize crop.

Key words: Agriculture, *Glomus iranicum* var. *tenuihypharum*, maize, Resid HC, seed coating.

ID 201 - Effect of *Funneliformis mosseae* on physiological and antioxidant response of *Physalis peruviana* under phosphorus stress

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Introduction. The purpose of this research was to study the mechanisms underlying phosphorus stress in cape gooseberry (*Physalis peruviana* L.) inoculated with arbuscular mycorrhizal fungi (AMF).

Methods. Gooseberry' seedlings were cultivated in inert substrate with nutrient solutions, using different levels of phosphorus 6, 12, 25 and 50 mg P2O5 / kg-1 for non-inoculated plants (P6, P12, P25 and P50) and AMF inoculated (P12+AM, P25+AM and P50+AM).

Results and discussion. The results indicate a significant reduction in total dry weight (TDW), root and shoot for treatments P6, P12 and P25, compared to control-P50. The reduction in growth was 81.8% (P6), 49.5% (P12) and 24.3%, (P25), at 50 days. These treatments showed decreases in leaf number (LN), leaf area (LA) and root volume (RLD), which can be attributed to the reduction of photosynthesis rates. The previous results contrast with the TDW increase of AMF inoculated plants, of 10.3% (P25+AM) and 19.1% (P50+AM), with higher rates of photosynthesis, LA, LN and RLD, possibly due to the increase in Carbon demand for the symbiosis AMF. The increase in photosynthesis of non-mycorrhizal treatments was 21% in P12+AM, 45% in P25+AM and 47% in P50+AM in relation to non-mycorrhizal. Mycorrhizal treatments also showed an increase in the activity of antioxidant enzymes, catalase (CAT) and peroxidase (POD) and proline in leaves at 30 day along with a reduction in the loss of electrolytes, suggesting a greater stability of the membranes, probably due to the increase in antioxidant defense mechanisms.

Conclusion. In conclusion, the symbiotic association improved the parameters associated with biomass production in P25+AM (3.8%) and P50+AM (19.1%) in relation to the P50-control and promoted the increase in phosphorus stress defense with production of antioxidants and proline.

Key words: Antioxidants, arbuscular mycorrhizae, biomass, cape gooseberry, photosynthesis.

ID 178 - Living and dead nurse trees facilitate oak regeneration in the xeric woodlands of central Texas

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Introduction. Texas and Mexico are *Quercus* diversity hotspots, yet Texan oaks are declining due to drought, land development, grazing, and disease. In Central Texas, *Juniperus ashei*-*Quercus* spp. woodlands provide critical habitat for threatened bird species and are essential for maintaining limestone aquifers. Woodland management is heavily focused on clearing and burning juniper, using techniques developed in temperate oak woodlands. Here we established an experiment on the Eastern Edwards Plateau to examine whether low-impact management techniques could improve oak regeneration in this subtropical subhumid xeric ecosystem.

Methods. In November 2013, we planted two hundred *Quercus sinuata* var. *breviloba* acorns in each of three habitat treatments, replicated across six plots: i) live juniper-oak canopy, ii) dead juniper-oak canopy, iii) open invasive grassland. We tracked emergence in May 2014 and survival each year until harvest in October 2017. At harvest, we excavated five seedlings from each plot and recorded height, depth, biomass, ectomycorrhizal colonization, and foliar nutrition.

Results and discussion. Living and dead canopy facilitated seedling emergence and survival; only two open plots produced surviving seedlings. Survival increased with increasing juniper and oak basal area, shrub cover, and soil organic matter. Seedling biomass and foliar N, P, S were greatest in dead and open plots, whereas ectomycorrhizal colonization and foliar Ca, Mg, Mn were greatest in live plots.

Conclusions. Living and dead canopy trees facilitated *Quercus* seedling emergence. Seedling survival depended on proximity to larger trees and living roots. Planting acorns under a juniper-oak canopy, living or dead, proved an effective habitat management practice.

Key words: Drought, forest restoration, habitat management, juniper-oak woodland, nurse trees.

Oral Session 11 "Sustainable management II"

ID 91 - Effects of long-term fertilization of a young spruce plantation on soil organic matter chemistry, ectomycorrhizal fungal communities, and exoenzyme activities

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Introduction. Fertilization of forests can increase productivity and timber supply. Because fungi are the most important decomposers in forest soils, it is important to understand how operational fertilization affects the function of soil fungal communities. We examined the effects of long-term (c. 14 years) annual or periodic fertilization on the fungal community, organic matter chemistry, and degradative enzyme activities in the fermentation/humus (FH) layer of a young spruce plantation.

Methods. The site, (54° 20´ 126° 17´N), is in the Sub-Boreal Spruce Zone of British Columbia, Canada. Three plots had been fertilized annually, every six years, or left unfertilized. Proximate analysis was used to quantify non-polar extractables, water soluble extractables (WSE), acid-soluble, and acid-insoluble components of organic matter. Fungal DNA was sequenced using next generation sequencing.

Results and discussion. Although increased litter inputs in fertilized plots did not result in higher total organic content, WSE compounds increased. Overall fungal diversity and relative abundance of ectomycorrhizal fungi were not affected by fertilization, but the proportions of Agaromycotina, especially *Cortinarius*, decreased, while *Archaerhizomycetes* increased. The potential enzyme activities associated with cellulose and hemicellulose breakdown generally increased in the fertilized FH material, and were positively associated with abundances of *Wilcoxina*, *Piloderma* and *Amphinema* spp. and negatively associated with *Cortinarius* and *Cenococcum* spp. WSE and P were the soil characteristics best correlated with overall enzyme activities.

Conclusion. These results indicate that the ectomycorrhizal fungal community changes functionally and taxonomically in response to operational levels of fertilization and associated increases in litter inputs, but without a loss of diversity.

Key words: Enzyme activities, fertilization, forest soils, fungal diversity, organic matter chemistry.

ID 138 - Soil ecological engineering with arbuscular mycorrhizal fungi and their role as keystone taxa in agroecosystems

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Introduction. Arbuscular mycorrhizal fungi (AMF) are well known for their ability to promote plant growth and ecosystem functioning in natural communities. The importance of AMF for agro-ecosystems is, however, still unclear and it is poorly understood whether the management of AMF can promote plant productivity and contribute to more sustainable agro-ecosystems.

Methods. Here we tested various ways to manage AMF in agro-ecosystems. We first tested whether specific agricultural management practices can be used to promote AMF communities. We compared 60 agricultural fields and observed that organic management promoted AMF abundance compared to conventional management. Moreover, we analyzed the root microbiome in these fields and organically managed fields had much higher root microbiome complexity with a much higher number of keystone species (27 taxa) compared to conventionally managed fields (0 taxa).

Results and discussion. Forty percent of all keystone taxa represented AMF taxa, indicating that AMF play a key role in structuring microbial communities in agro-ecosystems. In next set of experiments, we tested whether it is possible to actively manipulate AMF in the field by applying inoculum in maize fields. The effects were highly variable and growth responses to field inoculation varied from –12% to +25% with a slight to significant positive effect in 2/3 of all fields. The inoculated fungus established in almost all tested field sites demonstrating that it is possible to manage AMF in agricultural soils.

Conclusion. Our results indicate that the management of AMF can be an important tool for a more sustainable agricultural production.

Key words: Agriculture, field inoculation, microbiome.

ID 308 - The fungal Champions League: Pathogens versus Mycorrhizas

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Introduction. Soil fungal diversity has key roles in regulating plant growth and fitness, which can be either positive or negative depending on the outcome of interactions between pathogenic and mycorrhizal fungi. Mycorrhizal fungi have key strategies such as the ability to form common mycorrhizal networks from neighbouring plants that may put them at a competitive advantage over pathogenic fungi in colonising roots.

Methods. Here, we report findings from experiments in grassland and subtropical forests that investigate the effects of fungal interactions on plant performance.

Results and discussion. In grasslands, we found that fungal diversity has a key role in shaping plant-soil feedback. Overall, plant soil feedback was negative indicating pathogenic fungi were net winners, but fungal species richness mattered: increasing species richness of arbuscular mycorrhizal fungi tended to mitigate negative effects of pathogens. In forests, seedling growth and fitness (survival) was contingent on the capacity of plants to form common mycorrhizal networks. However, these effects were only apparent for ectomycorrhizal seedlings and not arbuscular mycorrhizal seedlings, which also harboured a greater proportion of pathogens.

Conclusion. Our findings emphasise that mycorrhizal fungi and pathogenic fungi are in constant battle in both grassland and forests. We also show that common ectomycorrhizal networks can facilitate seedling growth and increase fitness, which likely enables these plants to gain canopy dominance in subtropical forests.

Key words: Common mycorrhizal networks, pathogens, plant-soil feedback.

ID 32 - Genetic variation in *Rhizophagus irregularis* influences soil respiration and soil structure in tropical soils under cassava cultivation

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Introduction. Closing the gap between current and required food production, while mitigating anthropogenic carbon emissions to the atmosphere, is a major constraint to sustainable agriculture. Arbuscular mycorrhizal fungi (AMF) act as stabilizers of soil structure through physical and chemical soil aggregation by encapsulating organic carbon within aggregates and protecting it from microbial activity. In previous field studies we have observed very large differences in cassava yield when inoculated with diverse isolates of *Rhizophagus irregularis*, suggesting that carbon dynamics belowground could be greatly driven by the fungus.

Methods. We carried out a field trial in Colombia to evaluate the effect of 12 genetically different isolates of *Rhizophagus irregularis* on both carbon dynamics, accumulation (soil aggregation) and emissions to the atmosphere (soil respiration) in soils under commercial cassava crops. Soil samples at 10 and 30 cm depth were taken to determine soil aggregate size fraction employing water stable aggregates methodology. Soil respiration was directly measured in the field by infrared gas analyser (IRGA, Li-COR 8100A) means.

Results and discussion. Results showed that soil aggregation and soil respiration were significantly affected by AMF-cassava symbiosis. Particle size increased differentially among different treatments. Increases in medium size aggregates at 10 and 30 cm depth and small size aggregates at 30 cm depth were observed. Soil respiration was found to be greater in some treatments. However, this was not correlated with soil aggregation.

Conclusion. These results show the potential of using AMF as an alternative to reduce carbon emission by increasing Carbon sink while increasing food production. Further analyses are being performed.

Key words: AMF, carbon storage, cassava, soil aggregation, soil respiration.

ID 75 - Missing links: the lack of host specific arbuscular mycorrhizal fungi and keystone species contributes to ecosystem retrogression in native Hawaiian forest restoration experiment

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Introduction. Terrestrial restoration approaches often neglect to consider how historic land use has altered belowground mycorrhizal communities. This is a considerable omission as native plant re-establishment often fails due to either biotic and/or abiotic constraints, both of which can be mitigated by arbuscular mycorrhizal (AM) fungi. In this study, we examined whether aboveground restoration practices were successful in restoring belowground AM fungal communities and their ecological interactions.

Methods. We sampled AM fungal communities from intact forest and restored forest habitats, and examined changes in community composition, diversity, and the ecological interaction networks among AM fungi and their hosts. We predicted that communities and their interactions would differ between habitat types, with networks from restored sites being less complex, making them more susceptible to perturbation than remnant forest networks.

Results and discussion. Community composition varied between habitats, with observed differences in the relative abundance of AM fungal families. Network analyses revealed that remnant forest networks were more specialized, which included host species displaying a higher degree of AM fungal specialization. Additionally, keystone AM fungal taxa were lacking in restored habitats and their network structure more susceptible to perturbations. Our results indicate that ecosystem succession may be hindered by a lack of host specific and keystone AM fungi, and that relative to remnant forests the ecological interactions among AM fungi and their hosts are not re-established simply through outplanting of native plant species.

Conclusion. We suggest that both community composition and the ecological complexity of mycorrhizal communities should be incorporated into restoration practices to help increase restoration success.

Key words: arbuscular mycorrhizal fungi, ecological networks, restoration, sub-tropical native forests, success.

ID 59 - Arbuscular mycorrhizae versus Ectomycorrhizae: Changes in community composition after revegetation in riparian ecosystems

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Introduction. Mycorrhizal symbioses are important in facilitating plant establishment and survival, these plant-fungi interactions may be key to the successful revegetation of disturbed or degraded environments. To date few studies have focused on the changes in mycorrhizal communities with revegetation and fewer still have included analysis of vegetation structure.

Methods. The study was carried out in riparian areas in 6 catchments around Melbourne, Australia. Three vegetation types were assessed in each catchment: sites with intact native vegetation, sites which had been revegetated within the last 5-10 years, and cleared sites dominated by pasture grasses. At each site a 25 m x 25 m quadrat was established for soil and vegetation assessments. Composite soil samples were analysed for physical, chemical and biological factors, including genetic analysis using ITS and 18S regions. Transects and quadrats were used to assess overstorey, midstorey and understorey vegetation. Multi-variate analyses explored the relationships between vegetation and soil factors.

Results and discussion. Arbuscular mycorrhizal fungi (Glomeromycota) were more closely associated with plant populations in cleared sites, whereas, ectomycorrhizal fungi were associated with. Soil pH and phosphorus levels differed between vegetation types, as did the proportion of native plant species present, at this stage it is unclear which of the above factors is driving the changes in mycorrhizal communities.

Conclusion. Our research found that the relative abundance of different mycorrhizal communities fluctuates with revegetation and may be related to abiotic soil properties and vegetation structure.

Key words: Arbuscular mycorrhizal fungi, ectomycorrhizal fungi, revegetation, riparian ecosystem.

ID 73 - Mycotrophic capacity and diversity of native arbuscular mycorrhizal fungi isolated from degraded soils

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Introduction. Arbuscular mycorrhizal fungi (AMF) are organisms that form mutualistic associations with most plants, favoring their development, especially those located in degraded areas. The objective of the work was to identify the different predominant native AMF morphotypes, and determine the percentage of colonization, and spore density in soils of the Cumbaza sub-basin in the region San Martin, Peru.

Methods. Soil samples were taken from degraded areas of Chirikyacu, Vista Alegre, El Chontal, San Antonio de Cumbaza, Aucaloma and Shapumba, and they were associated with 4 legumes cover crops, among them, *Cajanus cajan*, *Canavalia ensiformis*, *Crotalaria juncea* and *Vigna unguiculata*. A completely random design was used, considering 6 zones and 4 legumes with 3 replications.

Results and discussion. The results showed that the treatments with legumes had greater influence in the mycorrhizal colonization in comparison with the zones of study, being *Vigna unguiculata* the one that had greater colonization (75%). However, the number of spores was influenced mainly by the zones, where the Aucaloma treatment had the highest number (252 spores / 10 g of soil). Eleven native AMF morphotypes were identified, being those of the genus *Acaulospora* the most predominant.

Conclusion. The selection of predominant native AMFs and its multiplication in trap plants favored the increase of spores which could be used as inoculants of cover legume crops in the recovery processes of degraded areas.

Key words: Cover crops, degraded soils, legumes, spores, symbiosis.

ID 53 - Host response of nine coffee varieties to AMF

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Introduction. Arbuscular mycorrhizal fungi (AMF) are not host specific, but some evidence suggests that certain preference in association could exist. There are more than 130 coffee varieties and AMF inoculation during the nursery stage is common. The coffee breeding programs might have an impact on the interaction with AMF.

Methods. A 12 AMF species consortium was applied to germinated coffee plants. Nine plant varieties were inoculated with AMF and the pathogen *Phoma costarrisensis*, with three replicates and their corresponding controls. Plants were harvested 120 days after inoculation (DAI). Fresh and dry weight were measured for root, stalk and leaves, as well as AMF root colonization and damaged leaf area. We evaluated and compared the response of the coffee variety to the AMF, and to their interaction to the pathogen infection.

Results and discussion. Most of the varieties increased their growth when inoculated with AMF. Root colonization was different, although Criolla and Garnica varieties had higher growth with lower root colonization. AMF inoculation reduced *P. costarrisensis* leaf damage in most varieties. Despite the general outcome, Criolla and Garnica showed a significant positive response to the inoculation, and Blue Mountain did not show a benefit from AMF inoculation. A PCA analysis show that most of the effect measured where correlated to AMF inoculation, and the reduction of the pathogen damage was also correlated to this factor.

Conclusion. Despite AMF not being host-specific, there was a clear difference in plant response regarding the variety, where some did not benefit from the AMF at any variable.

Key words: AMF efficiency, coffee, damage reduction, plant breeding, specificity.

ID 264 - Understanding AM community assembly to increase plant community restoration success

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Introduction. Belowground microbial communities have become a topic of much concern in the restoration of disturbed systems. A recent paradigm shift has acknowledged that belowground plant symbionts can enhance our understanding of plant community assembly. It is evident that arbuscular mycorrhiza (AM) plays a key role in the rhizosphere microbiome and strongly influences grassland restoration. However, the role of the arbuscular mycorrhiza community in plant community assembly remains largely unknown. Our study looks at the types of AM species that are commonly found in high, low and monotypic plant community diversity levels to understand relationships between aboveground (high diversity) communities and associated AM species. By understanding how these complex systems are assembled, we can perhaps recreate mycorrhizal networks that increase plant community success. The goal of this study was to understand which key AM taxa are associated with diverse, restored plant communities.

Methods. Soil samples were collected at a tallgrass prairie restoration site in Platte River, Nebraska (USA) across various plant diversity levels (high, low, monotypic). Arbuscular mycorrhiza DNA was processed using qPCR and sequenced using Illumina Miseq to understand key AM taxa, phylogenetic relatedness, and network formation.

Results. Results to this study are forthcoming and bioinformatic analyses are being processed. Future research will include manipulation of plant community composition to determine how the AM community changes and recovers.

Conclusions. Results from this study will be used to help improve restoration success and create more sustainable microbial communities in a changing environment.

Key words: Arbuscular, grassland, networks, prairie, restoration.

ID 269 - Legacy effects of nursery practices on arbuscular mycorrhizal fungal (AMF) communities in seedling transplants of the imperiled Mulanje cedar (*Widdringtonii wrighteii*; Cupressaceae)

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Introduction. Most efforts to restore of populations of rare plant species have focused on strategies to minimize threats in combination with actions to increase the size of perilously small extant populations, most notably through plant reintroductions. Less attention has been paid to mycorrhizal community matching and its effects on plant–soil feedbacks. In this study, we examined arbuscular mycorrhizal fungal (AMF) communities in the critically endangered Mulanje cedar (*Widdringtonii wrighteii*, Cupressaceae), which exists in a few diminished forest fragments on Mt. Mulanje in south-eastern Malawi.

Methods. We sampled rhizosphere soils in remnant stands of Mulanje cedar as well as in nursery seedlings propagated in a lowland forest soil, seedlings transplanted in five locations across Mt. Mulanje, and the native plant community, and analyzed AMF community composition by high-throughput sequencing.

Results and discussion. We recovered 39 AMF taxa representing 16 genera. Natural Mulanje cedar stands hosted AMF communities comprising species of *Ambispora* (48% reads) and *Archaeospora* (15% reads). However, AMF communities in nursery and transplanted seedlings, and native plants were characterized by *Entrophospora* species (43-74% reads). Communities in transplanted seedlings also contained some AMF taxa typical of native vegetation (*Acaulospora*, *Paraglomus*). AMF communities covaried with soil organic matter content (natural stands), or soil nitrate levels (nursery, transplanted, native vegetation).

Conclusions. The strong differences in AMF communities and abiotic drivers in natural cedar stands versus nursery and transplanted seedlings indicates a persistent mismatch that could alter plant–soil feedbacks and influence larger-scale patterns and success of cedar restoration.

Key words: AMF, mismatched mycorrhizas, mulanje cedar, restoration.

Oral Session 12 "Mycorrhizal roles in people land interactions"

ID 72 - Resilience of *Rhizopogon*-Douglas-fir mycorrhizal networks 25 years after selective logging

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Introduction. *Rhizopogon vesiculosus* and *R. vinicolor* are sister fungal species that form ectomycorrhizas exclusively with Douglas-fir roots. Previous research showed that different age classes of trees were linked together by *Rhizopogon* genets and the largest trees acted as hubs in the network.

Methods. In the current study, the main objective was to determine the resilience of mycorrhizal networks 25 years following removal of large hub trees. We predicted that the targeted removal of mature trees would have a lasting impact on the network, with the network of the harvested forest having reduced connectedness compared with a non-harvested neighbouring forest.

Results and discussion. *Rhizopogon vesiculosus* was nearly absent in the non-harvested plots, whereas both species were prominent in the harvested plots. Initially, network analysis was based only on networks formed by *R. vinicolor* because they were well represented in both treatments. The networks formed by *R. vinicolor* was more densely linked in the non-harvested plots than the harvested plots. In other words, this network of harvested plots was highly connected, but it did not recover to the level of its link density found in the non-harvested plots. When we accounted for the difference in link density between the treatments, there were no other differences, apart from an edge difference and a greater vulnerability to fragmentation in harvested forests than in non-harvested forests.

Conclusion. When both *Rhizopogon* sister species were included in the analysis, both treatments had similar connectivity and limited vulnerability to fragmentation, suggesting a resilient mycorrhizal network following 25 years since selective logging.

Key words: Belowground resilience, cryptic species, fungal genotypes, mycorrhizal networks, selective logging.

ID 184 - Linking management decisions, mycorrhizal abundance, soil quality and pasture productivity in an agroforest frontier in the humid tropics of Mexico

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Introduction. Young, induced pastures resulting from conversion of native vegetation are highly extended in the tropics and are important for local economy. However, pastures are often abandoned after some years of management. Some studies point out that tropical rangeland degradation primarily occurs due to overgrazing and changes in plant communities and soil properties. Our main goal was to analyse the effect of different management practices on mycorrhizal abundance, soil quality, and forage productivity in the Lacandon region in southern Mexico.

Methods. We found 31 active rangeland sites and conducted semi-structured interviews to collect management information and landowners perceptions of pasture productivity. We determined some soil properties such as texture, organic matter content, infiltration rate, stable aggregates, available nutrients, pH and abundance of microbial functional groups (including arbuscular mycorrhizal fungi). Additionally, we measured productivity of palatable and unpalatable species monthly for five months in cattle exclosures established in each site.

Results and discussion. We found a positive relation between mycorrhizal abundance and time grazing intensity but no relation with plant productivity. Sand content and infiltration rate were negatively, and grazing severity was positively related to primary productivity. Grazing severity was also related to productivity of palatable grasses.

Conclusions. Our study showed that mycorrhizal abundance was influenced by several soil and vegetation factors and suggests a strong relation between livestock management decisions, soil quality and the maintenance of productivity of rangelands.

Key words: Ecosystem services, mycorrhizal abundance, rangeland management, soil quality.

ID 88 - Impact of introduction of arbuscular mycorrhizal fungi on the root microbial community in agricultural fields

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Introduction. Arbuscular mycorrhizal (AM) fungi are important members of root microbiome and can be used as biofertilizers for sustainable agriculture.

Methods. To elucidate the impact of AM fungal inoculation on the indigenous root microbial communities, we used high-throughput sequencing and an analytical pipeline providing fixed operational taxonomic units (OTUs) as output to investigate both bacterial and fungal communities of roots inoculated with a commercial AM fungal inoculum in six agricultural fields.

Results and discussion. AM fungal inoculation significantly influenced the root microbial community structure in all fields. Inoculation changed the abundance of both indigenous AM fungi and other fungal members in a field-dependent manner. Inoculation consistently enriched several bacterial OTUs, by changing the abundance of indigenous bacteria and introducing new bacteria through the inoculum. Some inoculum-associated bacteria were tightly interacted with the introduced AM fungi, some of which belonged to the genera *Burkholderia, Cellulomonas, Microbacterium, Sphingomonas,* and *Streptomyces* and could be the candidate mycorrhizospheric bacteria that help the establishment and/or functioning of the introduced AM fungi. Inoculated AM fungi also co-occurred with several indigenous bacteria with putative beneficial traits, suggesting that inoculated AM fungi could recruit specific taxa to confer a better plant performance. The bacterial families Methylobacteriaceae, Acetobacteraceae, Armatimonadaceae, and Alicyclobacillaceae were consistently reduced by inoculation, possibly due to the changes in the host plant status caused by the inoculum.

Conclusion. To our knowledge, this is the first large-scale study to investigate the interactions between AM fungal inoculation and the indigenous root microbial communities in agricultural fields.

Key words: High-throughput community analysis, inoculation, microbiome, network analysis, sustainable agriculture.

ID 142 - Arbuscular mycorrhizal fungi role in the sustainability of coastal environments from Yucatan, Mexico

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Introduction. Human development has caused the loss of different environments in coastal zones and, as a result, of biodiversity. Plants in coastal zones survive stressful environments caused by saline aspersion, fires, flooding and other abiotic stresses. Due to the arbuscular mycorrhizal interaction, plants survive in these extreme environments. The aim of this work is to identify the coastal environments and the arbuscular mycorrhizal fungi from the rhizosphere of the dominant plants, as well as the percentage of root colonization.

Methods. Research was conducted in the North coast of Yucatan. We set up transects and measured plant cover, the percentage of arbuscular mycorrhizal fungi (AMF), and the abundance of AMF spores from the rhizosphere.

Results and discussion. We identified 191 plant species and five plant communities (barrier Island, coastal dune, mangrove, peten and tropical low flooding forest) and two plant associations (tasistal and tular). More than 90% of plants analyzed showed arbuscular mycorrhiza root colonization. We found 24 species of AMF, and three of them had never been logged in Yucatan before. From this total, we recorded 22 species in coastal dune vegetation; 22 in mangrove and peten; 13 in tropical low flooding; and 12 in tasistal.

Conclusion. According to our results, the vegetation from the North coast of Yucatan presents a medium grade of preservation. The main causes of biodiversity loss are house building on coastal dunes, agricultural activities, and hunting in tropical low flooding forest; and the shrimp farms and duck hunting in the mangrove and peten.

Key words: Coastal vegetation, conservation, floristic composition, restoration, sustainability.

ID 28 - Mycorrhiza smart breeding and agroecosystem management to optimize food production and nutrition

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Introduction. We aim to reduce fertilizer costs and soil erosion by developing in situ management of mycorrhizas for resilient agroecosystems. Our research examines how plant genetics, agricultural practices, and soil conditions influence AM fungal abundance, diversity, and benefits. By discovering genetic and ecological mechanisms related to functional AM symbioses, our research expands the toolkits of plant breeders and land managers.

Methods. We determined AM responsiveness for *Sorghum bicolor* (model crop) genotypes. In corresponding field trials, we assessed the influence of soil amendments and field management on AM fungi, examining how associated AM fungi effect host-plant nutrition, including grain quality.

Results and discussion. In low-fertility soil, landrace (open-pollinated) genotypes were more highly colonized and significantly more responsive to AM fungi, while producing significantly more grain, with greater nutritional quality, compared to commercial (fertilizer responsive) genotypes. Alternative soil amendments and management practices maintained or improved grain yield and nutrition, supporting similar or greater AM fungal abundance, compared with conventional practices.

Conclusion. Our findings have led us to develop a framework for synergies between plant breeding, field management, and soil amendments that should direct future research efforts to increase benefits of AM fungi in food systems. Currently, we are expanding assessments to include plant gene-expression and AM fungal community composition across gradients of soil fertility and soil moisture, utilizing a panel of 28 sorghum genotypes that represents broad genetic diversity. Ultimately, the concept of ‘mycorrhiza smart’ agriculture can help optimize food production and nutrition while decreasing fertilizer use and stabilizing soils.

Key words: Agriculture, grain quality, sorghum, resilience.

ID 179 - Metagenomic analysis of arbuscular mycorrhizal fungi associated to native maize landraces in a Mexican traditional polyculture

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Introduction. Ocotepec is a small community in Veracruz where traditional maize polycultures (milpas) are the prevalent system for food subsistence. Male migration and women and children malnutrition are important problems. Malnutrition has been linked with the loss of crop diversity in milpas, and the introduction of inadequate fertilization practices. We studied arbuscular mycorrhizal fungi (AMF) diversity associated with the different native maize landraces used in Ocotepec, in order to design strategies that help rescue AMF diversity and improve plant/soil nutrition and diversity.

Methods. We designed an ITS-rDNA massive sequencing strategy to analyze AMF diversity from roots of four maize landraces grown (1) in a greenhouse under different Pi conditions and (2) from 12 milpas. The spore inoculum for the greenhouse experiment was taken from the same milpas set.

Results and discussion. Bioinformatics analysis suggested the presence of 61 species. We found 35 AMF species associated to all maize landraces and ten AMF specific to a particular landrace. We also identified seven species, which are negatively impacted by phosphate nutrition. Differences at the greenhouse vs. field conditions were also found.

Conclusions. We concluded that: 1) Maize diversity in traditional polycultures may contribute to maintain a high AMF diversity; 2) despite low genotypic variation between maize landraces, black maize harbors the most diverse HMA consortium. Considering this, and the fact that *Glomus* was the most abundant and diverse genera, using the black landrace and a *Glomus* consortium may represent an option to improve plant/soil nutrition in these milpas.

Key words: AMF to recover food diversity, poverty and malnutrition, traditional Mexican polycultures.

ID 299 - The genetic basis of mycorrhizal growth responses in spring wheat

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Introduction. All cereal crops can associate with arbuscular mycorrhizal fungi, but the resultant symbiosis is not always beneficial for the plant. Colonisation of the plants' roots by arbuscular mycorrhizal fungi can substantially influence plant nutrient uptake and biomass. While plant genotype is known to influence the extent of resultant mycorrhizal growth responses, the underlying genes remain unknown. Using a mapping population of 99 wheat lines, we have found substantial variation in plant growth responses to colonisation by arbuscular mycorrhizal fungi. For example, shoot biomass is increased by up to 85% following mycorrhizal colonisation in some lines but is reduced by up to 35% in others.

Methods. Using quantitative trait locus (QTL) analysis, we have identified the wheat genome regions associated with positive and negative mycorrhizal growth responses.

Results and discussion. These regions will be used for further work with the aim of understanding which genes are responsible for positive plant responses to mycorrhization. This will aid in the identification of targets that may be utilised by plant breeders to improve agricultural sustainability.

Conclusion. By identifying the community composition and structure in mycorrhizal wheat roots of both highly and poorly responsive lines, we will determine whether plant responses to mycorrhization are characteristic of the presence or absence of certain fungal groups or indicative of shifts in overall mycorrhizal fungal community structure.

Key words: QTL, response, sustainability, wheat.

ID 217 - Ancient Amerindian modification of Amazonian Ferralsols changes community composition of arbuscular mycorrhizal fungi but does not affect cassava root mycorrhization

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Introduction. Cassava (*Manihot esculenta* Crantz) arbuscular mycorrhization has been mainly studied in low-fertility soils as cassava grows well in such conditions. However, in the Amazon region where cassava was initially domesticated, local people also cultivate cassava in Anthrosols denominated Amazonian Dark Earths (ADEs). ADEs were created by ancient indigenous communities of the Amazon region (around 2000 to 500 years ago), and have more soil bases and available phosphorus (P) than surrounding Ferralsols. We studied if arbuscular mycorrhization of cassava was affected by differences in these two soil conditions in which it is cultivated.

Methods. Soil and cassava root samples were obtained from indigenous shifting agricultural plots. Fungal DNA was extracted using SSU rRNA gene primers NS31 and AML2 and amplicons were obtained using 454-sequencing.

Results and discussion. The amount of available P was the major difference between Ferralsols and ADEs. The community composition of arbuscular mycorrhizal (AM) fungi was different in each soil type ($p = 0.007$), sharing only 39% of virtual taxa (VT) between them. ADEs were richer in AM fungal species than Ferralsols. Differences in the diversity of AM communities between these two soil types did not affect the number of AM fungal VT colonizing cassava roots ($p = 0.26$).

Conclusion. We conclude that the AM fungal species composition of natural Amazonian Ferralsols changed by the ancient human activities that transformed Ferralsols into Anthrosols. However, this soil transformation did not affect the capacity of cassava roots to establish AM associations with a similar number of AM fungi colonizing individual cassava roots in both soils.

Key words: Amazonian Dark Earth, arbuscular mycorrhizas, ferralsols, *Manihot esculenta*, shifting cultivation.

ID 56 - The legacy effect of drought on fungal communities from agricultural land under contrasting management types

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Introduction. Conventional arable management leads to changes in soil water/nutrient retention and yields through compaction, reduced carbon sequestration, and loss of microbial diversity and abundance. Degraded soils are less resilient to perturbation including droughts, which are projected to increase in frequency and severity. Restoring soils through implementing grass-clover ley (long-term uncropped fallow) has been shown to increase organic carbon and crop yields, though little work has looked at the effects on microbial diversity or stress response.

Methods. Monoliths were collected from fields containing strips set aside for ley and conventional cropping, along with grazed pasture. Wheat was grown and subjected to severe drought or a regime emulating in-field conditions, coinciding with a less severe natural drought. Soil was sub-sampled after harvest and re-sown. At eight weeks roots and rhizosphere soil were sampled for total fungal and Arbuscular Mycorrhizal (AM) fungal community analysis through Illumina MiSeq amplicon sequencing.

Results and discussion. Ley and pasture soils conferred advantages to water retention after drought but not to community maintenance. AM fungal and total fungal richness and diversity under ambient conditions was higher in ley and pasture than arable soil. The severe drought had a negative legacy effect in the ley and pasture soils more pronounced than in arable soils through a significant reduction in total fungal diversity and proportion of AM fungi.

Conclusion. Ley restores soil properties to those like pasture and shows a benefit to water loss mitigation after drought but may come with the trade-off that the communities are more heavily impacted and require longer recovery periods.

Key words: Agriculture, diversity, drought, legacy effects, resilience.

ID 302 - A participatory approach to harness native mycorrhizae

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Introduction. Current crop management suffers from major limitations: alteration of natural resources, loss of biodiversity, risk to human health and dependence of farmers on external inputs. By promoting natural regulations, agroecology is an alternative approach. However, this kind of approach no longer offers one-stop solutions but calls for a set of biodiversity-based solutions that leave room for farmer initiatives. As regards mycorrhizae, introducing exogenous commercial strains is a commonly-used option to enhance plants' mycorrhization. However, results in the field have been less conclusive than those in controlled conditions.

Methods. In French Guiana, a participatory approach involving farmers, advisers and researchers, allowed to share knowledge and to identify levers and brakes to the use of mycorrhizae in market gardening production.

Results and discussion. Propositions by farmers aimed at enhancing indigenous mycorrhizal networks rather than introducing exogenous propagules in the field. On farm innovative devices were implemented on three farms to assess the potential of candidate propositions to increase, in nursery, roots' mycorrhization of cucumber (*Cucumis sativus*). Three modalities and an additional control were assessed: practices favoring native mycorrhizae by growing sorghum (*Sorghum bicolor*) in a tray, inoculation of cucumber seedlings with propagules of indigenous strains and inoculation of cucumber seedlings with commercial propagules.

Conclusion. Our results show that, in nursery, the enhancement of native mycorrhizal fungi is an efficient practice. Thus, smallholder farmers were drivers in designing agroecological technics harnessing native mycorrhizal fungi.

Key words: Agroecology, native mycorrhizae, on farm experiments, participative approach.

Friday July 5, 2019

Oral Session 13 "New methods and innovative questions and approaches"

ID 38 - Seasonality of ectomycorrhizal function at the spruce root-soil interface

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Introduction. Forest trees act as major suppliers of carbon into forest soils through litter production and rhizodeposition. Ectomycorrhizal fungi (ECM) produce their mycelia on expense of the rhizodeposited C and are thus dependent on the activity of their host. However, this activity changes seasonally in temperate and boreal coniferous forests with warm summers and cold and dark winters. The activity of the soil microbiome should reflect this seasonality.

Methods. Fungal community composition and its activity was observed in the course of the year in a temperate *Picea abies* forest, rich in ECM. In the tree roots, rhizosphere, bulk soil and litter, we have tracked the transcription of all fungi as well as of the locally abundant ECM *Russula ochroleuca*, *Amanita rubescens*, and *Boletus edulis*.

Results and discussion. The composition of fungal communities did not show substantial seasonal changes and the fraction of ectomycorrhizal fungi remained stable. Higher variation was observed in the ribosome production by individual fungal guilds. The seasonality in all compartments was, however, clearly observable on the level of transcriptional activity and composition of transcripts with most profound changes observed in the soil and rhizosphere compartments. Various types of C compound in different seasons with higher utilization of reserve compounds in winter and of biopolymers in summer. The increase of utilization of reserve compounds in the time of tree inactivity was also observed in the three ectomycorrhizal fungi.

Conclusion. The results show that the activity of ectomycorrhizal fungi is largely driven by the activity of their tree hosts.

Key words: Ectomycorrhiza, metatranscriptomics, rhizosphere, seasonality, temperate forest.

ID 64 - Field transcriptomics: learning from gene-coexpression networks towards optimization and prediction of mycorrhizal functioning in the field

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Introduction. The molecular basis of mycorrhizal formation and functioning has been studied through forward and reverse genetics in the model systems, by which many key genes in the symbiosis have been identified. We have little information, however, about how plants optimize resource allocation via coordinating the expression of these genes in the field where their productivity is constrained by various environmental factors.

Methods. To this end, we employed field transcriptomics. Maize roots and rhizosphere soils were collected both across the US Corn Belt and across Japan, and mRNA extracted from the roots were subjected to RNA-Seq and subsequent gene-coexpression network analysis with respect to the environmental factors.

Results and discussion. Nineteen coexpression modules were identified, e.g., those involved in water uptake, cell cycle/division, phosphate starvation, and mycorrhizal formation/functioning. In the mycorrhizal module most of the mycorrhiza-specific genes were enriched, while the phosphate-starvation module consisted of those involved in phosphate uptake and homeostasis. The members of mycorrhizal module were upregulated with increasing mycorrhizal colonization and the soil nitrate-phosphate ratio and downregulated with increasing leaf-phosphorus content, and those of the phosphate-starvation module also responded to some of the factors. The two modules are, however, regulated independently, suggesting that the plant maximizes the efficiency of phosphate acquisition via coordinating these two modules in a given environment.

Conclusion. The identification of the environmental factors for the mycorrhizal modules raises the possibility for improving mycorrhizal functioning via manipulating/managing the factors in the field and, further for construction of prediction models for its functional level in the field via deep learning.

Key words: Arbuscular mycorrhizal fungi, environmental, field transcriptomics, gene-coexpression network, maize.

ID 307 - Newest molecular methods for identification and quantification of fungi

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Introduction. Rapid evolution of molecular technologies has opened up new opportunities for identification and quantification of mycorrhizal fungi.

Methods. I demonstrate how the third-generation sequencing platforms PacBio Sequel and Oxford Nanopore MinION can be applied for identification of fungi from environmental samples in large-scale metabarcoding studies, addressing ultra-long fragments.

Results and discussion. New approaches with digital droplet PCR, spiked-in molecules, metagenomics and metatranscriptomics tools can be used as alternatives to lipid-based and ergosterol-based quantification methods. Specific blocking primers for plants and animals can be used to concentrate fungal amplicons from plant and animal samples when using general universal eukaryote primers.

Conclusion. I discuss cons and pros of these methods and recent, mostly yet unpublished, applications.

Key words: Omics, quantification, sequencing.

ID 30 - Using high-throughput shoot phenotyping to explore plant responses to arbuscular mycorrhizal fungi and nutrient availability over time

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Introduction. There are many reported benefits to plants of arbuscular mycorrhizal fungi (AMF), including positive plant biomass responses; however, AMF can induce a range of biomass responses from negative (growth depression), through to neutral, through to highly positive. The continuum of responses to AMF are highly dependent on the plant species in question. High-throughput phenotyping (HTP) technology permits repeated measures of an individual plant's aboveground biomass, providing data of growth over time. Here we present the first experiments that use HTP to explore the continuum of growth responses to AMF, in three different plant species.

Methods. We examined the effect on AMF inoculation on the shoot biomass of three contrasting plant species: a vegetable crop (tomato), a cereal crop (barley), and a pasture legume (*Medicago*). We also considered the interaction of mycorrhizal growth responses with plant-available soil nutrients by modifying the available zinc (Zn) and phosphorus (P) concentration in the soil.

Results and discussion. The *Medicago* plants grown at low soil P displayed highly positive growth responses to AMF, and also greater tolerance of toxic soil Zn concentrations. In contrast, the *Medicago* supplied with extra soil P showed neutral and negative growth responses to AMF. The barley and tomato plants also experienced growth depressions, and for each plant species, the appearance of the depression occurred at different times after planting.

Conclusion. These results illustrate how context-dependent mycorrhizal growth responses are, and the value of HTP approaches to exploring the complexity of mycorrhizal responses, especially with regards to interactions with soil nutrient availability.

Key words: Arbuscular mycorrhizal fungi, growth response, high-throughput phenotyping, phosphorus, zinc.

ID 35 - A method to quantify the contribution of arbuscular mycorrhizal fungi to plant phosphorus nutrition *in situ* in the field

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Introduction. Arbuscular mycorrhizal (AM) fungi can produce a huge extraradical hyphal network in the soil to help plant uptake phosphorus. However, the previous elevations of the contribution of AM fungi to plant P uptake are usually conducted in the pot conditions, and, it is still very difficult to study the contribution in the field.

Methods. The maize is planted in a PVC tube (20 cm in diameter) which are made holes and sealed with 30 µm mesh (permitting AMF hyphae but not roots to grow outside). There are also four PVC tubes with different diameters outside. The PVC tubes in different layers are knocked to produce the hyphal gradients of AM fungal hyphae associated with the crop roots. The crop P content and hyphal length are determined and the model between them is established. The contribution of AM fungi to crop P uptake *in situ* can be then calculated.

Results and discussion. We present external hyphae extend a huge biomass that was similar to the root in our device, at a suitable phosphorus level (Olsen P =10 mg kg-1), there was a positive linear correlation between the external hyphae biomass and plant shoot phosphorus uptake, the contribution of AM fungi to the plant was 57.4%. For every 155.90 mg increase in external hyphae biomass, phosphorus uptake in shoot of plant increases by 6.4 mg.

Conclusion. We developed a novel method to quantify the contribution of plant P uptake by AM fungi *in situ* in the field.

Key words: Hyphal gradients, *in situ*, mycorrhizal contribution, novel method, phosphorus uptake.

ID 216 - Plants linked by a common arbuscular mycorrhizal fungal hyphal network: zinc transfer and plant and fungal gene expression

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Introduction. Mineral nutrient redistribution within and among plants is key to an efficient use of fertilizers. To test whether arbuscular mycorrhizas can contribute to zinc (Zn) redistribution between plants, a foliar Zn application experiment was set up with plants connected by a hyphal network.

Methods. The plants were *Medicago truncatula* wild type J5 and arbuscular mycorrhizal-defective mutant TRV25, all grown in the same bi-compartmented autotrophic *in vitro* system with *Rhizophagus irregularis* strain MUCL41833 as connecting fungus. Zinc was applied as droplets to the leaves of the donor plant at 0.1 mg per plant of approximately 0.1 g DW.

Results and discussion. Zinc application increased the leaf and root Zn concentrations in the donor and root Zn concentration in the J5 receiver plant but not in the TRV25 plant. The observed redistribution of Zn was accompanied by an upregulation of the plant nicotianamine synthase gene in the roots of the mycorrhized receiver plant J5. The expression of two fungal Zn transporter genes in the intraradical mycelia of the mycorrhizal donor and receiver plants changed as well in response to Zn application, providing evidence that the fungus sensed and responded to the redistributed Zn. In short, this study demonstrated that Zn applied to leaves differentially regulates plant and fungal gene expression and that it can raise the Zn concentrations in leaves and roots of neighbouring plants connected by an arbuscular mycorrhizal fungus.

Conclusion. We hence suggest that the arbuscular mycorrhizal symbiosis has potential to contribute to a better use of foliar-applied fertilizer in stands of mycorrhized crop plants.

Key words: Arbuscular mycorrhiza, common mycorrhizal hyphal network, differential gene expression, foliar zinc.

ID 41 - Pyroloid *in vitro* germination. A novel method allowing to study these mixotrophic plants

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Introduction. Pyroloids i.e. plants belonging to the subfamily Pyroloideae recently became considerably important models for the study of mixotrophy. Representatives of this group are, at least during early ontogenesis, fully mycoheterotrophic. It has been, until now, impossible to germinate them for conservation, physiological or medical research.

Methods. Using a unique combination of cultivation techniques, we developed a novel protocol for *in vitro* axenic cultivation of Pyroloids. With this protocol we were able to germinate seeds, grew green leafy representatives of all Pyroloid genera and describe their anatomy during post-germination ontogenetic development.

Results and discussion. The seeds contain only tiny undifferentiated embryos surrounded by a thin layer of endosperm. Both, endosperm and the embryo contain storage lipids and proteins, which are converted into starch during the germination. The basal embryo pole grows into undifferentiated polar structure, which forms a first root meristem. Subsequently, roots form an extensively branched root system from which adventitious shoots will later develop. Usually, more than one shoot is produced by each plant. The undifferentiated, intermediary zone could be called a protocorm, because it is functionally convergent with protocorm of other mycotrophic or parasitic plants (orchids, lycopods, Rafflesiaceae). Similarly to orchids, only one embryo pole forms meristem. However, while Pyroloids produce primary root meristem, orchids form primary shoot meristem with adventitious roots.

Conclusion. We propose, that, the reduction of seed structure, reduction of one embryo meristematic pole and the conversion of lipidic and protein storage compounds into starch are convergent traits in mycoheterotrophic plants having dust seeds.

Key words: Convergent evolution, germination, *in vitro*, Pyroloideae, Pyroloids.

ID 108 - PacBio genome sequencing decompress genomes and shows that genomes of ectomycorrhizal mushrooms are larger than we think

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Introduction. The genomes of ectomycorrhizal fungi are rich in transposable elements and repetitive regions. These regions collapse genome assemblies in size and fragment them in greater number of contigs when short sequences are used for the assemblies (50-400 pb).

Methods. In this work, we compare the resulting assemblages of three sequencing platforms (Hi-Seq, Next-Seq and Sequel), generated by several strategies for two strains of *Laccaria trichodermophora*.

Results and discussion. When using the two Illumina libraries, individually or together, the best assemblies were obtained with SPAdes. The genome sizes were, for strain CA-11 of ~70Mpb (120,117 contigs, N50 ~4K, L50 ~5K), while for strain EF-36 they were ~49Mpb (2,953 contigs, N50 ~45K, L50 279). Using the PacBio libraries individually, genome sizes grew up to ~112Mpb for CA-11 (1,151 contigs, N50 151, L50 201), and ~59Mpb for EF-36 (87 contigs, N50 ~1.5M, L50 13). The disparity between the genomic sizes of both strains is evident. All analyzes and sequencing libraries show that EF-36 has a genomic size smaller than that of CA-11. The long sequences of PacBio (50% of them of> 20Kpb) resolve the repetitive regions better than Illumina short reads, obtaining larger genomes with less fragmented assemblages.

Conclusion. The growth of 60% of the small genome of EF-36 and 80% of the larger genome of CA-11 when using PacBiol long reads highlight the difficulty that repetitive regions and transposable elements offer to assemblers and their contribution to genome contents.

Key words: Genome assembly, long reads, transposable elements.

ID 79 - Cultural characteristics of ectomycorrhizal fungi

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Introduction. Ectomycorrhizal fungi have symbiotic relationships with plants. They are widespread and play important roles in forest ecosystems such as nutrient cycling and forest health. In Korea, about 1,900 species of mushroom species have been recorded and 35% of them are known as mycorrhizal fungi. To better understand and cultivate them, we isolated and tried to characterize some important ectomycorrhizal fungal species.

Methods. For this study, 32 genera 93 species 225 isolates of ectomycorrhizal fungi were used. Their growth was observed using PDA, MEA, SDA and MMNA at 25°C, and optimal media was investigated. Optimal temperature and pH were investigated using PDA and PDB, respectively. In addition, cellulase and laccase activities were measured using PDA media with CMC and ABTS, respectively.

Results and discussion. For the growth media, PDA was the best followed by MMN. 48 species 86 isolates grew faster on PDA than the other media. For most of the species, their optimal growth was at 25°C or 20-25°C. Only *Ramaria apiculata* and *R. fumigata* showed increased growth at 15°C and 9 isolates including *Amanita melleiceps, A. spissacea, Mattirolomyces terfezilloides, Pisolithus arhizus, Russula sanguinea, Scleroderma areolatum* grew well at 30°C. Optimal pH of the ectomycorrhizal fungi was from pH 4-8, but large portion of the fungi belonged to pH 4-5. 87 species 200 isolates showed cellulase activities and 70 species 141 isolates showed laccase activities.

Conclusions. These results could help improve knowledge of mycorrhizal fungi for their cultivation.

Key words: Cellulase, growth, laccase, pH, temperature.

Oral Session 14 "Models for mycorrhizal research and research for the future"

ID 133 - Implications of intraspecific variation in ectomycorrhizal fungal communities for host plant response to climate change

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Introduction. Changes in climate, including the combined effects of increased drought and heat stress, are affecting many of the world’s forested ecosystems. Ectomycorrhizal fungi can improve plant survival and growth in hot, dry conditions, but it has been challenging to understand the importance of these fungi to the responses of long-lived trees in the field.

Methods. We used long-term field studies, a moisture manipulation experiment in a common garden, greenhouse experiments and lab studies to examine the importance of host genetics and ectomycorrhizal fungal communities to drought tolerance in *Pinus edulis*, a conifer that has experienced widespread mortality due to a warming, drying climate.

Results and discussion. We found that: 1) seedlings had similar patterns of growth and mortality during drought as their maternal trees and their siblings suggesting that drought tolerance is inherited, 2) drought tolerance was strongly associated with ectomycorrhizal fungal species composition, with drought tolerant trees consistently associating with ascomycete fungi in the genus *Geopora*, 3) in lab desiccation trials, members of the genus *Geopora* tolerated dry soil conditions better than other genera of ectomycorrhizal fungi, and 4) neutron radiography showed that root colonization by *Geopora* increased water flow velocity in drought tolerant seedlings but had the opposite effect in drought intolerant seedlings.

Conclusion. These results show that intraspecific differences among plants in their interactions with ectomycorrhizal fungi contribute significantly to variation in drought tolerance and explain patterns of growth and mortality of mature trees with climate change.

Key words: Climate change, drought, ectomycorrhiza, host genetics, neutron radiography.

ID 177 - Models of mycorrhizae: from stability of the mycorrhizal mutualism to predictions of resource uptake across the landscape

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Introduction. A basic observation of mycorrhizal fungal communities is that plant roots host multiple mycorrhizal fungal species that vary in their degree of benefit to that plant. Understanding the forces governing mycorrhizal fungal coexistence and dynamics is fundamental to predicting the efficiency of the mycorrhizal mutualism in the landscape. I build a general framework for understanding the dynamics generated from the interplay of fungal competition and plant preferential allocation to the most beneficial symbiont.

Methods. We have demonstrated that non-beneficial mycorrhizal fungi have a competitive advantage in mixture consistent with not paying the cost of mutualism, that plants can preferentially allocate carbohydrates to the most efficient symbiont and this can overcome the cost of mutualism, and that the rate of preferential allocation depends upon plant resource limitation. We represent these processes in a series of mathematical relationships describing fungal dynamics and plant physiology, and investigate the dynamics use graphical, analytic, and simulation approaches.

Results and discussion. We identify that fungal coexistence within a plant root system should be common as a result from two qualitative processes: resource partitioning for preferentially and non-preferentially allocated plant resources and negative physiological feedback in plant preferential allocation. The model predicts that the efficiency of the mycorrhizal mutualism will decline with increasing soil resources levels and increase with increasing aboveground resource.

Conclusions. We develop a framework that both explains the persistence of high diversity of mycorrhizal fungi within plant roots and makes predictions for patterns in the efficiency of the mycorrhizal mutualism across environmental gradients.

Key words: Ecology, mathematical modeling, mutualistic efficiency, preferential allocation, stability of mutualism.

ID 39 - An emerging model of an invasive species: Populations of the death cap *Amanita phalloides* are highly sexual but dispersal limited

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Introduction. The death cap *Amanita phalloides* is a European ectomycorrhizal fungus invasive in California and an emerging model we are developing to understand the spread of ectomycorrhizal species. To understand whether the fungus moves across landscapes using vegetative mycelia or sexual spores, we generated genetic fingerprint and population genomics data from American and European populations. Few, large genets would suggest asexual propagation mediated by hyphae, while many, small genets would suggest dispersal mediated by sexual spores.

Methods. To test whether genets are ephemeral or persistent, we also sampled from the same American populations over time. In total, 13 populations were mapped and collected from the United States and Europe between 2004-2007; these populations were characterized using AFLP data. Between 2014-2015, populations in California were resampled and 3 new European populations added; these populations and specimens originally collected in 2004 were characterized using genome sequencing.

Results and discussion. In every population and at all-time points, populations were characterized by small genets. Often, data revealed each mushroom to be its own genet. No genet discovered in 2004 was rediscovered in 2014 or 2015. Moreover, geographic and genetic distances were often significantly correlated, even at small spatial scales

Conclusion. Spores are the tools used by the death cap to move across landscapes, but spores appear to travel very short distances, typically falling adjacent to the parent mushroom.

Key words: Ecosystem impacts, genet or body size, life history evolution, mutualism, spore.

ID 172 - Genomics of non-model arbuscular mycorrhizal fungi

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Introduction. Arbuscular mycorrhizal (AM) fungi form symbiotic interactions with the majority of terrestrial plants and have crucial roles for biodiversity, plant health and production. Because AM fungi are obligate symbionts and complete their life cycle below ground genomic research in this important group of fungi has been hampered by difficulties in obtaining enough high-quality DNA for genome sequencing. Only a few model species that can be grown in axenic conditions have been sequenced so far, revealing important insights into their ability to undergo sexual reproduction, high repeat content both in transposons and protein-coding genes, patterns of low within strain polymorphism and symbiotic machinery specific to these fungi.

Methods. In our group we have developed a novel method for single nuclei sequencing and genome assembly that allows us to explore the generality of these findings across the phylogeny of AM fungi.

Results and discussion. With newly generated genome data from 24 diverse AM fungal species, we review the AM fungal tree of life and discuss relationships among families in the tree. Further, within strain analyses that support homokaryotic genome organization of AM fungi and patterns of repeat elements will be discussed.

Conclusion. Our results bring the field of AM fungal genomics beyond a few model species to provide a better understanding of this important group of plant symbionts.

Key words: Arbuscular mycorrhizal fungi, genomics, non-model.

ID 36 - Hurricane disturbance affects the structure of rhizosphere fungal communities and mycorrhizal network in a Neotropical forest

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Introduction. Ecosystems are constantly being disturbed by extreme events and climate change will increase their frequency. In 2015, Patricia hurricane (category 4), landfall in Pacific coast producing damage in vegetation and this litterfall increases soil nutrients, our aim was to understand the effect of hurricane disturbance in rhizosphere fungal communities, with special interest in mycorrhizal network.

Methods. Ectomycorrhizal hosts roots from nine plots were sampled in 2016 and 2017, and then were sequenced with Illumina MiSeq. We obtained environmental data from plots and categorized it in low, recovery and high disturbance.

Results and discussion. We found positive correlation of light with fungal diversity, and negative correlation with soil temperature. Rhizosphere fungal community was less diverse one year after hurricane and increased two years after hurricane. Host identity has a direct effect on fungal the community. Ascomycota was the most diverse group in each sample. Glomeromycota were absent in high disturbance plots and common in recovery plots. Saprotrophs were the most common fungal guild in the high disturbance sites. Ectomycorrhizal fungi had more richness in plots with low and high disturbance. Mycorrhizal network was disconnected in 2016 producing high modularity, and recovered connections in 2017. The specialization of mycorrhizal network increased from one year to the next.

Conclusion. Fungal communities and mycorrhizal network were not resistant but are resilient to hurricane disturbance after two years.

Key words: Arbuscular mycorrhiza, cyclone, ectomycorrhizae, extreme events, Pacific coast, tropical dry forest.

ID 78 - Ecosystem consequences of shifts in arbuscular and ectomycorrhizas of a dual-colonized common tree species

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Introduction. Shifts in the relative abundance of arbuscular and ectomycorrhizal tree species can influence nutrient economies and carbon cycling within forests. Whether similar outcomes emerge from shifts in the relative abundance of ectomycorrhizas (EM) and arbuscular mycorrhizas (AM) in forests dominated by a single, dual-colonized tree species are unknown.

Methods. We surveyed pure stands of aspen (*Populus tremuloides*), a common tree species able to form both types of mycorrhizas, from the northern boreal forest to the southern edge of its distribution in Canada. Our intent was 1) to capture regional and local variation in EM and AM, and link that variation to 2) stand leaf traits, including resistance to decomposition (% lignin) and specific leaf area, and 3) carbon stored in 'fast' and 'slow' pools within the soil. These leaf traits, in part, may reflect stand nutrient economies, and the different soil pools represent the potential for a stand to store carbon. Importantly, we confirmed all sampled roots were aspen to circumvent confounding effects of host identity.

Results and discussion. Ectomycorrhizas were most variable across regions, and for AM, within stands. The amount of carbon stored in fast pools was insensitive to EM abundance, but the amount of carbon stored in deep, slow pools was negatively related to EM abundance. Preliminary results suggest that AM abundance is positively correlated with leaf resistance to decomposition.

Conclusion. While the abundance of AM seem to associate with leaf traits of aspen, EM may underlie soil carbon storage deep in the soil profile.

Key words: Aspen, biogeochemistry, carbon storage, forest composition, leaf traits.

ID 169 - Root demographics: How root stage distributions alter plant growth

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Introduction. Little is known about the impacts of root stage distributions on plant-soil feedbacks, soil resource cycling, or projections of plant growth. A plant's proportion of biomass in later stage roots and resource uptake efficiency are typically inverse with growth enhanced by maintaining high-uptake capable early stage roots. There are trade-offs in senesce scheduling for different root stages, but circumstance can skew distributions towards later stages. Objective is to explore the effects of stage distribution on plant growth, resource cycling, and root turnover, and determine the conditions for different stage distribution dynamics.

Methods. We apply a stage-based matrix population model using varying resource acquisition, survivorship, transportation capacity, and maintenance costs for root stages to analyze stage distribution across a plant's life. A simulated perennial plant expands into a 2-dimensional soil environment. Growth and ageing feedbacks integrate resource acquisition by roots and carbon production from photosynthesis.

Results and discussion. A parameter space search indicates greatest plant growth – root and leaf biomass – is associated with root distributions heavily skewed towards early stages. Regression tree analysis indicates root and leaf photosynthetic conversion rates and allocation strategy were the strongest predictors of plant growth. Additional analysis of root stage distribution (including spatial analysis) will indicate how changing spatial arrangement of root stages impacts growth, resource cycling and root turnover.

Conclusion. Allocation strategies favoring new root and leaf growth over root maintenance produces the greatest plant growth. These strategies produce early-stage skewed distributions. Strategies favoring root expansion and maintenance increase the spatial spread and produce late-stage skewed distributions.

Key words: Carbon cycle, demography, model, root turnover.

ID 18 - Identifying the variables that limit predictability in AM fungal-plant-herbivore interactions

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Introduction. How can we understand the natural world if we cannot predict the dynamics of species interactions? A growing number of studies on AM fungal-plant-herbivore interactions show these interactions occur but are context dependent. To address which factors most strongly influence AM fungal-plant-herbivore interaction dynamics, I present a predictive framework based on a machine learning approach analyzing multiple studies in two AM fungal-plant-herbivore interaction systems from my group.

Methods. I applied a machine learning approach to analyze data from both AM fungal-plant-herbivore interactions systems. Machine learning uses a permutation approach to identify which variables have the greatest influence on system dynamics (in this case which variables limit predictability). I used the random Forest program in R version 3.4.4, and ran 1000 permutations of a decision tree regression to come up with composite trees most closely predicting total plant or insect biomass from 10 variables.

Results and discussion. The analysis revealed that the experiment the data was collected from, the plant genotype, and the plant source material had the greatest influence on plant biomass in AM fungal–plant–herbivore interaction systems. By contrast, neither plant nor herbivore species influenced plant biomass. The factors with the greatest influence on insect biomass in AM fungal-plant-herbivore interaction systems were plant genotype, plant species, presence of an endosymbiont, and herbivore genotype.

Conclusion. The results suggest that in AM fungal-plant-herbivore interaction systems genotypic level effects will have the greatest modifying influence on plant biomass, while both species and genotypic level effects will modify the influence on insect biomass.

Key words: Across system comparisons, arbuscular mycorrhiza, biotic stress, machine learning, multi-species interactions.

ID 284 - Rapid changes of ectomycorrhizal fungal communities under global warming: implications from *Pinus pumila* forests on nine mountains

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Introduction. Recent global warming potentially affects communities of ectomycorrhizal (ECM) fungi, critical symbionts of major forest trees, and thus would have a large impact on forest ecosystems. However, previous knowledge concerning temperature effects on ECM fungal communities are confounded by covarying tree communities and should be rigorously tested.

Methods. We examined ECM fungal communities in alpine forests dominated by a single host species (*Pinus pumila*) distributed on nine mountains across > 1000 km in Japan, where temperature condition varies among the forests. Additionally, we explored global records of each fungal species to infer its potential temperature niche, and used it to estimate the temperature of the observed communities. Direct sequencing of rDNA ITS regions identified 154 ECM fungal species from 4134 ECM root-tip samples in total.

Results and discussion. Gradient analyses revealed a large contribution of temperature, especially summer temperature, to ECM fungal communities. The estimated temperature as above was significantly correlated with the actual temperature of the research sites, especially in summer seasons.

Conclusion. These results clearly indicate that ECM fungal communities are affected by temperature, especially summer temperature, without confounding host effects. Although alpine ecosystems are regarded as the most vulnerable to global warming, its impacts on below-ground microbes may be more serious than previously thought on above-ground species.

Key words: Alpine forest, ectomycorrhizal fungi, global warming, *Pinus pumila*.

New Phytologist

DETAILED PROGRAM POSTER SESSIONS

Monday July 1, 2019

ID 7 - Mucoromycotina fine root endophyte fungi form nutritional mutualisms with vascular plants

Grace Hoysted, Alison S. Jacob, Jill Kowal, Philipp Giesemann, Martin Bidartondo, Jeffrey G. Duckett, Gerhard Gebauer, William Rimington, Sebastian Schornack, Silvia Pressel, Katie Field

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Introduction. Fungi and plants have engaged in intimate symbioses that are globally widespread and have driven terrestrial biogeochemical processes since plant terrestrialisation >500 Mya. Recently, hitherto unknown nutritional mutualisms involving ancient lineages of fungi and non-vascular plants have been discovered. However, their extent and functional significance in vascular plants remains uncertain.

Methods. We measured bi-directional transfer of carbon-for-nutrients between the lycophyte, *Lycopodiella inundata* (representative of an early evolutionary transition from non-vascular to vascular plants) and Mucoromycotina (Endogonales) fine root endophyte fungi, for the first time, using radio- and stable-isotope tracers under both modern and Paleozoic-like atmospheres of 440 ppm and 800 ppm CO_2, respectively.

Results and discussion. We provide first evidence of abundant carbon-for-nitrogen exchange between an early-diverging vascular plant and Mucoromycotina fine root endophyte fungi regardless of changes in atmospheric CO_2 concentration. We also provide evidence that the same fungi colonise neighbouring non-vascular and flowering plants.

Conclusion. These findings fundamentally change our understanding of the evolution, physiology, interrelationships and ecology of underground plant-fungal symbioses in terrestrial ecosystems and our findings point towards a new physiological niche for the persistence of Mucoromycotina fungi from ancient to modern plants, both singly and in dual colonisation with Glomeromycotina fungi.

Key words: Arbuscular mycorrhizas, Endogonales, fine root endophyte (FRE), lycophytes, Mucoromycotina, mutualism.

ID 208 - Fern gametophytes of *Angiopteris lygodiifolia* and *Osmunda japonica* harbor diverse Mucoromycotina fungi

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Introduction. Mycorrhizal symbiosis between plants and fungi is ubiquitous, and has been played key roles in plant terrestrialization and diversification. Although arbuscular mycorrhizal (AM) symbioses with Glomeromycotina fungi have long been recognized as both ancient and widespread symbionts, recent studies showed that Mucoromycotina fungi were also ancestral symbionts and would thus be expected to co-exist with many land plants.

Methods. To explore whether Mucoromycotina colonize fern gametophytes, we subjected fungal associations with gametophytes of two distantly related ferns, *Angiopteris lygodiifolia* (Marattiales) and *Osmunda japonica* (Osmundales), to molecular analysis. Direct PCR amplification from intracellular hyphal coils was also performed.

Results and discussion. We detected Mucoromycotina sequences in the gametophytes of *A. lygodiifolia* and *O. japonica* at rates of 41% (7/17) and 50% (49/98) of gametophytes, respectively, and assigned them to 10 operational taxonomic units of Endogonales lineages. In addition, we used AM fungal-specific primers and detected Glomeromycotina sequences in all individuals examined. The results suggest that Glomeromycotina and Mucoromycotina colonized fern gametophytes simultaneously.

Conclusion. We found that Mucoromycotina were present in fern gametophytes of Marratiales and Osmundales, which implies that a variety of fern taxa have Mucoromycotina associations.

Key words: Arbuscular mycorrhiza, fine root endophyte, gametophyte, Mucoromycotina, Pteridophyte.

ID 147 - An endophytic fungi from *Rododendron* sp. is able to form ericoid mycorrhiza in *Vaccinium* sp. roots *in vitro*

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Introduction. Mycorrhizal associations have different anatomical features depending on the partners involved in the interaction. Ericoid mycorrhiza is stablished between plants belonging to the Ericaceae and Ascomycotan and Basidiomycotan fungi. Although this type of association is widely recognized in ericaceous plants, a little number of fungal species has been recognized as ericoid mycorrhizal forming fungi (EMFF). Here we characterized the anatomical features of the mycorrhizal association between an endophytic fungi isolated from *Rhododendron* sp. and *Vaccinium* sp. roots in *in vitro* conditions.

Methods. Field samples of *Rhododendron sp*. roots stained with trypan blue revealed the occurrence of hyphal coils in cortical and epidermal cells, and a hyphal network resembling a fungal mantle. A fungal isolate obtained from these roots was grown axenically and inoculated into flasks containing *in vitro* regenerated *Vaccinium sp*. plantlets. Trypan blue stain of roots from the *in vitro* plants revealed the presence of hyphal coils restricted to cortical, fully differentiated cells. In root meristems hyphal coils were also observed in developing cells, and a fungal network was present in meristems as in *Rhododendron* sp. roots.

Results and discussion. Molecular characterization of the fungal isolate indicates a close phylogenetic affinity to the Peniophoraceae. The occurrence of Basidiomycotan as EMFF has been scarce, and to our knowledge, there is not significant evidence that a fungus belonging to the Peniophoraceae could form ericoid mycorrhiza.

Conclusion. Our results demonstrate that the fungal isolate from *Rhododendron* sp. has the capacity of stablishing an interaction with roots of *Vaccinium* sp. that coincides with the ericoid mycorrhizal features.

Key words: Ericaceae, mycorrhizal anatomy, Peniophoraceae.

ID 220 - Fatty acids promote energy production of arbuscular mycorrhizal fungi under asymbiotic conditions

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Introduction. Arbuscular mycorrhizal (AM) fungi provide host organisms with soil minerals taken up via hyphal networks in the soil, and in return, receive carbon sources such as sugars and lipids derived from plant photosynthates. Recent evidence suggests that lipids synthesized by the host are transferred to AM fungi that possess no fatty acid synthase genes. Further, mutations in the host's lipid biosynthesis-related genes lead to the failure of this sound symbiotic interaction. To address whether lipids derived from plants are crucial for AM fungal growth, we evaluated energy production in AM fungi after the application of fatty acids.

Methods. *Rhizophagus irregularis* DAOM197198 were incubated in sterilized water or a synthetic complete medium with fatty acid salt. After the incubation, the germinating spores or hyphae were sampled and used for ATP measurement, staining with a fluorescent probe, JC-1 for monitoring the mitochondrial membrane potential and gene expression analysis. ATP content in germinating spores and germ tubes was determined 12 h after the application of fatty acids.

Results and discussion. ATP content after the application of a fatty acid was increased 2.4 fold than that in the absence of fatty acids. In addition, we also confirmed the activation of mitochondrial membrane potential via the application of fatty acid via JC-1 fluorescence staining. Moreover, genes involved in ß-oxidation were upregulated 3 h after the application of fatty acid.

Conclusion. These results indicate that AM fungi can utilize fatty acids as energy sources.

Key words: ATP, energy production, fatty acid, gene expression, mitochondrial membrane potential.

ID 226 - Acid phosphatase activity released from extraradical hyphae of arbuscular mycorrhizal fungi and fractions of phosphorus in soil

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Introduction. Arbuscular mycorrhizal (AM) fungi extend the extraradical hyphae into the soil to promote plant phosphorus (P) uptake. Soil P was divided into organic phosphate (Po) and inorganic phosphate (Pi), and the Po in the soil accounts for 20-80% of total P. We previously clarified that certain AM fungus release acid phosphatase (ACP). The purpose of this study was to clarify the relationship between ACP activity and soil P fractions.

Methods. *Allium fistulosum* plants were inoculated or uninoculated with AM fungi (*Rhizophagus clarus*) and grown on a two-compartment pot divided into a mycorrhizal compartment and a hyphal compartment. Pots were filled with sterilized Andosol to which 0.5 g P2O5 kg-1 was applied. Soil solution was collected from the hyphal compartment 40, 45, 50 and 55 days after sowing using mullite ceramic tubes. ACP activity in the soil solution were measured by using disodium p-nitrophenylphosphate. The soil in the hyphal compartment was continuously extracted by using the method established by Hedley (1982) and each P fractions in the soil was measured.

Results and discussion. The mycorrhizal colonization of the root was 97% in inoculated plants. The shoot dry weight and shoot P uptake were higher in inoculated plants than in uninoculated plants. ACP activity in the soil solution was higher in inoculated plants than in uninoculated plants from 40 to 55 days after sowing. P in soil was fractionated into Resin-P, NaHCO3-Pi, and NaHCO3-Po (available phosphorus), NaOH-Pi, NaOH-Po, and HCl-P (unavailable phosphorus).

Conclusion. We discuss the relationship between ACP activity and these soil P fractions.

Key words: Acid phosphatase, hyphal exudate, organic phosphate, soil phosphorus fraction.

ID 242 - Gene co-expression analysis and modeling reveal distinct gene regulatory networks for phosphate acquisition in mycorrhizal plants

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Introduction. Although arbuscular mycorrhizal fungi play a predominant role in phosphate (Pi) acquisition of the plants, information about molecular networks regulating Pi acquisition in mycorrhizal plants is limited.

Methods. *Nicotiana benthamiana* was inoculated with 0-500 spores of *Rhizophagus clarus* HR1 and grown at different Pi levels (50-500 μM) for 6 weeks, and then RNA was extracted from the roots of 125 plants. RNA-Seq and subjected to LASSO modeling for constructing a molecular marker to estimate amounts of Pi taken up through the mycorrhizal pathway (MP) and also to co-expression gene network analysis with respect to Pi status. A molecular marker consisted of 8 root-expressed genes enabled to estimate the amount of Pi taken up through the MP.

Results and discussion. Correlation coefficients between actual values and estimated values were 0.97. The marker illustrated that a large fraction of Pi was taken up through the MP in the mycorrhizal plants. Gene co-expression analysis revealed that the genes encoding mycorrhiza-specific Pi transporters and fatty acid biosynthetic enzymes were tightly co-expressed, forming a 'mycorrhizal module', but this module did not respond to the Pi levels. Interestingly, differential gene regulatory network analysis showed that members of the modules, including hub genes, of which expression was regulated in response to the Pi levels differed between the mycorrhizal and non-mycorrhizal plants.

Conclusion. These results suggest that gene regulatory networks for Pi acquisition are shifted to a more complex system by mycorrhizal formation, in which not only Pi acquisition but also carbon-Pi trade-offs between the fungal symbiont are optimized.

Key words: Gene co-expression, mycorrhizal pathway.

ID 243 - Iron reduction as a potential mechanism to improve phosphorus nutrition by EMF

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Introduction. Phosphorus (P) uptake from soils can be challenging because the phosphate ions released from mineral and organic sources can become unavailable through adsorption on iron (Fe) oxides or precipitate with Fe3+ in the soil. Production of Fe-reducing metabolites by ectomycorrhizal fungi (EMF) may release P adsorbed on Fe oxides in the soil and thereby enhance uptake.

Methods. In a field experiment we incubated ingrowth meshbags amended with phosphate bound to the Fe oxide goethite and tested to what extent P and Fe were lost from the meshbags in P-limited soils with different abundance of EMF. We found P and Fe losses from the bags only in sites with significant EMF growth suggesting dissolution of the goethite by the action of EMF to obtain P, possibly through production of Fe reducing compounds.

Results and discussion. To further investigate if EMF produce Fe-reducing compounds in response to P limitation, we grew P-starved and non-starved *Paxilus involutus* mycelium in axenic cultures with different P sources: orthophosphate, apatite, phytic acid and P bound to goethite. At the end of the experiment we measured the Fe-reducing capacity of the growing medium and found that P starvation significantly stimulated *P. involutus* Fe-reducing capacity and that the highest values for Fe-reduction were found in the apatite.

Conclusion. We report for the first time that Fe reducing capacity by EMF can be stimulated by P starvation and dependent on the P source provided. The potential to produce Fe-reducing metabolites as a strategy for P mobilization is a research area that warrants further exploration.

Key words: Apatite, ectomycorrhizal fungi, goethite, iron oxides, iron reduction, *Paxillus involutus*, phosphorus.

ID 306 - Systemin modulates defense responses in roots of tomato plants (*Solanum lycopersicum*) during the pre-colonization stage of the mycorrhizal symbiosis

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Introduction. Most angiosperm plants form a symbiotic association with arbuscular mycorrhizal fungi (AMF). It has been observed that a suppression or down regulation of the defense response takes place in the root in order to permit mycorrhizal colonization. The degradation of chitooligosaccharide fragments by mycorrhiza-specific chitinases has been recently proposed to mediate this repression of the defense response.

Methods. In this work we describe the effect that the exogenous application of systemin, a plant polypeptide needed for the activation of a systemic defense in response to wounding and insect herbivory in leaves of *Solanum lycopersicum*, exerts on ß-glucanase and chitinase activity the first 12 hours of the pre-colonization stages of the mycorrhizal process in tomato roots when added together with spore suspensions of three different species of arbuscular mycorrhizal fungi (AMF).

Results and discussion. The application of exogenous systemin to tomato roots induced the rapid expression of a battery of signal pathway systemic wound responsive genes, and induced the rapid and transient in vitro activity of chitinases but not glucanases. However, when added together with the spores of AMF, systemin differentially modulated he activity of these enzymes in a way that was dependent of the AMF species tested. Modified lytic activity was preceded or accompanied by the induction of the RbohD, LoxD and PLA2genes at the first two hours after initial contact.

Conclusion. These results indicate that exogenous systemin is perceived in the roots where it modulates a local defense response in the presence of AMFspores.

Key words: Arbuscular mycorrhizal fungi, chitinases, glucanases, reactive oxygen species, systemin.

ID 159 - *Funneliformis mosseae* alters soil fungal community dynamics and composition during litter decomposition

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Introduction. Although arbuscular mycorrhizal fungi (AMF) are believed to be non-saprophytic, recent studies have indicated that AMF are able to influence litter decomposition through interacting with the soil fungal community. However, it remains unclear exactly which constituent groups of the soil fungal community respond to AMF during litter decomposition, and in what ways. In order to fill this knowledge gap, we investigated the effect of AMF on soil fungal communities in a subtropical forest in southwestern China.

Methods. Our experimental set-up included a dual microcosm unit with two treatments: *Trifolium repens* inoculated with AMF (AM) and uninoculated (NM). Soil sampling was carried out at different times (T0, T90, T120, T150 and T180) and Illumina sequencing was used to detect changes in soil fungal community composition.

Results and discussion. We found that the composition and operational taxonomic unit richness of the fungal communities, at higher taxonomical levels (e.g. phyla, order), remained stable across treatments. However, the relative abundance of key genera, including *Mycena*, *Glomerella*, *Pholiotina*, and *Sistotrema*, were significantly affected by AMF inoculation. Soil fungal community structure was also significantly altered by AMF inoculation during the later stages of litter decomposition, but the diversity of the soil fungal community was unaffected.

Conclusion. Our study provides new insight into understanding the interaction between AMF and soil fungal communities during litter decomposition.

Key words: Culture independent technique, Illumina sequencing, litter decomposition, soil fungi, soil microbial.

ID 194 - Reconstructing food webs involved in utilization of organic N by arbuscular mycorrhizal fungi

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Introduction. Arbuscular mycorrhizal fungi (AMF) obviously lack efficient mechanisms to mineralize complex sources of organic nutrients in soil. Rather, they rely on interaction with other soil microorganisms to get a share of such resources. Yet the exact identities and metabolic pathways involved in utilization of organic N by the AMF hyphae remain largely unknown, partly because of the complexity of microbial interactions in soil.

Methods. Therefore, we took a synthetic approach here to improve our understanding of organic N re-cycling in AM fungal hyphosphere. *In vitro* cultivation systems were constructed each with a root compartment delimited from the rest by root-exclusion mesh, the hyphal compartment, and labeling/bacterial compartment with no diffusion contact to the rest. When AMF hyphae reached the edge of the labeling compartment, a medium containing either 15N-NH_4Cl or 15N-labeled chitin was added to the labeling compartment.

Results and discussion. The AMF hyphae were let to colonize the new niche for 3 weeks, and then different strains of soil bacteria were added to the labeling compartment, and incubated for another 2 weeks. Thereafter, the 15N transfer was quantified from the labeling compartment to the AMF hyphae in the hyphal compartment, and to the roots. Whereas about 10% of the 15N was appearing in the AM hyphae and the roots if provided as mineral (NH_4Cl) source, irrespective of the bacterial identity, two bacterial strains (both *Paenibacillus* sp.) significantly increased 15N uptake from chitin as compared to other bacteria.

Conclusion. These results directly demonstrate that specific prokaryotes may facilitate AMF access to organically bound N in soils.

Key words: Bacteria, chitinolysis, hyphosphere, *in-vitro*, nitrogen.

ID 202 - Effect of native arbuscular mycorrhizal fungi on the initial growth of chili pepper *Capsicum* spp. and its potential to reduce the reproduction of *Meloidogyne incognita*

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Introduction. The arbuscular mycorrhizal fungi (AMF) improve the growth of *Capsicum* species, which results in seedlings resistant to biotic stress, such as the reduction in the severity of the damage induced by the nematode *M. incognita*.

Methods. In the greenhouse was estimated, the effect of the colonization of three native AMF of deciduous forest; *Funneliformis geosporum*, *Claroideoglomus claroideum* and *Glomus ambisporum*, 47 days after inoculation (dai) in *Capsicum chinense* and *C. annuum*. And at 97 dai, it was estimated the reproduction reduction of *M. incognita* and severity decrease of the disease in *Capsium* species.

Results and discussion. At 47 day, AMF colonized the roots of *Capsicum* spp., with high percentages of total colonization: *C. annuum* (94 to 99%) and *C. chinense* (76 to 98%), without significant differences among the AMF species. There were significant differences due to the effects of seedling species on the height ($F = 112.21$, $p \leq 0.0001$) and fresh root weight ($F = 27.17$, $p \leq 0.0001$) and on the effect of the interaction of AMF and species of *Capsicum* in all growth variables. At 97 day, all AMF reduced the severity of the disease ($F = 28.16$, $p \leq 0.0001$) compared to the oxamyl nematicide and the control. In *C. chinense* the application of oxamyl reduced the number of eggs and females of *M. incognita*, whereas in *C. annuum* the inoculation of *F*. geosporum, *G. ambisporum* and oxamyl reduced by 60% and 57% the number of eggs and females of *M. incognita*, respect to the control.

Conclusion. Native AMF present potential as growth promoters and biological control agents against *M. incognita* in *Capsicum* plants.

Key words: *Capsicum, C. claroideum, F. geosporum, G. ambisporum, M. incognita.*

ID 228 - Hyphosphere characterized by bacterial and fungal communities of *Gigaspora margarita* and *Rosellinia necatrix* from soil and host rhizosphere

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Introduction. Mycorrhizal fungi contribute to forming hyphosphere in soil ecosystems. Soil microbes are keys in declining *Rosellinia necatrix* (Rn), fungal pathogen of white root rot disease, by a hot water treatment. The efficacy of the treatment was often stable in orchards managing with cover crops, many of which were arbuscular mycorrhizal. This study aimed to know whether hyphosphere can be characterized by bacterial and fungal communities of *Gigaspora margarita* (Gm) and Rn and their changes in heat stress.

Methods. Gm inoculated onions were grown separately from sterilized soil by a sheet, and a soil solution was added every week. After Rn-growing filters were inserted in the soil compartment, half of the cultures were heated with a 44-h program, maximum 40oC for 1 hour, and the others were not. 16S rRNA gene and fungal ITS region were analyzed at suspensions of Gm extraradical hyphae, Rn filters, roots (R), and soil (S). Principle component analysis (PCA) and Shannon diversity index were calculated with OTUs.

Results and discussion. Diversity indices of microbial communities of both Gm and Rn hyphospheres were decreased by the heat treatment, but those of R and S were not. In PCA, control revealed the highest correlation between Gm and Rn, where *Pseudomonas* sp. (Proteobacteria) and *Spizellomyces punctatus* (Chytridiomycota) were high relative values. After treatment, the bacterial community sustained the correlation.

Conclusion. These results suggested that the presence of characteristic bacteria and fungi associated with the fungal hyphae. Further studies using other soils, model systems, and fungal hyphospheres.

Key words: AMF extraradical hyphae, microbial community, NGS, PCA, white root rot.

ID 251 - Arbuscular mycorrhizal fungi compete with ammonia oxidizing archaea and reduce nitrification in agriculture soil

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Introduction. Nitrification is an essential component of the nitrogen cycle whereby ammonia is oxidized by ammonia oxidizing bacteria (AOB) and archaea (AOA) to nitrite, which is subsequently oxidized by nitrite oxidizing bacteria to nitrate, and both processes can be carried out by complete ammonia oxidizers (comammox). Arbuscular mycorrhizal fungi (AMF) can transport significant amounts of ammonium and nitrate to host plants, but their preferred source of nitrogen may be in the form of ammonium. AMF may have a greater ability to capture the less mobile ammonium before it is converted by nitrifiers. Therefore, AMF may compete with AOA, AOB and comammox for ammonium, and consequently reduce nitrification.

Methods. To test this theory, microcosms containing agriculture soil were planted with either the tomato BC1-mutant (non-AMF system) or the wildtype pair (AMF system), or no plant, and spiked with urea or dried blood at a rate of 50 or 200 ppm of nitrogen. Soil nitrate concentrations were determined colormetrically and the abundance of nitrifiers quantified using qPCR.

Results and discussion. Under high dried blood, net nitrification and AOA abundance decreased in the AMF system, and AOB and comammox increased in both the AMF and non-AMF system. Results suggest that AMF compete for ammonium to the detriment of AOA.

Conclusion. AMF can impact nitrification and nitrifier abundances. Understanding the fundamental role that AMF play in influencing reactive nitrogen fluxes in the soil has vast potential for contributing to nitrogen use efficiency in agroecosystems and a reduction in nitrate leaching and the greenhouse gas nitrous oxide.

Key words: Agriculture, ammonia oxidizing archaea, arbuscular mycorrhizal fungi, nitrification, nitrogen cycle.

ID 69 - Mycorrhizal fungi and zinc nutrition in pecan trees

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Introduction. In soils with alkaline pH the availability of zinc for the pecan tree *Carya illinoinensis* is reduced, the contribution of Zn is by foliar application, in the semi-arid regions a solution of zinc sprinkled on the foliage evaporates quickly, which reduces the penetration of the nutrient into leaves.

Methods. In the field were four treatments: 1: trees without Zn contribution; 2: Zn foliar; 3: edaphic Zn (CZ); and 4: edaphic Zn with MycoRoot® (1x106 esp/g of *Pisolithus arrhizus* + 1x106 CFU/g of *Azospirillum brasilense*). Applications and evaluations for 4 years.

Results and discussion. The treatment of Zn to the foliage exhibited the greatest bearing shoot length and the control without zinc the least. In four years of evaluation, the treatment that best supports this variable is leaf Zn, followed by C+M, in part this reflects a dilution effect, given the greater vegetative growth of C+M and CZ. This treatment also shows a slight but sustained tendency to improve bud and leaf growth. In nutrient measurements in the foliage, the application of C+M averages 32 ppm and the CZ 24 ppm, lower than the control without Zn. It is also observed that C+M the nutrient in the foliage increased 24%, and the growth tended to be higher.

Conclusion. Induced mycorrhization promotes growth and increases the yield of young and adult pecan trees. The efficiency of a pecan root to absorb Zn from the soil is related to its ability to mycorrhize.

Key words: Edaphic zinc, mycorrhizae, nutrition, pecan tree, production.

ID 70 - Dynamics of phosphorus absorption in chile habanero (*Capsicum chinense* Jacq.) assisted with *Rizhophagus intraradices* in partially autotrophic culture *in vitro*

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Introduction. Phosphorus (P) is vital for the development of plants and has a low solubility in the soil, causing a shortage zone around the roots and limiting plant growth due to nutritional deficit. Arbuscular mycorrhizal fungi (AMF) help to improve the nutrition of plants, through their network of hyphae that explore places where roots cannot reach.

Methods. This research evaluated the phosphorus uptake in habanero pepper seedlings in a partially *in vitro* system, inoculated with *Rizhophagus intraradices*. One to four habanero chili seeds from the Chichen Itzá hybrid were placed in 12x8 cm glass jars with 20 mL of MS medium, at 25 DDG they were transplanted into Petri dishes with modified MS medium (in the P concentration: 0.500, 0.850, 1 g L-1). The roots were in contact with the medium and the plant protruded through a hole. Using a design with factorial arrangement giving a total of 6 treatments with 10 repetitions.

Results and discussion. A different behavior was observed in the parameters of plant, physiological and fungal growth, depending on the concentration of P in which they developed.

Conclusion. Significant differences were observed in the P uptake showing greater efficiency in the inoculated treatments.

Key words: Efficiency of P uptake, habanero pepper, *in vitro* mycorrhization.

ID 100 - Arbuscular mycorrhizal symbiosis: A new generation technology for sustainable agriculture

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Introduction. Abiotic stresses such as heavy metals HMs, salinity, etc. have become a major threat to crop productivity, especially in legumes. Constant changes in climate and deterioration of environment hamper plant growth, induce metabolic perturbations as well as reduce nitrogen fixing ability of legumes. Arbuscular Mycorrhizal Fungi (AMF) are widespread micro-organisms which are able to impart stress tolerance by increasing nutrient acquisition, absorptive surface area, modulating soil enzyme activities, osmolytes and antioxidant production as well as synthesis of glycoproteins. However, a significant functional diversity has been reported among the different fungal species depending upon host plant, endophyte and soil.

Methods. Experiments were conducted to investigate the relative effectiveness of native and exotic AMF species (*Rhizophagus irregularis*, *Funneliformis mosseae*, *Claroideoglomus claroideum*, *Claroideoglomus etunicatum*) in ameliorating metal and salt induced metabolic responses of two legume species- *Cicer arietinum* L. and *Cajanus cajan* (L.) Millsp.

Results and discussion. AM inoculations enhanced abiotic stress tolerance via reducing uptake of toxic ions (Na+, Cd2+, As+3, As+5) as well as production of reactive oxygen species (ROS). Moreover, increase in nutrient acquisition, nitrogen fixing potential, antioxidant production, proline biosynthesis, regulation of carbohydrate metabolism and asada-halliwell pathway were recorded which ultimately led to increase in plant biomass and yield. Among the different AM fungi, exotic species were more effective than native, of which *Rhizophagus irregularis* provided maximum stress tolerance as compared to the other species.

Conclusion. AMF colonization was a promising strategy for abiotic stress management in legume plants. Therefore, AMF can be a new generation technology for sustainable agriculture.

Key words: Abiotic stresses, arbuscular mycorrhiza fungi, asada-halliwell pathway, functional diversity, legume.

ID 109 - Ectomycorrhizal exoenzymatic activity is tightly coupled with host foliar nutrition

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Introduction. Phosphorus deficiencies are increasingly recognized as a major constraint to ecosystem productivity across the temperate rainforests of British Columbia. Forest trees acquire much of their phosphorus through the activity of their ectomycorrhizal associations, which can use exoenzymatic activity to access otherwise inaccessible organic P.

Methods. Through measuring phosphorus-specific exoenzymatic activity of ectomycorrhizal root tips, and soil and foliar characteristics along a phosphorus edaphic gradient, we set out to evaluate the drivers of exoenzymatic activity across coastal ecosystems. Sampling took place on 12 sites across southern Vancouver Island, Canada.

Results and discussion. Along the gradient, Pi declined 9-fold from less-weathered, east coast Brunisols to more strongly weathered, west coast Podzols, resulting in the P content of highly weathered sites being ~ 84% Po. Reductions in foliar P% confirmed P deficiencies over most Podzol sites. We assayed phosphatase (phosphomonoesterase & phosphodiesterase) activities on the surfaces of individual ectomycorrhizal root-tips to test the hypothesis that phosphatase activities would increase as soil Po/Pi increased. Phosphatase activity on the mycorrhizoplanes was inversely related to soil Pi content, especially phosphodiesterase (adj-R2=0.59; P=0.002), which increased ~2.5X from less-weathered to more weathered soils. There was no relationship with Po. Interestingly, phosphodiesterase activity was negatively related to foliar P% (adj-R2=0.58; P=0.002), and even more tightly coupled, positively, to foliar N:P ratio (adj-R2=0.73; P<0.001), increasing in activity ~4.5X along the gradient.

Conclusion. We conclude that fungal phosphatase activity was most strongly aligned with host P status in relation to N, rather than with P availability alone.

Key words: Ectomycorrhizae, exoenzymes, foliar nutrition, phosphorus, soil nutrition.

ID 134 - Hyphosphere functional microbiome assemblage is affected by phosphorus forms

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Introduction. Arbuscular mycorrhizal fungi-bacteria interactions in the hyphosphere play an important role in mediating the organic P transformation and turnover in soil. However, functional microbiome involved in organic P mineralization remains poorly understood. The aim of this study was to analyze bacterial communities on alkaline phosphomonoesterase (ALP) and ß-propeller phytase (BPP) gene in the hyphosphere, with application of different phosphorus forms in a microcosm experiment.

Methods. Using a compartmented microcosm, leek was grown with or without the AM fungus Funneliformis mosseae in root compartment, and the extraradical mycelium of F. mosseae was allowed to grow into a separate hyphal compartment containing 0, 50 mg P kg^{-1} as KH_2PO_4 or phytin. High-throughput sequencing technologies were employed to analyze the response of ALP- and BPP-harboring bacterial communities associated with extraradical mycelia of *F. mosseae* to phosphorus forms in the hyphosphere.

Results and discussion. The community structures of ALP-harboring bacteria, not BPP-harboring bacterial structures, were significantly changed in response to different P forms. The predominant community compositions of ALP-harboring bacteria were *Sinorhizobium*, *Bradyrhizobium*, *Pseudomonas* and *Ralstonia*, and specifically, P*seudomonas* had higher relative abundance in organic P treatments than those in control and inorganic P treatments. Likewise, the major bacteria harboring the BPP gene was *Pseudomonas*, however, the difference among three P treatments on relative abundance was not detected.

Conclusion. These results reveal the profound differences in ALP- and BPP-harboring bacterial communities at genus level in the hyphosphere, giving a new insight to link microbial flora and function in P cycling.

Key words: Alkaline phosphatase, bacterial community composition, ß -propeller phytase, hyphosphere, P forms.

ID 139 - The phosphorus in the arbuscular mycorrhizal association and the growth of *Acaena elongata* L., in a temperate forest of Mexico City, Mexico

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Introduction. Phosphorus is an essential nutrient for plant growth, but it is limited in the soil of temperate forests, so plants in these ecosystems have developed strategies to maximize its absorption, such as the arbuscular mycorrhizal (AM) association. The main objective was to analyze the response of the AM association based on the growth of *Acaena elongata*.

Methods. Under four concentrations of phosphorus: control (0 g P kg^{-1}), low (0.05 g P kg^{-1}), intermediate (0.2 g P kg^{-1}) and high (2 g P kg^{-1}), we predict that the growth will be positively associated with the AM colonization under a low concentration of phosphorus and will be negatively associated in a high concentration of P. The seedlings were harvested every two months, during one year, to obtain growth averages, the P content in plant tissue and the AM colonization.

Results and discussion. There were significant differences between treatments and between harvests for AM colonization and growth. The highest values in the growth measures occurred in the treatment of low concentration and high of added P. The AM colonization was significantly lower at the highest concentration of P. The direction of the correlations established between the growth measures, the concentration of P in plant tissues and the AM colonization were influenced by the concentration of P in the soil.

Conclusion. The availability of phosphorus in the soil directly influences the dynamics of the arbuscular mycorrhizal association, maintaining a mutualism in conditions of limited, but not in conditions of abundance of P.

Key words: Arbuscular mycorrhizas, fertilization, plant growth, temperate forest, weed.

ID 144 - *Fusarium* spp. promotes the symbiotic germination of *Dendrobium wangliangii*

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Introduction. Under the natural conditions, orchid seeds require compatible orchid mycorrhizal fungi (OMF) for germination. Therefore, understanding the compatible mycorrhizal fungi for each orchid species is crucial for the conservation of endangered orchid species. *Dendrobium wangliangii* is an endangered and epiphytic orchid with tolerance to seasonally extreme arid conditions and occurs exclusively in the hot-dry valley area of southwestern China. Thus, it is important to identify the germination-promoting OMF for its conservation.

Methods. The *ex situ* seed baiting technique was used for obtaining the protocorms of *Dendrobium wangliangii*, and the symbiotic fungi were isolated from the protocorms. The strains were sequenced and identified. The effective symbiotic fungi that could promote the germination of *Dendrobium wangliangii* were screened by the symbiotic germination of the seeds with the isolations.

Results and discussion. The protocorms of *Dendrobium wangliangii* were produced by symbiotic germination technology. 11 pure colonies were successfully isolated from the protocorms. Using molecular sequencing, 9 isolates were identified as *Fusarium*, 1 were *Chaetomium* and 1 were assigned to *Alternaria*. Through the symbiotic germination of *Dendrobium wangliangii*, 2 from *Fusarium* sp. KP137445.1), 1 from *Fusarium solani* JX869487.1 and 1 from Uncultured *Fusarium* KC311554.1 effectively promoted seed germination of *Dendrobium wangliangii*. The germination rate of the four treatments was over 41.10±4.79%, which was significantly higher than that of the control group ($P<0.05$).

Conclusion. *Fusarium* spp. are an effective symbiotic fungus that promoted the germination of *Dendrobium wangliangii*.

Key words: *Dendrobium wangliangii*, *Fusarium* spp., orchid, seed baiting technique, symbiotic seed germination.

ID 188 - Response of three cover crops to phosphate-solubilizing fungi and arbuscular mycorrhizal fungi inoculation

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Introduction. Cover crops prevent soil erosion, improve the physicochemical and biological properties of soil. Arbuscular mycorrhizal fungi (AMF) and the phosphate-solubilizing fungi (PSF) are used as an agroecological alternative in crops. This research aims to evaluate the effect of the AMF and PSF inoculation on three cover crops.

Methods. Greenhouse experiment was stablished with a randomized experimental design, with three cover crops: *Canavalia ensiformis* (Ce); *Mucuna pruriens* (Mp); *Clitoria ternatea* (Ct) and with four levels of inoculation: AMF consortia (Rizofermic), PSF *Penicillium brevicompactum*, both inoculants and non-inoculated for three cycles of 50 days. The variables measured were: AMF colonization and plant fresh weight. A factorial ANOVA and a Tuckey HSD were used. 10-day old plants were inoculated with 10 g of Rizofermic and 1x108 UFC x mL-1 of PSF, harvesting 30 days after inoculation.

Results and discussion. In first cycle there were significant differences (F= 70; p= 0.0) between treatments inoculated with AMF. In Mp had 37.6% and Ce 22.8% with AMF+PSF. Fresh weight of plants showed differences where Mp+PSF and Ce with AMF+PSF had the highest colonization (F= 457; p= 0.0). The second cycle, the fresh weight had differences (F=793; p=0.0), where Ce+PSF had 52.7, Mp 25.7 and Ct+AMF 5.7.

Conclusion. Co-inoculation can yield a higher benefit to cover plants than individual inoculation.

Keywords: Biofertilizers, interactions, microorganisms, nutrition, soil.

ID 193 - Exploitation of different organic nitrogen sources in soil by the AM fungal networks

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Introduction. Although lacking a potent exo-enzymatic repertoire to access organic nutrient sources, arbuscular mycorrhizal (AM) fungi have repeatedly been shown to proliferate their hyphae in soil patches enriched with organic nitrogen (N), obtain N from such soil zones, and sometimes also transfer significant amounts of the N to their plant hosts. It appears that AM fungal hyphae acquire the N from organic sources mainly via so-called soil microbial loop, involving primary decomposers and their grazers. Yet, direct comparison of different organic N sources and their exploitation efficiency by AM fungal hyphae is still largely lacking.

Methods. Here we analyzed, using direct 15N-isotopic labeling, the fate of plant leaf litter or fungal chitin in a root-free zone of mycorrhizal and non-mycorrhizal pots.

Results and discussion. At five weeks after adding the different N sources into the pots, mycorrhizal plants contained about 20 times more of the 15N than did their non-mycorrhizal counterparts. In contrast, greater 15N retention in the labeling patches, but also higher overall 15N losses from the pots, were often observed in the non-mycorrhizal as compared to the mycorrhizal pots. The treatments amended with chitin lost 50% or more of the 15N during the five weeks of cultivation, as compared to losses not exceeding 50% in the plant litter treatments.

Conclusion. Interestingly, only about 20% of the chitin carbon actually remained in the pots after five weeks of cultivation (measured using dually 13C-15N-labeled chitin), irrespective of the mycorrhizal treatment, indicating efficient mineralization in the root-free zone of both, mycorrhizal and non-mycorrhizal pots.

Key words: Immobilization, nitrogen, root-free zone, stable isotopic labeling, transfer.

ID 195 - Investigation of plant interactions across common mycorrhizal networks using rotated cores

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Introduction. Arbuscular mycorrhizal (AM) fungi influence plant mineral nutrient uptake and growth, hence, they have the potential to influence plant interactions. The power of their influence is in extraradical mycelia that spread beyond nutrient depletion zones found near roots to ultimately interconnect individuals within a common mycorrhizal network (CMN). Most experiments, however, have investigated the role of AM fungi in plant interactions by growing plants with versus without mycorrhizal fungi, a method that fails to explicitly address the role of CMNs.

Methods. Here we propose a method that manipulates CMNs to investigate their role in plant interactions. Our method uses modified containers with conical bottoms with a nylon mesh and/or hydrophobic material covering slotted openings, 15N fertilizer, and a nutrient-poor interstitial sand. CMNs are left either intact between interacting individuals, severed by rotation of containers, or prevented from forming by a solid barrier.

Results and discussion. Our findings suggest that rotating containers is sufficient to disrupt CMNs and prevent their effects on plant interactions across CMNs. Our approach is advantageous because it mimics aspects of nature, such as seedlings tapping into already established CMNs and the use of a suite of AM fungi that may provide diverse benefits.

Conclusion. Although our experiment is limited to investigating plants at the seedling stage, plant interactions across CMNs can be detected using our approach which therefore can be applied to investigate biological questions about the functioning of CMNs in ecosystems.

Key words: Common mycorrhizal networks, competition, extraradical mycelium, facilitation, mycorrhizal fungi.

ID 205 - Period of colonization of endomicorrhizas in tomato plants under greenhouse

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Introduction. Arbuscular mycorrhizae (MA) establish a mutual symbiosis between fungi and plants. The use of MA has been of great importance in the agricultural sector for its ability to increase the absorption of nutrients, such as phosphorus and nitrogen, stimulate growth, increase resistance to abiotic stress (drought, salinity, heavy metals) and biotic stress caused by pests and diseases, increases tolerance to water stress, and contributes to the improvement of soil structure.

Methods. The estimation of the period of infection and degree of advancement of fungi MA in root, an application was made in tray and another in transplantation of commercial products based on mycorrhizas in tomato under greenhouse conditions, by clarifying and staining mycorrhizae.

Results and discussion. After 58 days of the first application, the presence of MA mycelium in root tissue was observed; after 100 day of the application whas determinated the mycorrhization percentage of 36%.

Conclusion. The early inoculations of MA in short cycle crops favor the benefits of their establishment, given the long times for infection and colonization of the mycorrhiza, ensuring that their infection is during the vegetative growth and its use in the stage of requirement of the crop.

Key words: Endomicorrhizas, mycorrhization percentage, tomato.

ID 206 - Effect of radicular exudate on mycorrhizal infection

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Introduction. The mycorrhizal relationship favors nutrition processes, root exploration, soil structuring and root architecture among other advantages. Crops established in soils with adverse conditions of drought or salinity problems may be favored by the presence of mycorrhizae. The infection process begins with a series of fungal and root secretions that favor and regulate the colonization of the root by the fungus. Various signs of root exudation define the success of the infection.

Methods. Apple trees of 8-month-old in the nursery were inoculated into the irrigation system with a complex of ecto and endo-mycorrhizal fungi mixed with a inductor of root exudates (Exuroot®) in the irrigation water. Six months after application, treated and control trees were extracted, the evaluation was done by washing the root zone, and mycorrhizal staining of root segments.

Results and discussion. A greater amount of root mass of 15% was observed in the trees inoculated with endo and ecto mycorrhizae with Exuroot® compared to the control. In addition, mycorrhizal colonization was 55% greater in the Exuroot® treatment than in the control.

Conclusion. The application of mycorrhiza complexes accompanied by an inductor of root exudates favors root development and the establishment of mycorrhizae.

Key words: Aplee trees, endo and ecto mycorrhizae, inductor of root exudates.

ID 211 - First insights into stable isotope signatures of arbuscular mycorrhizal fungi

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Introduction. Arbuscular mycorrhizal (AM) fungi form associations with 71% of all land plants; however, our knowledge on their role in ecosystem carbon and nutrient cycling is limited. Stable isotope approaches are important tools for deciphering nutrient dynamics within plant-fungus-associations, but they are limited by sampling and identification difficulties of hyphae in the field. For saprotrophic (SAP) and ectomycorrhizal fungi (EcM), fruiting bodies were identified to resemble the isotopic signatures of belowground hyphae, which remains a challenge for AM fungi lacking fruiting bodies. Here, we applied methods to isolate AM hyphae from roots and soil to measure their stable isotope signatures.

Methods. Two AM-forming plants were inoculated with spores of *Rhizophagus irregularis*. Hyphae were isolated from soil following a modified approach by Brundrett et al. (1994) and from roots by applying an enzymatic (modified after Saito 1995) and a mechanical approach. Stable isotope natural abundances of 13C and 15N were determined with an EA-IRMS.

Results and discussion. AM hyphae were successfully isolated from both soil and roots with all mentioned approaches. Their stable isotope signatures are located between autotrophic plants and EcM/SAP fungi, with the AM fungi being more 13C enriched compared to plant leaves and roots and less 15N enriched than EcM and SAP fungi.

Conclusion. Overcoming the methodological obstacle of using fruiting bodies as supposedly adequate surrogate for fungal hyphae, the combination of hyphal isolation and determination of isotopic patterns will largely enhance our understanding of mechanisms of carbon and nutrient transfer between the plant and the soil via mycorrhizal fungi.

Key words: Arbuscular mycorrhiza, fruiting bodies, hyphae extraction, stable isotope natural abundance.

ID 218 - Mycorrhizal colonization, growth and foliar concentration of nutrients in seedlings of pecan *Carya illinoensis* (Wang.) K. Koch and pistachio *Pistacia atlantica* Desf. inoculated with ecto- and endomycorrhizal fungi

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Introduction. The pecan and pistachio orchards are established with trees produced in nurseries. The fungi associated with pecan are *Astraeus*, *Gyrodon*, *Pisolithus*, *Russula*, *Scleroderma*, *Tuber* and *Tylopilus*. Some members of the *Carya* genus establish associations with *Glomus*, *Gigaspora* and *Sclerocystis*. In the species of the *Pistacia* genus the colonization is by arbuscular mycorrhizal fungi.

Methods. They were inoculated with ecto fungi (Mycor-Tree®, 4x106 and 4x105 spores of *Pisolithus tinctorius* and *Scleroderma* sp.) and endomycorrhizal fungi (*Glomus* sp. Zac-19 and *Glomus intraradix* AM-CP) pecan and pistachio seedlings. The following variables were measured: percentage of mycorrhizal colonization (by counting macroforms for ectomycorrhizae and of vesicles and arbuscules for endomycorrhizas), height and diameter of the stem and foliar concentration of nutrients.

Results and discussion. Pecan roots were ectomycorrhizal, colonization from 0 to 83%. Ornamented hyphae of *Pisolithus tinctorius* were identified. The pistachio roots were endomycorrhized with *Glomus intraradix* with colonization from 0 to 78%. A linear, positive and highly significant relationship between mycorrhization and stem growth was found, with r^2= 0.64 to 0.74 in pecan and r^2= 0.63 to 0.77 in pistachio. In pecan the ectomycorrhization favored the foliar concentration of Zn and in pistachio the endomycorrhization did with the Cu.

Conclusion. The pecan seedlings formed ectomycorrhizae and pistachio endomycorrhizae, the growth of seedlings was greater as the degree of mycorrhizal colonization increased. The ectomycorrhization increased the foliar concentration of Zn in pecan and the endomycorrhization of Cu in pistachio.

Key words: Ectomycorrhizae, endomycorrhizae, *Glomus*, growth, *Pisolithus*.

ID 225 - Species difference of acid phosphatase activity in hyphal exudates of arbuscular mycorrhizal fungi

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Introduction. Organic phosphorus (P) accounts 20-80% of the total soil phosphorus. Some plants have ability to hydrolyze organic P by secreting acid phosphatase (ACP). Previous study demonstrated that arbuscular mycorrhizal fungi (AMF), *Rhizophagus clarus*, secret ACP from its extraradical hyphae. However, the ability of different AMF species to produce ACP and its effect on plant growth are not known.

Methods. *Acaulspora* sp., *Glomus* sp., and *Diversispora gibbosa* were isolated from *Gmelina arborea*, *Artocarpus champeden*, and *Dipterocarp* mixed forest, East Kalimantan, Indonesia. *Allium fistulosum* were uninoculated or inoculated with these three AMF species and grown on a two-compartment pot filled with sterilized Andosol to which 0.5 g P2O5 was applied. Soil solution was collected from the hyphal compartment 45, 50, 55 and 60 days after sowing using mullite ceramic tubes. The ACP activity in the soil solution was measured by using disodium p-nitrophenylphosphate. AMF colonization, shoot dry weight, shoot P concentration and hyphal length in the hyphal compartment were measured.

Results and discussion. AMF colonization of all inoculated plants was 98%. The hyphal length of inoculated treatment ranged from 66 to 90 cm g- dry soil. ACP activity was detected in soil solution of all AMF species. The ACP activity in soil solution of *D. gibbosa* was higher than uninoculated and other AMF species. AM colonization of these three species increases the shoot dry weight of *A. fistulosum*.

Conclusion. These results demonstrate that the ACP activity in hyphal exudates is different among AMF species.

Key words: Acid phosphatase, hyphal exudate, hyphal length, organic phosphorus, species differences.

ID 236 - Two arbuscular mycorrhizal plant species with different morphotypes (*Arum maculatum, Paris quadrifolia*) are distinguished in their stable isotope natural abundance

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Introduction. Fungal root endophytes are either beneficial – represented by a bi-directional nutrient transfer between the plant and the fungus (mycorrhizas) – or antagonistic (mycoheterotrophy). Mycoheterotrophs exploit the fungi for carbon-nutrients. Stable isotope approaches are an elegant tool to unmask those cheaters. For the globally distributed arbuscular mycorrhizae (AM) two types can be distinguished: *Arum*-type (after *Arum maculatum*) forming hyphae along cortical intercellular airspaces, *Paris*-type (after *Paris quadrifolia*) forming intracellular hyphal coils. So far, every achlorophyllous mycoheterotrophic AM plant species reveals the *Paris*-type, however green *Paris*-type species were rarely analyzed for mycoheterotrophy. We aim to compare *Arum maculatum* and *Paris quadrifolia* with the expectation that *Paris*-type species are enriched in 13C and 2H in analogy to hyphal coil forming mycoheterotrophs.

Methods. *Arum maculatum* (n = 10), *Paris quadrifolia* (n = 10) and co-occurring plants as references (n = 30) were sampled in two separated forest sites (Germany). Plant material were measured for 13C, 15N (EA-IRMS) and for 2H and 18O (TC-IRMS).

Results and discussion. *Paris quadrifolia* were significantly enriched in 2H, 13C compared to reference plants and additionally in 15N compared to *Arum maculatum* while no differences were found for 18O.

Conclusion. For the first time, we could show that the arbuscular mycorrhizal subtypes reveal differences in their natural stable isotope abundances. The relative enrichment in green *Paris quadrifolia* individuals shows strong similarities to the situation in partial mycoheterotrophic plants also colonised by hyphal coil forming fungi. To validate this, more analyses are highly recommended which is currently work in progress

Key words: Arbuscular mycorrhizae, *Arum*-type, mycoheterotrophy, *Paris*-type, stable isotopes.

ID 248 - Carbon to phosphorus exchange rate in relation to host-preference in AM fungi

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Introduction. The majority of land plants establish mutualistic symbioses with arbuscular mycorrhizal (AM) fungi, that benefit both partners by mediating uptake of essential plant nutrients fueled by host's photosynthates. AM fungi form large multinucleate spores, nuclei can migrate and mix within developed extraradical mycelial networks that link different plants. The promiscuous nature of AM symbiosis where both partners simultaneously engage in multiple interactions, makes the symbiosis potentially sensitive to the emergence of cheater strains, i.e. strains that increase their fitness at the expense of the other host.

Methods. Our experiment is designed to test if fungal cheaters can emerge when a single AM fungus simultaneously colonies two different host plants. To study the symbiotic performance in a dual host system, we will apply 33P isotopes to five-months-old systems containing one native and one novel plant (C3 and C4) that are linked by hyphal network to investigate carbon for phosphorus exchange rate. In addition, plant and fungal fitness, will be estimated and root colonization rate will be measured.

Conclusion. Fungal fitness will be analyzed in relation to the estimated carbon to phosphorus traded with the two hosts.

Key words: AM fungi, dual host system, host- preference, nutrient exchange, symbiotic performance.

ID 265 - Root colonization with arbuscular mycorrhizal fungi and supplementary P fertilization improve nutrient status, growth and physiological performance of *Anthurium pedato-radiatum* Schott.: Araceae

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Introduction. *Anthurium pedato-radiatum* is an endemic Mexican wild species. This perennial and herbaceous plant with beautiful leaf morphology has great potential for commercial cultivation as ornamental. Ubiquitous mycorrhizal fungi associate with *A. andraeanum*, a close relative of *A. pedato-radiatum*, however, for most of the 700 *Anthurium* species only limited information has been reported.

Methods. Young micropropagated plantlets were used to run a factorial experiment with 2-levels of mycorrhizas (+AM, -AM) and four P fertilization regimes (0, 22, 44 and 66 ppm). After sixteen months of greenhouse culture we evaluated plant growth, plant physiology and photosynthetic performance, and the nutrient status in foliar tissues.

Results and discussion. Non-mycorrhizal plants remained free of colonization while the inoculated showed typical fungal structures. Under P-stress mycorrhizas enhanced overall plant growth, physiological performance and nutrient status when compared to uninoculated plants. Significant effects in most experimental variables were recorded as the rate of P fertilization increased in both –AM and +AM plants but 66 ppm P was excessive. Mycorrhizal plants had increased P, Ca, and S but lower contents of Fe, Zn and Mn than -AM plants under all P levels. The nutrient status was significantly improved with increases of P supply, which promoted higher growth. Nutrient disorders such as antagonistic (P-Ca, K, S, Mg, Fe, Zn) and synergistic (P-Mn, N,) interactions were observed.

Conclusions: *Anthurium pedato-radiatum* is a mycorrhizal plant. Both, P-level and mycorrhizas enhanced overall plant growth, physiological performance and nutrient status. Differences in P fertilization promoted nutrient antagonistic and synergistic interactions.

Key words: *Anthurium*, arbuscular mycorrhizas, mycorrhizae, plant nutrition.

ID 298 - Microbial dynamics and functionality influenced by phytate of soybean plants

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Introduction. Reduction of chemical fertilizer is an ultimate need to restore our soil for better plant growth and health. In plants, phytate is a primary storage of phosphorus (60-90%), and it can reduce inorganic phosphorus supplementation by 30-50%.

Methods. Emphasising on organic farming, we used phytate as organic phosphate source and microbial suspension originated from naturally grown environment. We keep the other nutrient source constant and want to evaluate the effect of phytate on microbial community structure dynamics. Also we will quantify the pattern of microbial community structure against each treatment using 16S rRNA and ITS based gene sequencing using Next Generation Sequencing, and perform a functional analysis of sequencing data against reference database. In order to identify the functional traits linking clusters thriving on phytate, we will select the most abundant taxon in the enriched clusters. We are also interested in finding out if any Arbuscular Mycorrhizal Fungi (AMF) is present in the microbial community and how AMF(s) interacts with other microbes, or is AMF playing any key role in recruiting other microbes in response to phytate.

Results and discussion. We are assuming that this study might yield a common theme of phytate solubilizing taxa including AMF consistent with observations that might be used for phosphorus dissolution in order to reduce inorganic phosphorus for soybeans.

Conclusion. The project emphasizes a comprehensive understanding of nutrient-related changes to the root-associated microbiota to the growth and development of soybean plants.

Key words: AMF, phytate, soybean.

ID 304 - A semi-hydroponic cultivation system associating *Anchusa officinalis* with arbuscular mycorrhizal fungi for optimal production of plant secondary metabolites

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Introduction. *Anchusa officinalis*, from the Boraginaceae family, is known for its therapeutic properties (e.g. anti-inflammatory and anti-viral) attributed to the production of bioactive metabolites. These plants interact with various microorganisms including arbuscular mycorrhizal fungi (AMF), which are suspected to stimulate the production of secondary metabolites (SMs).

Methods. To investigate the role of AMF on the production of SMs, a semi-hydroponic (S-H) cultivation system was set up. The system consisted of pots filled by perlite and containing plants of *A. officinalis* mycorrhized (M) or not (NM) by one of the following AMF strain [*R. irregularis* (MUCL 41833), *R. clarus* (MUCL 46238), *G. aggregatum* (MUCL 49408) and *R. intraradices* (MUCL 49410)]. A nutrient solution was circulated on the plant roots via peristaltic pumps. Plant growth parameters as well as root colonization were assessed. The extraction and semi-quantification of the SMs was measured in the shoots and roots, using HPLC-PDA-ELSD and UHPLC-HRMS.

Results and discussion. Whatever the AMF strain, all the plants were colonized by the fungi, with values ranging from 76% (MUCL 41833) to 91% (MUCL 46238). Curiously, root biomass and total plant biomass were lower in the M *versus* NM plants. Two major SM peaks were observed in all the AMF treatments with slight differences among fungi and with the NM controls.

Conclusion. This experiment demonstrated the potential of AMF to colonize *A. officinalis* under S-H cultivation conditions. Plant growth promotion seemed decreased as compared to the controls, while no differences were noticed in SMs production. Further experiments are needed to better comprehend the possible role of AMF on SMs production.

Key words: *A. officinalis*, arbuscular mycorrhizal fungi, circulatory semi-hydroponic cultivation system, *R. irregularis*, secondary metabolites.

ID 154 - Guild patterns of basidiomycetes community associated with *Quercus mongolica* in Mt. Jeombong, Republic of Korea

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Introduction: Depending on the mode of nutrition exploitation, major fungal guilds are distinguished as ectomycorrhizal and saprotrophic fungi. It is generally known that diverse environmental factors influence fungal communities; however, it is unclear how fungal communities respond differently to environment factors depend on fungal guilds.

Methods: we investigated basidiomycetes communities associated with *Quercus mongolica* using 454 pyrosequencing. We attempted to detect guild pattern (ectomycorrhizal or saprotrophic fungal communities) by comparing the influence of geography and source (root and surrounding soil).

Results: A total of 515 mOTUs were detected from root (321) and soil (394) of *Q. mongolica* at three sites of Mt. Jeombong in Inje County. We found that patterns of diversity and community structure were different depending on the guilds. In terms of alpha diversity, only ectomycorrhizal fungi showed significant differences between sources. In terms of community structure, however, geography significantly influenced the ectomycorrhizal community, while source appeared to have a greater influence on the saprotrophic community.

Conclusions: A guild-based view will help to elucidate novel features of the relationship between environmental factors and fungal communities. Geography is likely a major factor determining EMF communities, while source was more important for SPF communities.

Key words: Ectomycorrhizal fungi, guild-based view, Mongolian oak, pyrosequencing, Sebacina.

ID 61 - DSE colonization alleviated Cd toxicity of maize by remodeling host cell wall and Cd subcellular distribution pattern

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Introduction. The subcellular re-distribution of metal ions altered by numerous biotic and abiotic factors (e.g. mineral nutrients, or root-associated endophytes) repeatedly confirmed the vital role of the modifications in cell wall (CW) in heavy metal response, while the process and the physico-chemical properties of the remodeling CW, functioning a compartment as a sink for toxic metals in plant, is still obscure.

Methods. Under 0 and 200 μM Cd stress, the response of CW was analyzed comparatively between the maize (*Zea mays*, B73) inoculated with one dark septate endophytic fungus (DSE, *Exophiala pisciphila*) and the uninoculated control.

Results and discussion. Compared with the uninoculated controls, *E. pisciphila* significantly increased the activities of CW-related enzymes, e.g. pectin methylesterase (PME), phenylalnine ammonialyase (PAL), and peroxidase (CWP), and up-regulated the genes expression of cell wall biosynthesis, resulting in the remodeling CW under metal stress. *E. pisciphila* colonization enhanced the chelation of functional groups responsible for metal binding and immobilization in plant CW. Also, *E. pisciphila* colonization significantly altered Cd cellular/subcellular distribution in maize roots CW, via reducing Cd transportation to xylem, instead of the enhanced Cd accumulation in epidermis, cortex, and endodermis cells.

Conclusion. These results suggested that the enhanced Cd cellular/subcellular compartmentalisation in maize roots CW via increasing CW binding capacity and reducing Cd transportation unloading from the xylem to leaf was a powerful altered strategy to confer maize tolerance against Cd toxicity by *E. pisciphila*.

Key words: Cadmium tolerance mechanism, cell wall, dark septate endophyte, *Exophiala pisciphila*, maize.

ID 67 - Do microbes support plant growth on natural bituminous soils?

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Introduction. Naturally occurring bituminous soils in the Northern Alberta, Canada provide a unique opportunity to investigate whether we can utilize beneficial relationships between soil microbes and trees to reclaim sites containing hydrocarbons. Here, we test if mycorrhizal fungi isolated from natural bituminous soil, bituminous-free soil, or disturbed soil containing hydrocarbons differentially affect host tolerance to hydrocarbons.

Methods. We collected soil inoculum from three sites within northeastern Alberta, where mature forests have established on natural bituminous soils, and from another three adjacent forest sites free from hydrocarbons. Finally, we collected soil inoculum from a recently disturbed mining site. We grew *Populus tremuloides* for 72 days in five soil types (i.e. natural bituminous soil, bituminous-free soil, disturbed bituminous soil and soil with 1% and 5% hydrocarbons) either inoculated or not with soil inoculum from each site.

Results and discussion. *P. tremuloides* seedlings were smaller in presence of hydrocarbons. Seedlings grown in 1% and 5 % hydrocarbons were 46% and 22% shorter than those grown in natural bituminous-free field soil, respectively. Overall, soil inoculum did not significantly impact seedling height.

Conclusion. Although hydrocarbons reduced plant growth this response may not necessarily be linearly related to hydrocarbon concentration as seedlings were shortest in 1% than in 5% hydrocarbons. Furthermore, soil biota may either not be important in this context or take longer than 72 days to arise.

Key words: Arbuscular mycorrhizal fungi, ectomycorrhizal fungi, hydrocarbons, natural bituminous soil, *Populus tremuloides*.

ID 221 - Ectomycorrhizal community composition in Submediterranean oak secondary forest under changing environmental conditions

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Introduction. Past human activity in the Karst area of Slovene Submediterranean has resulted in soil erosion from the vast area. After abandonment of pastures 30-40 years ago, area was spontaneously encroached by various woody species, among which pubescent oak (*Q. pubescens* Willd.) is prevailing. The area is characterized by frequent summer droughts, wildfires and presence of two distinct types of bedrock – calcareous (with rendzic leptosol) and eutric cambisol. Abiotic factors are strongly limiting vegetation thriving in this area, but on the other hand, ectomycorrhizal fungi may have beneficial effects.

Methods. To characterize ectomycorrhizal fungal (EMF) communities of pubescent oak on two types of bedrock and under rainfall exclusion simulating climate change with longer drought periods, soil cores from three plots (calcareous, calcareous + rain exclusion, eutric cambisol) were collected from June 2016 till May 2018. From each soil core, ectomycorrhizal morphotypes associated with oak roots were isolated, morpho-anatomically characterized, and sequenced using ITS1/ITS4 markers. Assembled sequences were identified using UNITE database and molecular identification was compared and combined with morpho-anatomical identification.

Results and discussion. Effects of season and plot were observed on community composition of oak EMF. The lowest general EMF richness and the lowest seasonal variability in species richness was observed on rendzic plot with rain exclusion. Percentage of vital ectomycorrhizal tips was dependent only on season, with peaks in late spring/early summer.

Conclusion. Climate change with accompanied longer droughts in already extreme sites may result in impoverishment of EMF communities, which can subsequently lead to decrease in spectrum of EMF functionality in such environments.

Key words: Abiotic stress, climate change, drought, encroachment, Karst.

ID 227 - Microbial communities in potentially toxic metal contaminated soil before and after remediation

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Introduction. Soil is a limited resource and soil contamination with potentially toxic metals is a global problem. Soil remediation procedure with EDTA (chelant – ethylenediaminetetraacetic acid) is a good solution for cleaning contaminated soils. However, there is limited knowledge on how this procedure affects soil microorganisms, including plant symbiotic arbuscular mycorrhizal (AM) fungi.

Methods. The impact of soil remediation with EDTA on the availability of Pb, Cd and Zn in soil, mycorrhiza and microbial community developement was investigated. We designed a mesocosm experiment in which we included two types (acidic and calcareous) metal contaminated soil, and control (non-contaminated) soil, before and after remediation. All the three types of the original (non-remediated) soils differed in soil properties, especially in the pH and soil organic matter content, and total metal concentration. We also included plants (*Lolium perenne*) and added inoculum (rhizosphere soil) as treatments. Microbial communities were characterised using molecular methods.

Results and discussion. After soil remediation procedure practically no AM fungal colonisation was detected in plant roots. However, within two years of experiment duration functional mycorrhiza was established either by spontaneous dispersal of mycorrhizal propagules from the environment or by additional inoculation.

Conclusion. Continuous growth of plants in remediated soil was an important factor not only for development of AM fungi, but was also highly correlated with overall microbial biomass and abundance of gene markers for specific microbial groups (archaea, bacteria and fungi) and functional genes.

Key words: Arbuscular mycorrhiza, heavy metal polluted soil, microbial communities, remediation, revitalization.

ID 229 - Effect of inoculation with arbuscular mycorrhizal fungi and plant growth promoting bacteria on growth and development of *Theobroma cacao* L. affected by cadmium

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Introduction. Peru is the second producer of organic cocoa, with 1.7% of world production. Many authors have reported that *Theobroma cacao* L. could bioaccumulate cadmium, affecting its its commercial activity in international markets. Beneficial microorganisms such as arbuscular mycorrhizal fungi (AMF) and plant growth promoting bacteria (PGPB), can alleviate cadmium toxicity of plants. In this work we study the effect of AMF and PGPB on cocoa growth and development at two cadmium concentrations.

Methods. A greenhouse experiment was established with a substrate of 0, 2 and 10 ppm of cadmium inoculated with two AMF: cocoa fungal consortium (CM), and *Rhizophagus intraradices*, (RI); a PGPB: *Rhizobium vallis* (RV) and combination of both AM and PGPB. A control treatment without inoculation was also considered. At harvest, plant morphometric parameters were determined.

Results and discussion. CM, RI and the interaction treatments with RV resulted in a high relative water content with values of up to 98% each, in all Cd concentrations tested. Chlorophyll content was significantly greater when plants were inoculated with RV (47.4) at 2 ppm Cd compared with the control. Height of the plants were greater when inoculated with RI + RV (36.1 cm) at 2 ppm Cd and with RI (34.8 cm) at 10 ppm Cd. Results showed that RI favored shoot dry weight (7.0 g) at 10 ppm Cd and RV stimulated root dry weight (2.4 g) at 0 ppm Cd.

Conclusion. Our results suggest positive effect of beneficial microorganisms on cocoa growth in presence of Cd. The implications of these interactions will be discussed.

Key words: Cadmium, cocoa, heavy metals bioaccumulation, *Rhizobium vallis*, *Rhizophagus intraradices*.

ID 230 - The influence of wheat microbiomes on drought stress

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Introduction. Drought stress (DS) is a limiting factor of the development, and yield of crops such as wheat. Plants respond throughout intrinsic mechanisms, also through interactions with microorganisms such as arbuscular mycorrhiza (AM) formed between the root system and the fungi of the subphylum Glomeromycotina. The plant gives carbohydrates; in return, the fungus gives nutrients and water.

Methods. Four wheat landraces from Afghanistan (A205 and A207), Bolivia (B5), and Colombia (C333) were inoculated with soil containing AM fungi; sterilized inoculum and a filtered soil solution were used in non-mycorrhizal treatment. Chlorophyll content and dry weight (DW) were measured. DS was imposed on inoculated 30-days-old plants during two weeks maintaining 40% field capacity. To observe the AM colonization, a root sample was stained.

Results and discussion. The AM fungi did not colonize any plant of the inoculated treatment. The chlorophyll values showed a statistical significance only in A207 in well-watered conditions compared with DS. Aerial DW was higher in well-watered plants in all landraces; C333 and B5 under DS presented the same amounts of root DW as well-watered treatment.

Conclusion. DS was imposed during the vegetative phase in a short period, which could have affected the growth of the aerial part, letting the roots to expand to increase the water uptake. Although DS had an impact on DW, the chlorophyll content apparently was not affected by this condition when the values were compared.

Key words: Arbuscular mycorrhizal fungi, chlorophyll content, drought stress, dry weight, spring wheat.

ID 239 - Soil ectomycorrhizal fungal communities under chronic N deposition

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Introduction. Nitrogen (N) is a limiting factor in most temperate and boreal forests that trees have adopted to through e.g. soil and root fungi. Long-term N deposition caused by human activity can disturb natural forest ecosystem homeostasis including both soil and trees. As nitrogen is also required for soil and root fungi, tree roots and their direct interactions with the soil environment through symbiotic fungi and indirect interactions with free-living saprotrophic fungi may be adversely affected by elevated**.**

Methods. The objective of the research was to define the response of soil ectomycorrhizal communities to long-term elevated artificial N loads. Soil samples were collected in 7 forest sites located in N-E the United States fertilized with inorganic N resulting in the total wet N deposition ranging from ca. 3 to 60 kg ha^{-1} yr^{-1}.

Results and discussion. Next-generation sequencing (4 mln reads) revealed 698 OTUs out of which 76 were ectomycorrhizal or possibly ectomycorrhizal (1.4 mln reads). Species of *Russula*, *Lactarius* and unidentified Russulaceae dominated (560k), followed by *Cenococcum* (270k) Atheliaceae (170k), Thelephoraceae (90k), *Cortinarius* (80k), and Sebacinaceae (40k).

Conclusion. *Lactarius* spp., unidentified Russulaceae, Atheliaceae, Sebacinaceae, and Thelephoraceae tend to dominate in fertilized soils. However, other site-specific environmental variables are also significant in the response.

Key words: Chronic nitrogen deposition, ectomycorrhizal fungi, nitrogen fertilization, soil.

ID 259 - Optimizing Arbuscular Mycorrhizal Use in Agriculture to Reduce Heavy Metal Uptake in Crops

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Introduction. Soil pollution with heavy metals (HM) is a serious worldwide environmental issue particularly affecting agriculture. The consumption of crops grown in HM contaminated soils can have adverse public health effects. Arbuscular Mycorrhizal fungal (AMF) inoculants are thought to confer a range of benefits in agricultural systems, and studies show AMF inoculation can either increase or decrease plant symbiont accumulation of heavy metals depending on a range of conditions and factors. This study contributes to an understanding of the mechanisms through which AMF adsorb HM in agricultural soils to optimize restoration of degraded and heavy metal contaminated agricultural soils and limit HM uptake into food crops.

Methods. A controlled column experiment is set up to investigate the parameters by which AMF sorbs target HMs of concern in agricultural crops. Lettuce is inoculated with AMF isolated from our reference sites and grown in sterilized soils from our partner sites in a column experiment over a 3-month period. Treatment combinations will be HM concentration and AMF inoculum source. Factors that will be changed include pH, amendment with P fertilizer, soil moisture content, AMF with N fixing bacteria inoculum, AMF with endophytic fungi, and whole soil (unsterilized) from our reference site.

Results. Experiment is in progress and results will be available for poster presentation at the conference.

Conclusions. We hypothesize that optimizing AMF applications to adsorb heavy metals will be part of the transition to sustainable agriculture, and ultimately, achieving food security in the context of a shifting climate, growing population, and soil degradation and pollution issues.

Key words: AMF, heavy metals, soil quality, soil restoration, sustainable agriculture.

ID 260 - Effect of inoculation with arbuscular mycorrhizae on the survival of *Araucaria araucana* subjected to drought

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Introduction. It has been reported that arbuscular mycorrhizal fungi (AMF) increase the survival and yield of plants in conditions of low water availability. The present study evaluated the response of *Araucaria araucana* (*Araucaria*) to post-mycorrhizal drought, in order to evaluate the effect that the association with AMF has on the survival of plants, and on morphological and physiological parameters.

Methods. Plants of *Araucaria* were inoculated with HMA consortiums from the sectors: Nahuelbuta National Park (NNP), Conguillio National Park (CNP), China Muerta Natural Reserve (CHMNR) and Tolhuaca National Park (TNP), of the last two from sectors conserved and affected by the fire. The plants were maintained for 5 months under greenhouse conditions. Subsequently, they were subjected to drought: 1 irrigation per week (for 4 weeks) and without irrigation (for 3 weeks). Morphological and physiological parameters were evaluated.

Results and discussion. Five months after the inoculation of *Araucaria*, greater colonization (%) was observed in the inoculum from conserved sectors of NNP, CHMNR and TNP in comparison with their respective inocula from sectors affected by fire, this being reflected in the Morphological-physiological parameters at the end of the period of drought.

Conclusions. The treatments that had the inoculation of the AMF in general presented a better response to the drought in comparison to the non-inoculated ones (controls). These results show that the inclusion of AMF in *Araucaria* plants should be a variable to be considered in ecological restoration programs, considering an optimized rhizosphere for field conditions.

Key words: Arbuscular mycorrhiza, photosystem II efficiency, plant quality, relative water content.

ID 274 - Disturbance and stability act as selection pressure for arbuscular mycorrhizal fungi in a volcanic ecosystem

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Introduction. Arbuscular mycorrhizal (AM) fungi play a significant role in the establishment of vegetation during early primary succession. We demonstrated that in a volcanic ecosystem there is nested structure in AM fungal community along an elevation gradient towards a crater, in which soil disturbance is one driver for the nestedness. In this study, we evaluated the significance of periodic soil disturbance as selection pressure for the fungi in a pot experiment.

Methods. Three soil-core samples containing rhizosphere soil and roots were collected from each of four Miscanthus sinensis plants grown in the grassland at lower elevations in Mt. Tarumae in Japan. DNA was extracted from the roots in one of the three samples. The second sample was sieved with a 4-mm mesh to destruct hyphal networks of the fungi (disturbance), while the third one was not (intact). *M. sinensis* was grown in these soils in a greenhouse for 12 months, during which the soils in the disturbance treatment were sieved every month. Roots were harvested every other months for DNA extraction. AM fungal LSU rDNA was amplified from the DNAs and sequenced by MiSeq.

Results and discussion. AM fungal richness was consistently decreased during the culture period similarly in the two treatments. Compositions of the communities were significantly differentiated between the treatments, in which different taxa responded differently; e.g., two *Rhizophagus* OTUs disappeared after 6 months by disturbance, whereas three *Acaulospora* OTUs were unresponsive to disturbance.

Conclusions. These observations suggest that both disturbance and stability act as selection pressure for AM fungi.

Key words: Community structure, selection pressure, soil disturbance, volcanic slope.

ID 315 - Arbuscular mycorrhizal fungi (AMF) retain the photosynthesis efficiency and improve rice growth under drought stress

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Introduction. Drought limits soil water and nutrients availability for rice (*Oryza sativa*), and subsequently reduces its growth and productivity. Arbuscular mycorrhizal fungal (AMF) colonization may improve rice growth under drought by maintaining the photosynthesis efficiency for longer. This study aimed to investigate the role of AMF symbiosis in maintaining the photosynthesis efficiency of the rice plants growing under drought stress.

Methods. We conducted a three-factorial greenhouse pot experiment with two rice varieties (KDML 105 and SR1); with high and low AMF colonization, under well-watered and drought conditions. We measured the photosynthesis efficiency by measuring leaf stomatal conductance and the maximum quantum yield of photosystem II (Fv/Fm) over time. The measurements were taken every two days over 14 days of drought. Plant biomass and grain yield were measured at harvest.

Results and discussion. Drought reduced the stomatal conductance and Fv/Fm. However, this reduction was less severe in plants with high AMF colonization. Shoot biomass was also significantly greater in plants with high AMF colonization than in plants with low AMF colonization. Furthermore, the increase of AMF colonization tended to increase rice grain yield.

Conclusion. Overall, higher AMF colonization in rice roots improved the growth of rice via maintaining plant stomatal conductance and Fv/Fm of the rice plants under drought stress.

Key words: Drought, mycorrhizae, photosynthesis, rice, stomatal conductance.

ID 33 - Unipartite and bipartite mycorrhizal networks associated to *Abies religiosa*: understanding community structure to select facilitator plants and fungal links

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Introduction. *Abies religiosa* is a tree in risk due to climate change scenarios. A proposed management measure is assisted migration; however it is mandatory to solve the low sapling survival rate using facilitator plants. Our objective was to identify potential facilitator plants and the mycorrhizal fungus that connects saplings of *Abies religiosa* to the mycorrhizal network by modelling unipartite and bipartite interaction networks.

Methods. We obtained the rhizosphere from 17 potential facilitator plants and we Illumina sequenced the ITS2. We constructed unipartite and bipartite networks for the interaction.

Results and discussion. We identify plant and fungal nodes with the largest degree and the lowest average shortest path: *Salix paradoxa*, *Cortinariaceae* sp._965_SH033131.07FU, *Genea* sp._24_SH191238.07FU, *Rhodoscypha* sp._466_SH208437.07FU, *Russula firmula*_sp.2_KX812987, and *Tomentella* sp._215_SH002650.07FU. However, other plants and fungi of potential importance due to their position in the networks were detected.

Conclusion. We found strongly modular network architecture which suggests that these networks have a high resilience to random perturbations.

Key words: Connectivity, environmental-decision-making, keystone-species, plant-fungal bipartite network.

ID 92 - Do ectomycorrhizal fungi compensate for decreasing fine root area in old forests?

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Introduction. Ectomycorrhizas (EcM) provide enhanced resource acquisition to hosts. Therefore, rather than increase fine root area, trees may invest in EcM to support resource needs. However, the ability of EcM to provide resources to hosts varies and may be linked to functional traits such as exploration type. Here, we quantify fine root area and the functional composition of EcM on roots of a dominant tree species to test the hypothesis that EcM able to explore more soil volume become more prevalent with stand age and soil depth, conditions presumably representing decreased resources.

Methods. Replicated 20 × 20 m plots were established across an age-gradient of *Pinus banksiana* stands in western boreal forest, Canada. Soil cores were collected in five locations per site and divided into three depth increments, 0–15 cm, 15–30 cm, and 30–90 cm. Pine roots were extracted, and surface area of fine roots was measured. We then classified ectomycorrhizal pine roots into simplified exploration types, 'contact' or 'distance', based on presence of emanating hyphae or rhizomorphs.

Results and discussion. Both fine root area and the proportion of distance-EcM were highest in middle-aged stands (~33 years old). This pattern was especially pronounced at deeper soil profiles, i.e., > 15 cm.

Conclusion. Contrary to our prediction, the proportion of distance-EcM was not highest in old stands. This finding suggests that 1) host resource needs are low in young and old stands, or 2) our hypothesized functioning of these exploration types needs revaluation.

Key words: Chronosequence, exploration type, pine, soil depth.

ID 141 - Endo- and ectomycorrhizal fungi in an Amazonian rain forest soil of Colombia

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Introduction. It is assumed that arbuscular mycorrhiza is the dominant mycorrhiza in tropical forests. However, recent studies indicated that ectomycorrhizas naturally occur in tropical ecosystems. We evaluated the presence of arbuscular mycorrhizal (AM) and ectomycorrizal (EM) fungi in a tropical rain forest of the Colombian Amazon region with acid low-fertility Oxisols.

Methods. Two composed soil samples of the area and 20 soil samples around *Pseudomonotes tropenbosii* trees were collected to study mycorrhizal fungal communities. Ectomycorrhizal fungal DNA was extracted from soil samples around *Pseudomonotes tropenbosii* trees following the methodology proposed by Tedersoo et al. (2014). Arbuscular mycorrhizal fungal DNA was obtained for the two composed soil samples using SSU rRNA gene primers NS31 and AML2 as described by Öpik et al. (2013). AM and EM fungal sequences were obtained using 454-sequencing.

Results and discussion. Forest was rich in Mimosaceae, Fabaceae, Lecythidaceae, and Arecaceae plant families, considered arbuscular mycotrophical plant species. However, *Pseudomonotes tropenbosii*, a member of the family Dipterocarpaceae also occurred in this forest. *Pseudomonotes tropenbosii* is considered an ectomycotrophical species. A total of 25 AM fungal VT (VT; phylogenetically-defined taxonomic units) of seven genera (*Acaulospora*, *Archaeospora*, *Claroideoglomus*, *Glomus*, *Gigaspora*, *Paraglomus* and *Rhizophagus*) and 57 ectomycorrhizal fungal OUT´s from the Thelephoraceae, Russulaceae, Clavulinaceae and Sclerodermataceae families were obtained from the forest soil samples.

Conclusion. Results indicated that ecto- and endo-mycorrhizal fungi co-exist in this Amazonian forest. Ectomycorrhizal fungal OTU´s might indicate that other EM host plants might exist in this forest and that mycorrhizal status of the different plant species there could not be well established.

Key words: Amazon, arbuscular mycorrhizas, ectomycorrhizas, *Pseudomonotes tropenbosii*, tropical rain forest.

ID 152 - Coinoculation of *Pinus greggii* Engelm. arbuscular and ectomycorrhizal fungi

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Introduction. Mexico has one of the highest rates of deforestation at the international level, which demands the development of strategies for successful reforestation. Although the roots of Pinaceae are usually colonized mainly by ectomycorrhizal fungi, the presence of arbuscular mycorrhiza has also been recorded. The objective of this work was to evaluate the growth and photosynthetic rate of *Pinus greggii* inoculated with arbuscular mycorrhizae originated from pine forest soil (HMApf) and with the ectomycorrhizal fungus *Laccaria proxima* (Lp).

Methods. Seeds of *P. greggii* were superficially sterilized with 30% H_2O_2 and planted in a mixture of river sand, ground pine bark and forest soil (ratio 2: 2: 1) in forest containers. A random block experimental design was used. There were 4 treatments: i) plants inoculated with HMApf soil; ii) plants inoculated with Lp; iii) plants co-inoculated with HMApf + Lp and iv) Non-inoculated plants.

Results and discussion. 365 days after sowing the presence of hyphae, vesicles, arbuscules and microsclerotia of dark septate fungi was recorded in the roots of *P. greggii* in plants inoculated with HMApf. Likewise, increments of up to three times in the height of co-inoculated plants were registered in comparison with non-inoculated plants or plants inoculated only with arbuscular mycorrhiza or ectomycorrhiza. The photosynthetic rate increased conspicuously in the plants co-inoculated with the HMApf + Lp, in comparison with non-inoculated plants. The treatment inoculated with Lp presented Hartig net, external hyphae and mantle.

Conclusion. It is concluded that co-inoculation with arbuscular mycorrhizal fungi and ectomycorrhizal fungi should be considered when carrying out pine reforestations.

Key words: Consortium, Pinaceae, reforestation, symbionts.

ID 187 - Shift on the arbuscular mycorrhizal communities with changes of land use

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Introduction. The Andean mountain forest has experienced a rapid change in land use in the last 100 years, shifting the natural forest to pastures and cropland. In order to evaluate how the changes in land use impact on the biodiversity and functionality of arbuscular mycorrhizal fungi (AMF), we evaluated the compositional and functional parameters of AMF communities from three important land use types in the Colombian Andes.

Methods. Soils from natural forests, pastures and tomato tree plantations were sampled at five farms. AMF diversity in soil was evaluated by Illumina MiSeq, the infectivity and symbiotic efficiency of the native AMF communities by greenhouse biotests.

Results and discussion. The change from forest to pasture or cropland induced changes in both the composition and the potential infectivity of AMF communities. Surprisingly, the biotests revealed very low AMF infectivity in the forest soils as compared to cropland and pasture. The efficiency of the AMF communities in providing plant benefits was correlated with their infectivity.

Conclusion. This shows that changes in land use in Andean mountains change the functional and composition parameters of AMF communities. The low infectivity of the forest AMF communities, along with their compositional divergence indicates selection of ruderal AMF by the land use changes and loss of other functional traits in the AMF communities. Thus, due to changes in land use, important groups of living beings are possibly replaced, which may affect the long-term functionality of the ecosystem.

Key words: Andean forest, land use change, mycorrhizal composition, mycorrhizal infection, pastures.

ID 190 - Arbuscular mycorrhizal diversity in soil, root and rhizosphere for coffee and its native forest relatives in Monteverde, Costa Rica

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Introduction. In the greenhouse, arbuscular mycorrhizal (AM) fungi differ in their colonization of roots vs. soil. These differences appear to be conserved at the family level and reflect differences in functional roles.

Methods. We used coffee (*Coffea arabica*) at three farms in Costa Rica, and eight forest species from the same plant family growing in adjacent forests, to test predictions about community composition of AM fungi via high-throughout ITS2 sequencing at three spatial scales (bulk soils of coffee fields and forest, the rhizosphere of individual plants, and roots) as a function of environment and host relatedness.

Results and discussion. AM fungal communities differed across plant hosts, but differences correlated more strongly with environment than host. They also differed between forest and coffee soils, with Glomeraceae predominating in forest and Gigasporaceae more frequent in coffee than in forest. In roots of most forest species, we detected only Glomeraceae and unidentified families, while in coffee and relatives growing in sunnier spots in the forest, root communities also included Gigasporaceae, Acaulosporaceae or Diversisporaceae. In contrast, rhizosphere communities included multiple families. These findings are consistent with conserved differences in functional roles of AM fungi, with the Gigasporaceae prevalent where plant nutrient demand is high and outside the root rather than in it.

Conclusion. The Glomeraceae was a larger proportion of the community in forest than in coffee and within the root rather than the rhizosphere, consistent with a role in pathogen protection. Multiple families in the forest rhizosphere suggest similar roles to Gigasporaceae without the same demand for carbon.

Key words: Arbuscular mycorrhiza, coffee, community ecology, root vs. rhizosphere, Rubiaceae.

ID 196 - Response of pine root-associated fungi to the impact of nesting great cormorant colony

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Introduction. Colonies of piscivorous birds nesting in forests bring in loads of allochtonous material, including nutrients (N, P) and other elements in amounts much exceeding atmospheric depositions. This eventually results in tree death and total change of an ecosystem.

Methods. In 2012-2014, we studied the effect of increasing ornithogenic impact on ectomycorrhizal (EMF) and other root-associated (RAF) fungi in a Scots pine forest affected by great cormorants' colony. By molecular and morphological approaches we identified RAF species from root tips and EMF species from root tips and sporocarps collected in three designated study zones: D (active nesting zone), E (colony edge), and G (pristine forest).

Results and discussion. Number of species bearing sporocarps steadily decreased in zone E and was significantly lower than in zone G. Number of EMF species in root tips were higher in zone E compared to zone G. No sporocarps were observed in zone D. Numbers of RAF species showed no clear trend for D and G zone and insignificant increase in E zone. Number of root tip morphotypes was significantly lower in D zone and steadily decreased, was stable (and highest) in zone G and fluctuated in zone E. Number of mycorrhizal root tips was lowest in D zone, remaining rather stable.

Conclusion. Our study has shown that in nutrient-poor forests increasing load of N and P initially resulted in decrease of EMF sporocarp formation and subsequently, even though trees are still alive, resulted in fast and significant decrease of EMF association with roots.

Key words: Ectomycorrhiza, nutrients, ornithogenic, *Pinus sylvestris*, *Phalacrocorax carbo*.

ID 209 - Arbuscular mycorrhizal communities at different root orders collected at Japanese cedar forests in the central Japan

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Introduction. The aim of this study was to clarify community structures of arbuscular mycorrhizal (AM) fungi associated with Japanese cedar, *Cryptomeria japonica*, in the central Japan.

Methods. We collected three soil blocks within a 1 ha stand at seven cedar artificial forests in five prefectures. Root systems of the cedar were retrieved and 1st to 3rd order roots were used for colonization and molecular identification of the fungi.

Results and discussion. AM structures in both *Arum* and *Paris* types were found in all the samples, and AM colonizations tended to decrease as root orders. Using a next generation sequencing via Ion PGM, quality filtered AM sequences were assigned into a total of 48 MOTUs ranging from 21 to 28 MOTUs per stands. AM richness in 1st order roots was significantly higher than that in 3rd order roots. The most dominant AM taxa was Glomeraceae (58.3%) followed by Acaulosporaceae (22.9%) and Diversisporaceae (6.3%), and the sequence abundance was exclusively accounted by Glomeraceae (97.0%). No significant MOTU clusterings were detected among stands and root orders. MOTUs in the 3rd roots were a subset of the lower order roots.

Conclusion. These results suggest that AM community structures are less obvious in local scale and lower order roots involve diverse AM taxa and play roles for nutrient acquisition in fine scales.

Key words: *Cryptomeria japonica*, morphological type, next generation sequencing, *Paris* type.

ID 212 - Mycorrhizal mediation of invasive species soil legacy in a changing climate

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Introduction. Climate change and invasive species are threats to most ecosystems. Riparian trees of the southwestern USA are experiencing warming temperatures while interacting with non-native tamarisk (*Tamarix* spp.), a nonmycorrhizal tree that reduces the abundance and diversity of the mycorrhizal fungi upon which native trees depend. While many native Fremont cottonwoods (*Populus fremontii*) now grow in association with tamarisk (“experienced”) others occupy uninvaded sites (“naïve”). We tested the hypotheses that, relative to naïve cottonwoods, experienced cottonwoods would: H1) perform better in tamarisk legacy soil and H2) have lower mycorrhizal colonization and mycorrhizal growth response (MGR). We also hypothesized that H3) tamarisk legacy soil and warm temperatures would increase colonization by dark septate endophytes (DSE) and reduce colonization by ectomycorrhizal (EM) and arbuscular mycorrhizal (AM) fungi.

Methods. We used a fully factorial greenhouse experiment to examine the effects of temperature, soil legacy, and source population on cottonwoods and their associated fungi.

Results and discussion. Experienced cottonwoods performed better than naïve cottonwoods in tamarisk legacy soil as hypothesized. Contrary to H2, experienced cottonwoods had higher MGR, but similar EMF, AMF, and DSE. AMF and EMF were altered by tamarisk legacy soil as predicted, but DSE were more abundant in cooler temperatures.

Conclusion. Warm temperatures had fewer negative effects than tamarisk legacy soil. Experienced cottonwoods grew well in tamarisk legacy soil, partly due to their responsiveness to inoculation with mycorrhizal fungi, suggesting inoculation as an important restoration strategy.

Key words: Climate change, invasive species, restoration.

ID 219 - The response of native and invasive shrubs to a diverse soil fungal inoculum

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Introduction. Invasive species are major contributors to the loss of biodiversity and ecosystem function, yet the importance of microorganisms, both arbuscular mycorrhizal fungi (AMF) and pathogens, in promoting invasion remains unclear.

Methods. We tested the roles AMF and soil pathogens play in plant invasion with a multifactorial greenhouse experiment using 17 native and invasive shrub species of eastern North America. Inoculation treatments included: (1) AMF plus other soil microorganisms, (2) microbial soil filtrate of microorganisms only, (3) sterilized soil and filtrate. The live inoculum and microbial filtrate were created from soils composited from diverse field sites with numerous invasive and native shrub species.

Results and discussion. Results for aboveground variables show: 1) irrespective of treatment, non-natives had greater aboveground mass, larger leaves and higher specific leaf area, relative to native species, 2) native and invasive species had equivalent positive responses to AMF, 3) aboveground variables did not differ between the sterile and live microbial wash treatments, suggesting that there was no negative effect of pathogens.

Conclusion. Our results indicate that invasive and native shrub species equally benefit from AMF, and soil pathogens do not influence plant growth. These results may be due to: 1) a lack of systematic difference in how native and invasive plant species respond to AMF, or 2) different plant species optimizing mycorrhizal associations by partnering with different subsets of the AMF community. Our aim is now to integrate belowground plant trait data, and fungal community sequencing, to explore these alternative explanations.

Key words: Arbuscular mycorrhizal fungi, invasive species, shrub, soil pathogen.

ID 234 - Plant root-fungal interactions in a neotropical freshwater wetland

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Introduction. Wetlands in Neotropics harbor high fungal diversity, including arbuscular mycorrhizal fungi (AMF) and dark septate endophytes (DSE). This study evaluated the interaction of plant roots with AMF and DSE in a freshwater wetland belonging to a hotspot of biodiversity.

Methods. Properties of soils and the water column, floristic composition, root colonization by AMF and DSE, and molecular identification of AMF inside roots were studied.

Results and discussion. Soils were Gleysol, and flooded during the rainy season. Most of identified plant species were herbaceous, with the native *Cyperus articulatus* and the invasive *Mimosa pigra* as the dominant species. Seven of 8 analyzed plant species exhibited differential co-colonization between AMF and DSE. Repeated sampling for one year under flooding/dry conditions demonstrated that *C. articulatus* and *M. pigra* were mainly associated with DSE and AMF, respectively. A positive correlation between dissolved O2 in the water column and fungal colonization was observed in *C. articulatus*. Glomerales and Archaeosporales were molecularly identified inside roots containing arbuscules of *M. pigra*.

Conclusion. Findings highlight differential coexistence between AMF and DSE in plant roots; fungal colonization was influenced by flooding/dry conditions in a neotropical wetland; the community of AMF inside arbusculated roots of *M. pigra* includes at least four clades.

Key words: Arbuscular mycorrhizal fungi, *Cyperus articulatus*, dark septate endophyte fungi, gleysol, *Mimosa pigra*.

ID 240 - Root mycobiome of different truffle producing forest in Serbian lowlands

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Introduction. Balkan Peninsula, an easternmost of Europe’s three great southern peninsulas is a biodiversity rich area characterized by different terrain elevations, geological formations, as well as climatic zones. Forest ecosystems in the Balkan peninsula are characterized as truffles producing habitats depending upon the dominant vegetation type. It is known that the aboveground vegetation as well as seasonal dynamics impacts the belowground microbial diversity. However, very little is known about root inhabiting fungal communities of truffle producing habitats of Balkan peninsula in Serbian lowlands. Therefore, we investigated the impact of forest type and season on the root associated fungal diversity and community composition.

Methods. The root samples were collected from soil cores of three different truffle producing forests at three time points representing different seasons. Genomic DNA was isolated from pooled root samples. We used Paired-end illumina sequencing approach to target the ITS2 rDNA fragment of the root associated fungal communities.

Results and discussion. We found a significant effect of seasonal variation on the fungal alpha diversity (ANOVA $p < 0.05$) in the white truffle producing forest. Beta diversity analysis indicated that the root associated fungal communities differ significantly between truffle producing forests (PERMANOVA F=4.8, df=2, p=0.001).

Conclusion. Dominant tree species, season, and their interaction shapes the root associated fungal community composition in the lowland forest ecosystems.

Key words: Balkan Peninsula, ectomycorrhiza, ITS2, mycobiome, truffle habitats.

ID 252 - Initial tissue carbon fractions predict sporocarp necromass decomposition in mycorrhizal and saprotrophic fungi

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Introduction. It is now clear that a sizable portion of soil organic matter in terrestrial systems is derived from fungal material, leading to current interest in the rates and drivers of fungal necromass decomposition in soils. Recent work suggests that fungal necromass decomposition in soil is best described mathematically using a two-pool model of decomposition originally developed for plant litter. This model consists of a labile “fast pool” which is described using an exponential decay constant (i.e. k value) for mass loss, and a second “slow” pool which can potentially persist for years and is represented as an asymptote.

Methods. We decomposed 28 sporocarp tissues across 23 fungal species and described their decay rates using the two-pool decomposition model. We characterized the initial carbon fractions of each tissue type using a sequential leaching procedure widely used to describe plant carbon fractions in plant litter decomposition studies (e.g. cell-soluble components, cellulose, lignin). We then compared these fractions with chemical traits previously used to predict fungal necromass decay, including tissue N concentrations, melanin concentrations, and FTIR spectra.

Results, discussion and conclusion. Soluble cell components, represented by mass lost after a neutral detergent extraction, accounted for over half of total tissue mass in all but one fungal tissue (mean 58%, range 34-77%). We found that this fraction was the best predictor of the fast pool in our decomposition models. Tissue contents removed by an acid detergent extraction, likely representing bound proteins, represented 20% of tissue contents (range 14-28%) and best predicted the slow pool in our decomposition model.

Key words: ANKOM, carbon cycling, decomposition, necromass, soil organic matter.

ID 253 - Tree neighbour diversity and mycorrhizal trait affect the rhizosphere microbiome assemblages of tree species pairs

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Introduction. Soil microorganisms are essential to plants for the cycling and uptake of nutrients. Previous research has shown that subtropical forests harbor a great amount of microbial diversity. However, the role of neighborhood diversity and the plant mycorrhizal trait on the rhizosphere microbial diversity are not well understood. Thus this project studied the rhizosphere soil microbial composition of tree species pairs in a Chinese subtropical forest ecosystem.

Methods. Rhizosphere soil samples were collected using soil cores, freeze-dried and microbial genomic DNAwas extracted. The bacterial (V4 region of 16S rRNA) and fungal (ITS2 fragment of rRNA) amplicon libraries were sequenced using a paired-end approach with Illumina MiSeq. Bioinformatic analysis of the sequence data was performed using mothur based custom pipeline. The specific research questions were tested by R based statistical analysis.

Results and discussion. PERMANOVA analysis revealed a significant effect of tree neighbourhood diversity on both fungal and bacterial communities ($P<0.003$ & $P<0.008$ respectively). Tree mycorrhizal type has shown significant effect on fungal communities ($P<0.001$) whereas there was no significant effect on bacterial communities.

Conclusion. Neighbourhood diversity affects the rhizopshere microbiome as compared to tree mycorrhizal type in this particular ecosystem.

Key words: Microbiome, mycorrhiza, neighbourhood diversity, rhizosphere, tree species pairs.

ID 256 - Small scale spatial distribution of orchid mycorrhizal fungi in a tropical tree canopy

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Introduction. Mycorrhizal fungi are critical for establishment of orchids, and spatial distributions of orchid mycorrhizal fungi (OMF) may thus constrain orchid distributions. While the greatest diversity of orchids is found in tropical tree canopies, OMF in these habitats have been little studied compared to terrestrial ones. Here we investigate the small-scale spatial distributions and substrate preferences of these fungi in a tropical rainforest canopy.

Methods. To capture spatial structure of fungi at various spatial scales, we sampled fungi from over 300 points on 35 branches along a 250 m transect in Tapantí National Park, Costa Rica. Each sample was subdivided by substrate type, including live bryophytes, litter, and host tree bark. Five branches were sampled intensively with a focus on the sub-meter scale. We used Illumina sequencing of ITS2 to identify fungi and analyzed OTUs assigned to Tulasnellaceae, Ceratobasidiaceae, and Sebacinales.

Results and discussion. Along a single branch, OMF show positive spatial autocorrelation at distances less than a meter. At the scale of our study site, fungi are spatially clustered at distances up to 40 m. Although the OMF community as a whole does not segregate by substrate, individual OTUs are indicators of different substrates. OTUs also vary in their commonness and spatial distributions.

Conclusion. OMF in the tree canopy have patchy distributions, even at the sub-meter scale along single branches and are found in diverse canopy substrates. Because orchids depend on these fungi for establishment, we expect that orchids are limited to sites containing compatible fungi. Mycorrhizal specialist orchids should be particularly restricted.

Key words: Epiphyte, orchid, spatial, tropical.

ID 263 - Mycorrhizas and host tree mortality in the Piñon-*Juniper* woodland

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Introduction. Forest disturbances, including drought and associated mortality, are increasing globally. Fungi likely influence the recovery and resilience of these systems. To better understand how mycorrhizal fungal communities respond to disturbance we evaluated responses in the codominant piñon pine (*Pinus edulis*) and juniper (*Juniperus monosperma*) woodland.

Methods. In 2017 a simulated mortality experiment was conducted to determine species-specific above/belowground traits involved in ecosystem hydrology of the piñon-juniper woodland. To impose mortality, we girdled all adult trees of one species per plot (3 piñon, 3 juniper, and 3 control plots). To evaluate the fungal response, soil cores were collected the year of the treatment and the year following. We then collected and morphotyped all living fine roots. Dry weights were used to determine abundance of fungi and DNA was sequenced for identification.

Results and discussion. Piñon fine root biomass decreased significantly one year after piñon girdling. Juniper-girdled plots displayed the same trend with juniper root biomass. Several dominant fungi were found across all 9 plots, including taxa known to affect drought tolerance in piñon pine like hypogeous taxa *Rhizopogon* and *Geopora*.

Conclusions. Mycorrhizal fungi possess species-specific traits that contribute to their host and ecosystem's response to disturbance. In this ongoing experiment, we have documented strong changes in abundances of fine roots and associated fungi that will tip the balance between different guilds (AM vs EMF; Ascomycota vs Basidiomycota). These shifts thereby impact seedling dynamics (resilience), soil hydraulics, decomposition, and carbon flux, all of which are being measured.

Key words: Communities, disturbance, drought, mycorrhizae.

ID 267 - Functionality of arbuscular mycorrhizal fungi in the dry tropic: a landscape analysis

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Introduction. The relationship between above- and belowground components of an ecosystem has usually been explained through structural variables such as diversity and species richness (arbuscular mycorrhizal fungi (AMF) diversity is positively correlated to plant diversity). However, this relationship is seldom true in field studies. One complementary approach is the functional one. Some of the variables that allow us to estimate the functionality of AMF are mycelia production, and percentage of colonization because they indicate the carbon allocated to fungi, we expect that if the mutualistic relationship exists over time, we will record higher quantities of mycelia. Our objective was to estimate and compare the mycelia production and the intraradical colonization in two contrasting environments.

Methods. We sampled two sites (Cuyo and Río) of sand dune shrubland (SDS) and tropical dry forest (TDF) at the Reserva de la Biosfera Ría Lagartos, Mexico in the dry and rainy seasons. Per each sample point, we obtained mycelia and colonization percentage, and performed physicochemical soil analyses. We applied analyses of variance to test site and season effects.

Results. Mycelium length and colonization percentage significantly differed between sites and seasons in TDF but not in SDS, the highest values corresponded to Cuyo. Also, we found the highest carbon and organic matter values in Río.

Conclusions. The AMF-plant relationship has a differential functionality depending on the prevailing environmental conditions, while Cuyo has a lower availability of nutrients and, therefore, the mycorrhizal mutualism is strengthened, in Rio occurs the opposite, however, under harsh environmental conditions, this trend is not maintained.

Key words: AMF, colonization percentage, functionality, mycelium length, Ría Lagartos Reserve.

ID 280 - Mediterranean woody plant species influence the phylogenetic structure of arbuscular mycorrhizal fungal communities

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Introduction. Arbuscular mycorrhizal (AM) fungi are obligate plant symbionts that have important functions in most terrestrial ecosystems. They exhibit low taxonomic diversity but some degree of preferences for their plant hosts. However these patterns are usually recorded for herbaceous plants being the studies including woody plants scarce. Here, we aimed to describe the bipartite association network in two Mediterranean woody plant communities and their symbiotic AM fungi.

Methods. We sampled two Mediterranean forests in spring and autumn and analyzed the AM fungal community by means of SSU rDNA illumina sequencing.

Results and discussion. The network included 32 plant species and 78 AM fungal OTUs. The host plant species strongly determined the AM fungal community composition. In addition, a significant relationship between the phylogeny of AM fungi and plants was found. Moreover, the plant hosts showed a different degree of taxonomic and phylogenetic diversity that seemed to be related with plant traits: the higher the plant species, the less OTU richness and more phylogenetically clustered AM fungal communities.

Conclusions. The study of woody plant species can shed light on the drivers of AM fungal community assembly, regarding both functional diversity and evolutionary history of plant fungal interactions.

Key words: Association networks, community assembly, trees and shrubs species.

Thursday July 4, 2019

ID 9 - The succession of Arbuscular Mycorrhizal community in the Wheat cropping system

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Introduction. Arbuscular mycorrhizal fungi (AMF) are symbiotic with more than 80% of plants on land. They provide more nutrients for plants by expanding the absorption area of roots by mycorrhiza and hyphae. Microbial interactions activate organic phosphorus and play an important role in improving the utilization efficiency of soil cumulative phosphorus in farmland systems. With the artificial cultivation, the amount of applied phosphorus increased, and the soil fertility changed significantly, especially the soil available phosphorus increased remarkably. However, the change of the diversity of AMF, one of the soil biological fertility indicators, has not been reported yet.

Methods. High-throughput sequencing.

Results and discussion. In this study, the long-term positioning test station in Yangling Loess Fertility and Fertilizer Benefit Test Station, Shanxi province, self-built station, 10 years of root system as research objects, through the long-term positioning test conditions including three different fertilization treatments (NK, NPK, NPKM) changes in tillage and fertilization systems, changes in AM fungal mycorrhizal diversity within roots. High-throughput sequencing results showed that the diversity of AMF in roots was stable and influenced little by external factors, three different fertilization treatments showed the same trend.

Conclusion. The result indicated that the diversity of AM fungi community in the roots was stable by external fertilization.

Key words: AMF, fungal diversity, high-throughput sequencing, phosphorus.

ID 153 - Effect of fairy ring bacteria on the growth of *Tricholoma matsutake in vitro* culture

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Introduction. *Tricholoma matsutake* (pine mushroom), as a valuable edible fungus, interacts with pine trees (Pinaceae and Fagaceae). Recent studies have shown that diverse bacteria co-exist in the fairy ring, and suggest that the fairy ring bacteria may influence on the growth of *T. matsutake*. However, the effect of the fairy ring bacteria on the growth of *T. matsutake* is largely unknown.

Methods. In this study, we isolated fairy ring bacteria and investigated their effect on the growth of *T. matsutake* in co-culture experiments. In addition, the relationship between bacterial effects and nutrient conditions was tested using different media with varying glucose concentrations.

Results and discussion. A total of 237 bacteria (28 species) were isolated from fairy rings of four different *T. matsutake* producing areas: Proteobacteria (17 species), Firmicutes (7 species), and Actinobacteria (4 species). Burkholderiaceae (*Burkholderia* and *Paraburkholderia*) was most abundant in the fairy ring bacteria communities. Most bacteria showed a negative effect on the growth of *T. matsutake* when it grew on glucose rich medium (20 g/L). In glucose deficient medium (2 g/L), however, some bacteria promoted the growth of *T. matsutake*. In addition, the mode of interaction between bacteria and *T. matsutake* is different, depending on the glucose concentration.

Conclusion. The role of bacteria in the growth of *T. matsutake* is changed depending on nutrition conditions, which suggests that *T. matsutake* growth promoting bacteria may be used as bio-fertilizer in forest soil for increasing productivity of *T. matsutake*, although they cannot be used in nutrient-rich medium.

Key words: Fairy ring, growth promoting bacteria, *Paenibacillus*, pine mushroom, *Tricholoma matsutake*.

ID 197 - A leafless epiphytic orchid, *Taeniophyllum glandulosum* Blume (Orchidaceae), is specifically associated with the Ceratobasidiaceae family of basidiomycetous fungi

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Introduction. Leafless epiphytes in the Orchidaceae undergo a morphological metamorphosis in which the root has chloroplast-containing cortical cells and is the sole photosynthetic organ for carbon gain. All orchids are entirely dependent on mycorrhizal fungi for their carbon supply during seed germination, and this mycorrhizal association generally persists in adult plants. However, our knowledge of the mycorrhizal association of leafless epiphytic orchids remains limited, and the contribution of the mycorrhizal association to nutrient acquisition in these orchid species is largely unknown.

Methods. In this study, the mycorrhizal fungi of a leafless epiphytic orchid, *Taeniophyllum glandulosum*, were identified molecularly using 68 mature plants and 17 seedlings.

Results and discussion. In total, 187 fungal internal transcribed spacer sequences were obtained, of which 99% were identified as Ceratobasidiaceae. These sequences were classified into five operational taxonomic units (OTUs) based on 97% sequence similarity. The most frequent sequence was OTU1, which accounted for 91% of all Ceratobasidiaceae sequences, although other phylogenetically distinct Ceratobasidiaceae fungi were detected. These results show that *T. glandulosum* is specifically associated with a particular group of Ceratobasidiaceae. All mycorrhizal fungi found in *T. glandulosum* seedlings belonged to OTU1, which was also found in adult plants on the same host tree. The mycorrhizal fungi from 13 host tree species were compared, and *T. glandulosum* was preferentially associated with OTU1 on 11 tree species.

Conclusion. *T. glandulosum* is specifically associated with Ceratobasidiaceae fungi and this specific association remains throughout the orchid life cycle and is found on divergent host tree species.

Key words: Ceratobasidiaceae, epiphytic orchid, high mycorrhizal specify, leaflessness, orchid mycorrhizal fungi.

ID 222 - Mycorrhizal symbiosis in plants of two temperate forest of Mexico

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Introduction. Temperate forests are a reservoir of forest resources, fungi and medicinal plants that are associated with mycorrhizal fungi. There are few studies on arbuscular mycorrhiza in these ecosystems because forest species are obligate ectomycorrhizal hosts. This research evaluated colonization and AMF richness in 17 plant species from two temperate forests: i) Tlalmanalco state of Mexico and ii) Agua Escondida Taxco Guerrero.

Methods. In the study sites, transects were made to select the plants and collect from each plant species: i) root samples to evaluate colonization; ii) soil samples to evaluate the species richness of AMF and, iii) only in Agua Escondida sporomes of ectomycorrhizal fungi were collected.

Results and discussion. The results indicated that all plant species are in symbiosis with AMF and contributed to alpha diversity. Mycorrhizal colonization was high and depended on the plant species; ranging from 45% for *Castilleja teniuflora* to 85% for *Maurandia* sp. The highest species richness of AMF was recorded in *C. tenuiflora* (17spp.), *Salvia elegans* (16) and *Lupinus campestris* (17), while the lowest richness was recorded in *Geranium seemanni* (9), *Mentha* sp. (5) and *Salvia lavanduloides* (2). The plants, together, reported more than 50spp. of AMF distributed in 12 genera: *Acaulospora*, *Ambispora*, *Diversispora*, *Dentiscutata*, *Gigaspora*, *Entrophospora*, *Funneliformis*, *Glomus*, *Pacispora*, *Racocetra*, *Rhizophagus* and *Scutellospora*. Also, twelve species of ectomycorrhizal fungi were recorded in the forest of Agua escondida; highlighting *Amanita* and *Ramaria* with 7 and 4 species.

Conclusion. In the temperate forests of Mexico coexist of the arbuscular mycorrhizal and ectomycorrhizal symbiosis; they also harbored a great diversity of AMF and ectomycorrhizal fungi.

Key words: Diversity, medicinal plants, mycorrhizal colonization, richness AMF.

ID 232 - *Septoglomus mexicanum*, a new species of arbuscular mycorrhizal fungi (Glomeromycota) from semiarid regions in Mexico

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Introduction. *Septoglomus mexicanum* is described as 1 new species of arbuscular mycorrhizal fungi (AMF) based on morphological and phylogenetic analysis.

Methods. It was isolated from rhizospheric soil of two endemic Mexican legumes: *Prosopis laevigata* and *Mimosa luisana*, which grow in Mexican semiarid regions.

Results and discussion. *Septoglomus mexicanum* is characterized by forming globose spores (154.5-)202.8(-228.9) µm diameter, and a spore wall consisting of four layers (SWL1-SWL4): outer wall layer (SWL1) semi-permanent hyaline, (1.7-)3.2(-4.3) µm thick; SWL2 permanent, laminated and smooth, orange to reddish orange, (3.1-)4.5(-6.1) µm thick; SWL3 laminated, smooth, reddish orange to reddish brown, (4.1-)5.1(-5.7) µm thick; and SWL4 semi-flexible layer similar in color to SWL3, (0.93-)1.2(-1.4) µm thick. None of the spore wall layers stains with Melzer´s reagent. The subtending hypha has a color from yellowish to golden and presents a septum on spore base. *Septoglomus mexicanum* can be distinguished from all other *Septoglomus* species by spore size and color, spore wall structure (four layers), and by color change of the subtending hypha. Phylogenetic analysis based on the AMF extended DNA barcode covering a 1.5 kb fragment of the small subunit (18S), internal transcribed spacer region (ITS1-5.8S-ITS2) and the large subunit (28S) of nuclear rRNA genes, place *S. mexicanum* in the genus *Septoglomus* separated from other described *Septoglomus* species; especially *S. turnauae* with whom it could be morphologically confused.

Conclusion. The sequences in public databases suggest that *S. mexicanum* has not yet been previously detected, so it ranges to 149 Glomeromycota species registered in Mexico, representing 47.4 % of the known species worldwide.

Key words: Arbuscular mycorrhizae, deserts, fungal species, Leguminosae, 1 new taxon.

ID 233 - Diversity of arbuscular mycorrhizal fungi in agricultural systems in acidic andisols

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Introduction. In southern Chile the crop production is predominantly established on volcanic soils. These soils have limitations for production, such as their high P-fixing capacity and high levels of exchangeable Al. To address these conditions, farmers have implemented a series of strategies, among them, increased activity of arbuscular mycorrhizal fungi (AM). This symbiosis will be conditioned partly by the intensity of land use and agricultural management, both aspects related to sustainability and the nutrient cycle and, on the other hand, to the structure and composition of the morning fungi community along with the functionality to promote fitness plants to this condition of environmental stress.

Methods. The aim of this study was to define the agro-edaphoclimatic areas in different agricultural production systems with different degrees of intensity of agronomic management and to compare AM fungi status, focused on colonization, mycelia and spore volume. Three regions were selected in the area of traditional crops. Within these crops, different types of agronomic management were considered, from the conventional, a mixture of conventional and organic that could be called integrated or intermediate and finally organic management.

Results and discussion. After the analysis of fungal propagules, a higher intensity of these was obtained in organic-managed soils and in systems with lower intensity of soil use.

Conclusion. The most representative species corresponded to the following families: Acaulosporaceae, Pacisporaceae, and Paraglomeraceae.

Key words: Acidic soils, agricultural system, aluminum, AMF diversity, land use.

ID 254 - Relationship between 18S rRNA gene polymorphisms and endobacterial communities in a strain of *Gigaspora margarita*

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Introduction. *Gigaspora margarita* shows 18S rRNA gene polymorphisms within a spore, which vary between spores of an isolate and between isolates. This fungus harbors either *Candidatus moeniiplasma glomeromycotorum* (CaMg) or *Candidatus glomeribacter gigasporarum* (CaGg) or both. This study aims to investigate the relationship between the rRNA gene and endobacterial polymorphisms in *G. margarita*, and the effect of continuous cultivations on the diversities.

Methods. Two lines of a strain (GmC) verified by M13 mini-satellite primer were used; MAFF line (2013, 2017) was established in 1987, and HU line (2006, 2017, 2018) was subdivided from the MAFF in early 2000. The lines were maintained by culturing with a multiple spore inoculum more than annually. DNA from surface-sterilized single spores was analyzed by PCR-DGGE for arbuscular mycorrhizal fungal (AMF) 18S and bacterial 16S rRNA genes.

Results and discussion. Within GmC, four types of AMF polymorphisms were observed in total; the oldest HU was three types, recent two years' HU and MAFF were one type, different from each other, where endobacterial patterns were consistent with a combination of two CaMg bands and one CaGg band. The relative abundance of one of CaMg was stable between HU and MAFF, but those of the others varied within and between the lines. The results suggest that the diversity of endobacterial polymorphisms within a *G. margarita* strain tend to be lower than that of rRNA gene.

Conclusion. Furthermore, continuous cultivation at a small-scale suggested lowering diversity of rRNA gene polymorphisms found in the spore population in a strain within several years.

Key words: Arbuscular mycorrhizal fungi, DGGE, endobacteria, *Gigaspora margarita*, rRNA gene polymorphism.

ID 261 - Checklist of the Glomeromycota in the Tehuacán-Cuicatlán Valley, Puebla-Oaxaca, Mexico

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Introduction. Diversity of arbuscular mycorrhizal fungi (AMF) is critical for maintenance of desert vegetation, since water and nutrient deficiencies commonly constrain plant growth in dry ecosystems, thus AMF diversity can vary due to that plant species have different AMF communities associated to survive. This work provides a checklist of AMF species in the Tehuacán-Cuicatlán Valley (TCV).

Methods. AMF specimens deposited in the Laboratory on Legume Biosystematics (Universidad Autónoma Metropolitana-Iztapalapa, Mexico) were examined, and their microenvironments, plant communities and plant species recognized within the TCV.

Results and discussion. A total of 74 species of AMF have been found over more one decade of work, representing 49% of the registered in Mexico. *Acaulospora* and *Glomus* are dominant and frequently reported, and at least four new records and one new species of AMF have also been documented in this Valley. Of all AMF species, 36 spp. were recorded in xerophilous scrub, 28 spp. associated to four Mimosa species, 20, 22, 13 and 4 spp. in rhizospheric soil of *Prosopis laevigata*, *Neobuxbamia tetetzo*, *Coryphantha radians* and *Escontria chiotilla*, and *Stenocereus pruinosus* (established only in orchards), respectively; and 7 spp. under biocrusts inside or outside resource islands formed by *Mimosa luisana*. Likewise, we registered 17 spp. of AMF at open areas from scrub, 23 spp. in the "Milpa-chichipera" agroforestry system, and 19 spp. within corn-bean crops.

Conclusions. All examined conditions share on average 38% of the AMF species registered. Our results characterize the TCV as an important AMF reservoir, and suggest that this semiarid Valley may be biologically promising for Glomeromycota.

Key words: Arbuscular mycorrhizal fungi, leguminosae, Mexican deserts, mycorrhizae, semiarid regions.

ID 271 - Phylogenetic diversity of the species of the Phalloideae section of the genus *Amanita* in the states with the highest incidence of fatal mycetisms in Mexico

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Introduction. In countries where the consumption of wild mushrooms is frequent, hundreds of deadly mycetisms are reported every year, most of them related to white species of the genus *Amanita*. In Mexico, the impact of poisoning is underestimated, since there are many knowledge gaps about the subject. One of the most relevant is the ignorance of the species distribution over the territory. Therefore, the main objective of the present investigation is to evaluate the diversity and the phylogenetic position of the deadly species of the Phalloideae section of the *Amanita* genus scattered in the states with the highest incidence of mycetisms in Mexico.

Methods. The sporomas were collected in the forests surrounding the zones with the highest incidence of micetisms (Michoacán, Oaxaca and Chiapas). These were characterized and determined based on the established biological methods. In addition, copies were requested to the National Herbarium of the Institute of Biology, UNAM (MEXU). Morphological, molecular and ecological data was used to define species and their phylogenetic relationships.

Results. 34 sporomes and 25 copies of the MEXU have been collected. Of these, most have presented morphological variation, which shows differential patterns depending on the region where they were collected. At least four different molecular species have been identified.

Conclusions. The data obtained suggest that the species distributed in the study areas have a great morphological variety that may be species not described for America.

Key words: American species characteristics, poisonings, taxonomy.

ID 275 - Spatial and seasonal variation of ectomycorrhizae and sporocarps in mixed conifer/hardwood forests of southwest Oregon

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Introduction. Ectomycorrhizal fungi (EMF) profoundly affect forest ecosystems by mediating nutrient and water uptake, protecting roots from pathogens and environmental extremes, and maintaining soil structure and forest food webs. Conservation of EMF is predicated on baseline knowledge of their distribution in various landscape settings.

Methods. Experimental plots were installed in the Siskiyou National Forest, Oregon to compare spatial and seasonal variation of ectomycorrhiza (EM) morphotypes and sporocarps across a forested landscape. Fifteen Douglas-fir dominated stands of 7 ha each were sampled for ectomycorrhizae and sporocarps. The sampled stands were arranged in three blocks of 5 stands each and are located approximately 5-7 kilometers distant from each other within the Pistol River basin of southwestern Oregon.

Results and discussion. From 189 soil cores totaling a soil surface area of only 0.45 m^2, 192 ectomycorrhiza morphotypes were discerned. Nearly all of the thousands of root tips observed were ectomycorrhizal. Frequency of occurrence of each morphotype was used to determine the relative abundance of EM types within a particular soil core. The total number of EM types and mean relative frequency of each type were assessed. The mean number of types (12) per 350 cc soil core varied little among 14 of the 15 stands, yet only 10 ectomycorrhizal types were found in 25% or more of the soil cores while 60 types were restricted to single sample occurrences.

Conclusions. Stand-level differences in the results show we cannot assume uniformity of fungal populations in these stands and demonstrate the necessity and utility of thorough sampling before the application of logging treatments.

Key words: Biodiversity, ecosystem, fungi, long-term, mushrooms, truffles.

ID 278 - Richness and Diversity in Aquatic Environments: New Records of Arbuscular Mycorrhizal Fungi in Brazil

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Introduction. While symbiosis of arbuscular mycorrhizal fungi (AMF) is known to be widespread in terrestrial ecosystems, but there is limited knowledge about association in plants living in aquatic environments. The occurrence of AMF in aquatic roots was investigated, 19% from 79 AMF species are new records, and therefore, objective of this study was to report new records of AMF in aquatic environments.

Methods. Soil samples were colleted from 3 oligotrophic lagoons (Alcaçuz, Arituba, Carcará) at the APA Bonfim-Guaraíra, Rio Grande do Norte State, northeastern Brazil. Spores were extracted from soil by wet sieving and sacarose (70%) centrifugation.

Results and discussion. 79 AMF species were identified, mainly distributed in Glomeraceae (25 sp.), Acaulosporaceae (20 sp.), Dentiscutataceae (9 sp.), and Ambisporaceae (7 sp.). A total of 15 AMF morphotypes were identified as first record to aquatic condition: *Ambispora appendicula, Acaulospora denticulata, A. excavata, A. herrerae, A. ignota, A. spinulifera, A. spinosissima, Redeckera fulva, Dentiscutata hawaiensis, Fuscutata savannicola, Glomus spinuliferum, G. glomerulatum, G. trufemii, Oehlia diaphana, Sclerocystis sinuosa* and *S. coremioides*. *Ambispora appendicula, G. spinuliferum* and *G. glomerulatum* were found in the three lagoons. In Alcaçuz lagoon obtained the highest incidence numbers of new records (10 sp).

Conclusions. The study showed richness of mycorrhizal species in aquatic habitats and that there are still gaps in information and lack of quantitative data.

Key words: Aquatic habitat, aquatic plant, arbuscular, Glomeromycota, taxonomic diversity.

ID 281 - Molecular diversity of arbuscular mycorrhizal fungi community associated with *Cocos nucifera* in southeastern Mexico

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Introduction. Coconut (*Cocos nucifera*) is one of the major economic incomes for industry and farmers in Latin America, especially small landholders in southeastern Mexico. Mycorrhizal fungi represented a key to plant growth, productivity and especially relevant for organic agriculture. Mycorrhizal fungi are widespread in agricultural systems, and coconut has been well documented that is consistently colonized by AMF. Unfortunately, little effort has been carried out to identify the AMF colonizing roots.

Methods. We collected roots from eight different Green Dwarf coconut plantation in Yucatan and Quintana Roo and were sequenced with Illumina MiSeq platform using 18S rDNA gene.

Results and discussion. Rarefaction curves showed an acceptable AMF richness in coconut roots in with the samples analyzed. Phylogenetic analysis clustered sequences into 28 virtual taxa (VT), including one potential new VT taxa associated with coconut roots in Quintana Roo, Mexico. The higher number of VT were found in organic plantation. The *Glomus* and *Rhizophagus* genus were the dominant groups in both number of VT and number of sequences. Shifts in AM community composition were correlated with precipitation, percentage of carbonates and sand.

Conclusions. This study showed a high richness of native AMF fungi associated with coconut and variables such as percentage of carbonates and sand could explain a portion of the community variance and AMF diversity shifts at the local scale. Now, we are propagating AMF in trap cultures and searching for a suitable and local hostplant that increases native inoculum as an alternative for sustainable agriculture.

Key words: Arbuscular mycorrhizal fungi, coconut, diversity, next-generation sequencing.

ID 292 - Richness and abundance of arbuscular mycorrhizal fungi from rhizosphere soils of mono-cropped maize

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Introduction. Maize has been present in Mexico for more than 8700 years ago and it is grown all over the country. Arbuscular mycorrhizal fungi (AMF) play a key role in supplying phosphorus to plants and the maize is highly mycorrhizal dependent under low P in soil. Recording the occurrence of AMF populations in different ecosystems represents the first step toward understanding their functional diversity. The aim of this research was to evaluate the richness and abundance of AMF associated with the cultivation of maize with high inorganic fertilization.

Methods. This study was conducted in La Palma, Los Reyes, Michoacán, México (19°24'41" N and 101°42'12.999" W; 2198 ma.s.l.). Three plots were selected for this study and for each plot, three soil composite samples were taken in the dry season. The soil was sandy-clay-loam with pH 5.0 (H2O 1:2), P 0.53 mg/kg, organic matter 2.74%. Spores were extracted by wet sieving and sucrose density centrifugation, were counted and then mounted on slides with polyvinyl-lactic acid-glycerol with and without Melzer's reagent for their taxonomic identification.

Results and discussion. A total number of 16 AMF were recovered from soil samples: *Acaulospora denticulata, A. excavata, A. laevis, A. mellea, A. scrobiculata, A. spinosa, A. splendida, Entrophospora baltica. E. infrequens, Entrophospora sp., Pacispora coralloidea, Funneliformis mosseae, Scutellospora calospora, S. erythropus, Gigaspora margarita and, A. baetica* as new record for Mexico. Spore abundance was 15.5 spores g-1. *Acaulospora* was the dominant genus with high diversity of species adapted to acidic soils.

Key words: *Acaulospora baetica*, Glomeromycota, maize, new record, taxonomy.

ID 293 - Morphological and molecular characterization of ectomycorrhizae of *Phylloporus* (Boletales) and tropical *Quercus* species in Eastern Mexico

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Introduction. *Phylloporus* is distributed worldwide and recognized with tropical affinity, but in Mexico it has been recorded mainly in mesophytic and temperate forests. *Phylloporus rimosus* Bandala, Montoya & Garay and *P. quercophilus* Montoya, Bandala & Garay, however, were discovered in tropical oak forest at Eastern Mexico, an ecosystem seriously fragmented. *Phylloporus* is considered ectomycorrhizal, phylogenetically inferred as such, but the morphology of its ectomycorrhizae (ECM) and precise interactions have not been documented. Our objective was to provide morphological and molecular evidence at root tips of the ectomycorrhizal association of *Phylloporus* with tropical *Quercus* trees.

Methods. Basidiomes were weekly sampled (May-October 2016, 2017) and ECM´s obtained in 24 soil cores, in two monodominant stands of *Q. oleoides* and *Q. sapotifolia* at Veracruz, 750m altitude. To confirm the interaction, mycobionts in the ECM´s were identified through bioinformatic analysis of ITS region from rDNA. The phytobiont was detected by comparison of ITS sequences of leaves and ECM.

Results and discussion. The analyses inferred that *Phylloporus rimosus* and an unidentified species close to *P. rhodoxanthus* are associated with root tips of *Q. sapotifolia* and *Q. oleoides*, respectively. Descriptions of the morpho-anatomic features of ECM´s of both are presented.

Conclusion. The ectomycorrhizal interaction of *Phylloporus* at root tips level is confirmed, and its interaction with *Q. sapotifolia* and *Q. oleoides* at the tropical oak forest is diagnosed as well. Based on the programmed sampling we recorded an abundant fructification but a scarce presence of ECM´s of *Phylloporus* in both sites. Research supported by CONACYT CB-252431.

Key words: Ectomycorrhizal symbiosis, neotropics, tropical diversity.

ID 305 - Truffles diversity in alpine regions

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Introduction. The upper timber lane was rarely explored for truffles, both for commercial truffles and sequestrate fungi in general mainly because of lack of interest of commercial truffle hunters. The site conditions considering rock base, soil types and presence of potential ectomycorrhizal partners indicate their potential presence in high altitudes also by modelling approaches (Grebenc et al. 2010). For this reason, we focused on high altitude areas of the northern hemisphere.

Methods. We have sampled areas in the SE central Alps, Dinaric Alps, Himalaya – western part and Northern China (Inner Mongolia). We used either hunting approach or revision approach of soil or ectomycorrhiza sequencing data available.

Results and discussion. There was only one commercial species collected in the designated areas namely *Tuber aestivum* from beech and mixed beech-silver fir forests at high altitude (> 1500 m a.s.l.) (Grebenc et al., 2011). A novel true truffle species *Tuber petrophylum* (Milenkovi et al., 2015) closely related to Tuber melanosporum was described from similar sites. Novel ectomycorrizae from the genus *Tuber* were retrieved also from Himalaya, Inner Mongolia and Alps (Ilyas 2013; Jabeen and Khalid, 2014) including a broadly distributed novel *Tuber* species limited to the upper timber line.

Conclusion. Results indicate that the upper timber line in limestone/dolomite dominated areas are as suitable for truffles as any other area at lower altitude. A preliminary ecological model for predicting cultivation areas indicate potential for a successful cultivation and economically justified use of truffles as a plantation culture or as a supplementary inoculation species for environmental restoration purposes.

Key words: Alpine regions, distribution, diversity, hypogeous fungi, truffles.

ID 310 - Do native and invasive *Conyza canadensis* interact differently with AM fungi?

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Introduction. Plant invasions may represent a serious threat to local biodiversity. *Conyza canadensis* is native in North America and invasive in large parts of Europe and Asia. Despite being a ruderal annual, this species has been shown to promote the abundance of arbuscular mycorrhizal (AM) fungi. Here, we assessed if-and to what extent-AM colonization differed in the native and invasive ranges, and how these differences correlated with productivity.

Methods. We sampled 17 native populations from 4 biogeographical regions (Montana, California, Florida, Quebec) and 17 invasive populations from 4 biogeographical regions (Jordan, Kashmir, NW China, SE China). At each population, we sampled five *Conyza* plants and quantified shoot biomass, seed production and percent AM colonization. We also collected rhizosphere soil and measured concentrations of available nutrients.

Results and discussion. In the invasive ranges, *Conyza* grew bigger and set more seed, and soil pH and macronutrient availability were higher. All plants were highly colonized by AM fungi (72.3±24.5%). The relationship between AM colonization and shoot biomass differed between native and invasive ranges. AM colonization correlated negatively with *Conyza* biomass in the native ranges ($r = -0.66$, $P = 0.004$), whereas no such correlation was found in the invasive ranges ($r = -0.003$, $P = 0.99$).

Conclusion. We show that *Conyza* behaved as a typical invader and that interactions with AM fungi may differ across ranges. To gain a more mechanistic understanding of this biogeographical variation, we will investigate the plant-fungi interactions in common garden inoculation trials involving seeds collected from all populations.

Key words: Arbuscular mycorrhizal fungi, *Conyza canadensis*, invasion, productivity, soil properties.

ID 289 - Effect of P fertilization level on arbuscular mycorrhizal communities and maize growth under a tilled and no-tilled system

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Introduction. Arbuscular mycorrhizal fungi (AMF) was known to improve the P nutrition of *Zea mays* (Vivekanandan and Fixen 1991). It is necessary to increase the colonization rate of AMF for improve P nutrition. AMF colonization rates were increased with no-tillage (McGonigle and Miller 1993). However, there are few reports about changes in AMF community structure by no-tillage. Thus, we investigated how tillage affect the AMF community structure of *Zea mays* roots.

Methods. Field experiments were conducted from April to September 2018. We established four different amounts of P-fertilizer treatments (0, 50, 100, and 200 kg ha^{-1}) with or without rotary tillage to determine the diversity of AMF in maize roots using an Illumina Miseq Platform.

Results and discussion. AMF colonization rate were significantly decreased with the increase of P-fertilization. The colonization rate in no-tillage plot were significantly higher than that in tillage plot. Redundancy analysis showed that the tilled and no-tilled management noticeably altered the AMF communities in maize roots. In addition, the proportion of detected OTUs occurred specifically in no-tilled or tilled was 36.6% and 39.3%, respectively. However, there were no significant differences in the diversity of AMF communities among the difference of P-fertilization level.

Conclusion. Our results indicate that tillage management has more influence on changing AMF community structure in root than P-fertilization. However, we established only two different tillage intensities such as rotary tillage and no tillage. Thus, we should to determine how tillage intensity can alter the diversity of AMF communities in *Zea mays* root.

Key words: Amplicon sequencing, arbuscular mycorrhizal fungi, maize, no tillage, phosphorus fertilization.

ID 283 - Impact of different cover cropping on the arbuscular mycorrhizal fungal communities colonizing maize roots

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Introduction. Maintaining better host crops for arbuscular mycorrhizal fungi (AMF) in cover crop rotational systems can be important because having active AMF propagules present in the soil can allow for rapid colonization, better crop growth, and nutrient uptake. However, there is little information regarding the effects of different cover crops on AMF communities in subsequent maize (*Zea mays* L.) roots. Thus, we evaluated the molecular diversity of AMF community structure in the roots through the 2-year rotation using amplicon sequencing of the Illumina Miseq Platform.

Methods. Three different cover crop-maize rotational systems were established including winter wheat, hairy vetch, and brown mustard with or without incorporation of cover crop residue. We examined AMF colonization and communities in maize roots at the V6 stage.

Results and discussion. The AMF root colonization in the maize was significantly influenced by cover crop treatments. However, the AMF communities in roots with or without residue incorporation did not differ. Although the AMF communities colonizing maize roots were not influenced by cover crop residue management, the AMF communities were significantly changed by cover crop type.

Conclusions. Our results indicated that cover cropping rather than the incorporation of cover crop residues may be a key factor for shaping the AMF communities in maize roots. Thus, further investigation into the functional aspects of AMF communities in cover crop management will provide useful information on the role of AMF to improve crop productivity in cover crop rotational systems.

Key words: Amplicon sequencing, arbuscular mycorrhizal fungi, community structure, cover crops, maize.

ID 160 - Non-target effects of pesticides on maize growth and mycorrhiza formation in different fertilization settings

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Introduction. Arbuscular mycorrhizal fungi (AMF) can provide multiple crop benefits in agroecosystems, including improved plant growth and nutrition as well as stress alleviation, which however may be affected by agricultural practices such as pesticide applications. Here short term effects of pesticides on maize growth and mycorrhiza formation were examined in a greenhouse pot experiment with different fertilization settings.

Methods. A complete factorial design was employed with three factors: 1) Pesticides [without, Carbendazim (fungicide), Glyphosate (herbicide) and Carbofuran (insecticide)], 2) Organic matter in terms of maize straw (0 and 0.5%) and 3) Phosphorus mineral fertilization (0 and 100 mg P kg^{-1}). Maize hybrid plants were grown in low P soil in 1L pots for 8 weeks. Plant growth was measured in terms of shoot and root dry weight, and C, N and P shoot concentrations. Mycorrhiza formation was measured in terms of AMF root and soil colonization.

Results and discussion. All pesticides inhibited root and soil colonization by AMF, though effects were more pronounced for AMF soil colonization. Pesticides also strongly affected plant growth performance. Plant growth promotion was observed when combining Carbendazim and P, which coincided with the complete elimination of the mycorrhizal association, suggesting that Carbendazim was alleviating a possible plant growth suppression caused by the mycorrhizal association when P was not limited.

Conclusion. The three pesticides examined strongly affected the mycorrhizal status and growth of maize plants, which was further modulated by mineral P application. Our results suggest that pesticide applications are important to consider when managing and conserving AMF in agroecosystems.

Key words: Arbuscular mycorrhizal fungi, organic matter, pesticides, phosphorus fertilization.

ID 290 - Effect of arbuscular mycorrhiza on the interaction of invasive and native European plants

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Introduction. In a globalized world, plant invasions are common challenges for native ecosystems. Although a considerable number of invaders form arbuscular mycorrhiza, the role of arbuscular mycorrhizal fungi (AMF) in their interaction with native plants is little understood. For example, mycelia of AMF may help the invader to pre-empt nutrients for native plants or an invader may exploit common mycorrhizal networks nourished by native plants.

Methods. Here we present a glasshouse experiment asking whether AMF support invaders at the expense of native plants and whether the effect of AMF in disturbed soil differs from that in stable soil with established mycelial network. We tested three pairs of invasive and native plant species, all in the family Asteraceae, co-occurring in the central Europe. Pots were pre-planted with another native plant to establish mycorrhizal network before experimental disturbance.

Results and discussion. In general, AMF increased mass and P content of all plant species. The mass of two native species was independent on the competing plant (an invader or their own species) or slightly decreased by invader, regardless of mycorrhiza. The mass of the third native plant, *Inula conyzae*, was decreased by invader, *Echinops sphaerocephalus*, particularly in mycorrhizal treatment. Mycorrhiza shifted *Echinops-Inula* competition in favour of the invader; the effect was higher in disturbed soil. The presence of invader also decreased mycorrhizal colonization in *I. conyzae*.

Conclusion. To summarise, AMF supported invaders to the detriment of native plants in one of the three tested species pairs, demonstrating a variability of AMF effects on invader-native plant interaction.

Key words: Arbuscular mycorrhiza, plant invasions, plant competition, soil disturbance.

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ID 122 - The relationship between aboveground diversity and AMF on agroecosystems

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Introduction. Arbuscular mycorrhizal fungi (AMF) have the potential to benefit agroecosystems through their role in nutrient availability. Yet, little is known about how AMF community composition varies within agricultural landscapes and, more specifically, through a range of farm management practices. AMF form essential mutualism with more than 70% of vascular plants, including major crops. While AMF are not host-specific, mycorrhizal associations are also not random. Plant diversity is often proposed to explain the patterns of soil microbial diversity in which greater plant diversity increases belowground heterogeneity. Thus, in agroecosystems, a relationship between managed aboveground diversity (e.g. crop diversity) and belowground AMF diversity is expected.

Methods. In this study, we explore how diversifying crops in space and time, through intercropping or monocropping, in agroecosystems will impact AMF community composition through increasing plant heterogeneity. Specifically, we examine how AMF community composition varies between high plant diversity on farms (i.e. polycultures; >20 crop types) and low plant diversity on farms (i.e. monocultures; 1 crop type). We used microscopy and next generation sequencing on the fungal DNA barcode to characterize the AMF community.

Results and discussion. Our recent analyses compared how AMF root colonization and composition differs between polyculture and monoculture systems to determine if aboveground crop diversity influence belowground AMF in agroecosystems. Preliminary results show that AMF community composition correlates with greater plant diversity, and, thus dependent on cropping history.

Conclusion. Together, this research shows how diversifying farm management practices can create potential beneficial soil properties for farmers through belowground diversity.

Key words: aboveground - belowground interactions, arbuscular mycorrhizal fungi, diversified farming systems.

ID 199 - Arbuscular mycorrhizal fungal diversity response to fertiliser and crop rotation in wheat rhizospheres over multiple years

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Introduction. Arbuscular mycorrhizal fungi (AMF) are soil microbes that colonize up to 90% of all land plants and offer benefits in the form of nutrient acquisition, water retention, and resistance to pathogens and pests. AMF diversity is thought to respond to a range of biotic and abiotic factors in soil management practices. This was studied in a multi-year wheat field trial incorporating variation in fertiliser application (N and P) and crop rotation.

Methods. The AMF diversity in each sample was analysed by PCR amplification with AMF-specific DNA primers that span the small sub-unit to the large sub-unit of the ribosomal RNA gene and the products were sequenced using Illumina MiSeq. These primers were chosen for this study because they provide greater coverage and depth of AMF sequences compared to traditional fungal primers. The AMF diversity of individual samples differed by treatment in fertiliser type and amount and previous crop rotations of canola or chickpea.

Results and discussion. Bioinformatic analyses showed a strong correlation between AMF diversity and field trial conditions, particularly between the AMF genus Funneliformis and rhizosphere samples with no fertiliser treatments, and grown in conjunction with chickpea during rotation years. This indicates that treatments have a strong influence on AMF species diversity in agricultural trials, which may be explained by the filling of niches dictated by functional traits at the AMF genus or species level.

Conclusion. Further research on functional traits will elucidate how AMF can be strategically applied for reducing chemical inputs and water use in agriculture.

Key words: Arbuscular mycorrhizal fungi, bioinformatics, functional traits species diversity, wheat.

ID 224 - Microbiome transplants: a dirt simple method to enable urban forestry

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Introduction. Urban trees are essential infrastructure for sustainable cities. To grow well, trees need an array of beneficial microbes, among them the mycorrhizal fungi. Little is known about how to harness beneficial microbes to promote plant growth in cities. We aim to promote a simple protocol to provide urban trees with effective, local symbionts. As a first specific objective, we aimed to know how thoroughly urban trees are colonized by mycorrhizal fungi compared to rural trees.

Methods. 23 urban oak trees (18 in soft surfaces and 5 in hard surfaces) and 16 rural oak trees were collected in Bogotá, Colombia, and compared based on the percentage root colonization by ectomycorrhizae. 2 subsamples of each tree's roots were collected following a root tracing technique, then 4 2-ml tubes per subsample were prepared with root tip cuts to count the total root tips and colonized root tips in 8 stereoscope views per tube. A total of 64 measurements were obtained per tree.

Results and discussion. Two sample t-Tests show that there is a significant difference in the means of percentage root colonization between urban surfaces: higher percentage root colonization in hard surfaces than in soft surfaces. More generally, trees from forest presented higher percentage root colonization compared to urban oaks. Here we showed that in the city of Bogotá urban oaks are significantly less colonized compared to rural oaks; similar to some previous studies comparing urban and rural settings.

Conclusion. These findings, represent a significant step in proposing a strategy that uses root community transplants sourced from rural individuals in urban forestry.

Key words: Ectomycorrhizae, hard urban surface, percentage root colonization, soft urban surface, urban forestry.

ID 231 - Host identity rather than soil heterogeneity is the key determinant of the early ectomycorrhizal fungal community assembly for exotic and native pine seedlings

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Introduction. Exotic pine trees have been often introduced to novel places worldwide. Compared to the local native counterparts, how exotic pines interact with local soil microbes, such as symbiotic ectomycorrhizal (ECM) fungi, desires further investigation in order to better understand their establishment strategies and growth differences. Native masson pine (*Pinus massoniana*) and exotic slash pine (*Pinus elliottii*).

Methods. Seedlings were grown in soil cores collected from three different forest sites, with treatment of either intact (undisturbed) or homogenized (disturbed), to investigate the recovery of ECM fungal communities on seedlings roots. ECM root tips were collected at two times (3- and 6-month) and identified using high-throughput sequencing.

Results and discussion. We recovered ideal number (86%) of ECM fungal species from soils on native/exotic pine seedlings. Though native and exotic pines shared most of the ECM fungal species (79%), host identity was the key factor determining the early ECM fungal community assembly across the sites, in which native pine preferred *Rhizopogon* while exotic pine preferred to associate with most of ECM generalists (*Russula* and Thelephoraceae). However, in later succession, fungal communities of native and exotic pines seemed to be homogenized by *Rhizopogon* species. Additionally, five of the ECM fungal species showed unstable colonization with exotic slash pine seedlings in the community succession process.

Conclusion. This study documented that positive interactions among several pioneer ECM fungi shared by congeneric pine counterparts could facilitate exotic tree species establishment. However, more attention should be paid to the consequences of exotic trees on local forest ecosystem, such as host filtering of ECM fungal species and invasive potential.

Key words: Bioassay, community assembly, ectomycorrhizal fungi, exotic pine, *Rhizopogon*, *Russula*.

ID 270 - Mycorrhizal colonization and Indole-3-butyric acid on the vegetative propagation of *Stevia rebaudiana*

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Introduction. *Stevia rebaudiana* Bertoni is a low-calorie alternative natural sweetener that has gained worldwide interest. The growing global demand for stevia has made countries like Mexico begin to cultivate stevia extensively, however, one of the main challenges is the difficulty in propagating this crop.

Methods. We investigated the inoculation effect of arbuscular mycorrhiza (AM) and the application of Indole-3-butyric acid (IBA) concentrations on the vegetative propagation of *Stevia rebaudiana* through stem cuttings under greenhouse condition.

Results and discussion. Plants with the AM treatments (LC and CM consortiums) has lesser dry biomass of root (DBR) that the non-AM plants. Probably this reduction is related with the use of the AM mycelium to satisfy the absorption of water, because they presented up to 20% of the mycorrhizal colonization. On the other hand, application of powder IBA at 0.075% increased the DBR in relation at plants treated with powder IBA 0.15%, these results suggest that can be reduce the cost of the auxin application up to 50%. Finally, cuttings colonization by R*hizophagus intraradices* together with treatments of IBA solutions at 0.075%, generated the best effect of shoot growth.

Conclusions. The results of this work demonstrate for the first time the potential of AM to improve the rooting in crops of commercial interest such as *Stevia*.

Key words: Alternative plants to sugarcane, rooting, vegetative propagation.

ID 272 - Arbuscular mycorrhizal fungi native from acid soils as growth promoters in hybrid mayze

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Introduction. The adaptation to edaphic conditions and the specificity between arbuscular mycorrhizal fungi (AMF) and plants that form mycorrhizae confer advantages to the use of native strains of AMF. The aim of this work was to evaluate the effect of native AMF from acid soils on the growth of mayze hybrids.

Methods. Five consortia of native AMF and a commercial inoculum were evaluated as growth promoters in greenhouse hybrid maize plants. Inoculation with 80 spores was performed in the transplant in acid soil without sterilization. At 61 days after transplantation, plant height, stem diameter, fresh and dry weights of leaves, stem and root, leaf area, root volume and root colonization were recorded.

Results and discussion. Plants inoculated with the La Ciénega consortium grew 48% more than plants without inoculation (Tukey, $P \leq 0.05$). On the other hand, maize plants inoculated with the El Llano consortium presented fresh and dry biomass of root and leaf area greater by 30% than plants without inoculation (Tukey, $P \leq 0.05$). The highest colonization of the plants was presented with the El Llano inoculum with 94% and with the commercial inoculum they presented 80%.

Conclusions. This suggests that maize plants inoculated with native consortiums of acidic soils are able to carry out a growth promotion with respect to uninoculated plants, this biotechnology could be used in soils with acidity problems where mayze is grown.

Key words: Acid soil stress, biofertilizer, corn, consortia AMF.

ID 276 - Seed coating: a tool for delivering arbuscular mycorrhizal fungi to agricultural crops

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Introduction. Arbuscular mycorrhizal fungi (AMF) are well known for improving nutrient uptake, plant growth and tolerance to various abiotic stresses. Still, their large scale application has been hampered by the relatively high cost of inoculation and the need to attain a sufficient number of propagules per plant.

Methods. Different greenhouse and field experiments were performed with agricultural crops in order to assess seed coating as a feasible AMF inoculum delivery system and the inoculation effect on plant performance under different environmental conditions.

Results and discussion. There were no significant differences in root mycorrhizal colonization between plants conventionally inoculated with AMF in soil and those inoculated via seed coating, indicating that seed coating system can serve as an efficient system to inoculate agricultural crops. Overall, plant vigor, yield, nutrient concentration, photosynthetic potential and resistance to drought stress were boosted in plants inoculated with AMF through seed coating.

Conclusions. Our findings indicate that application of AMF via seed coating is a promising approach for sustainable field-based plant cultivation, as it has the advantage of reducing the amount of inoculum needed for successful inoculation.

Key words: Arbuscular mycorrhizal fungi, seed coating, seed inoculation, sustainable agriculture.

ID 285 - Variation of Arbuscular Mycorrhizal Fungal Communities along a Chronosequence of *Betula alnoides* Stands

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Introduction. This study was conducted to understand the ecology of AM of *Betula alnoides* plantation, a fast-growing and valued birch timber species prevalently planted in tropical and subtropical areas of Southern China.

Methods. This study was conducted in Puwen experimental forest farm in Xishuangbanna, Yunnan province of China, on a 3-year-old (P3y) and 12-year-old *B. alnoides* plantation (P12y) and in a nearby natural stand (zonal vegetation tropical montane rain forest, N). We explored AM fungal community composition change along the plantation chronosequence by combining morphological methods on rhizosphere soil AMF spores and Illumina MiSeq sequencing technique.

Results and discussion. The results pointed out a trend of AMF richness and diversity of two plantations was similar to natural stand, however, the specific AM fungal compositions of the three stands were distinctly different, the AM fungal composition of mid-aged stand (P12y) was more similar to that of *B. alnoides* in the natural forest (N) than the young-aged plantation (P3y). A set of soil properties (AP, AN, OM, TN and silt content) played a significant role in shaping the AM fungal communities.

Conclusion. AMF showed considerable resilience to the establishment of *B. alnoides* plantation, the P12y harbored AM fungal communities more similar to those in natural stand than in the P3y, which implied that the along the growing of plantation, driven by the improvement of environmental factors such as soil parameters, the AM fungal diversity and community composition could develop towards the natural stands.

Key words: Arbuscular mycorrhizal fungi, *Betula alnoides*, birch, plantation.

ID 301 - Effectiveness of native AMF from a Cuban agroecosystem vs. exogenous AMF on *Zea mays* L.

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Introduction. This study aimed to evaluate the effectiveness of native AMF against two exogenous inoculants on corn, under greenhouse conditions. The native mycorrhizal potential of an agroecosystem with a Pardo mullido soil belonging to "Mi Niña" orchard, from Caraballo, Jaruco Municipality, Mayabeque Province, Cuba, was characterized.

Methods. The AMF spores were multiplicated in trap cultures (*Sorghum bicolor*), obtaining 30-98 spores/g of soil at the five areas with different management, in which the orchard was subdivided for the study.

Results and discussion. The morphological spore identification showed 24 morphotypes, grouped in four families and eight genera. The molecular analysis revealed48 AMF OTUs distributed in three families and sevengenera. In both determinations the Glomeraceae family and the *Glomus* genus were the most representatives. One inoculum conformed by the native AMF and two exogenous strains (*Funneliformis mosseae* (INCAM-2) and *Rhizophagus irregularis* (INCAM-11)) were inoculated in corn plants, separately and several combinations of them, for a total of seven treatments. At 60 days after sowing, a better behavior of treatments inoculated with native AMF, INCAM-11 strain and their combination, was observed inplant growth (biomass, height, stem diameter, leaf number, chlorophyll content), plant nutrition (N, P, K leaf contents) and fungal variables (frequency, intensity, spore number). Results showed the efficiency of native AMF and the exogenous strain *Rhizophagus irregularis* (INCAM-11) for the edaphoclimatic conditions of studied agroecosystem.

Conclusion. We discuss the possibility to formulate a mix inoculum based on both AMFs for their optimized use as biofertilizer in soils with similar conditions.

Key words: Arbuscular mycorrhizal fungi, corn, metagenomic, 454 pyrosequencing.

ID 51 - Identification and *in vitro* selection of root-associated fungi for use in ecological engineering and ecosystem restoration of iron-ore tailings in subarctic tundra of Northern Quebec, Canada

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Introduction. Mining activities involve the removal of vegetation, healthy living soil, plant propagules and symbionts, and may alter soil hydrology and increase the risks of heavy-metal contamination. In northern ecosystems such as the subarctic tundra, these activities increase abiotic stress to a point that actions must be taken to promote ecosystem restoration. We hypothesize that the use of root plant symbionts can enhance the establishment and survival of plant communities on such drastically disturbed ecosystems.

Methods. Healthy roots were collected from six native plant species from the Schefferville mine site area in Northern Quebec, Canada. Fungal symbionts were isolated from root tips and pure isolates were identified based on rDNA internal transcribed spacer (ITS) analysis. Nine of the most frequently isolated fungi were used for an in vitro test in liquid media (GYME) amended with overburden, sterile or pure ferric iron. Ergosterol and organic acids were quantified by HPLC to monitor fungal growth and metabolites.

Results and discussion. A total of 376 cultivable fungi were identified, representing 106 taxa. Ericoid fungus *Rhizocyhus ericae* exhibited the best growth in the presence of mine tailings, followed by dark septate endophyte *Phialocephala fortinii*, who exuded the greatest amount of organic acids. *Cadophora finlandica* and *Meliniomyces bicolor* also exhibited good tolerance to amendments.

Conclusion. Root-associated fungi do not all respond the same way to mine waste. We selected the cultivable fungi that would be the most appropriate candidates for biotechnological applications of inoculants for use in reclamation of iron-ore mine waste in subarctic tundra of Northern Quebec, Canada.

Key words: Ecological restoration, fungal symbionts, mining, northern ecosystem.

ID 238 - Moving together with flat-mates: Sympatric arbuscular mycorrhizal fungi after three seasons in allopatric conditions

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Introduction. Inoculation with sympatric, presumably co-adapted mycorrhizal symbionts has been proposed to enhance the performance of plants sown or out-planted within revegetation programs. However, the establishment and persistence of the plants' sympatric mycorrhizal communities in allopatric soil-climatic conditions is rarely investigated.

Methods. A field transplant experiment with *Bouteloua gracilis* at four localities has been utilized to address this question. At each (climatically and edaphically defined) locality, the grass was out-planted either inoculated with its "home" community of microorganisms (originating from the site of seed collection) or with the out-planting site’s "away" microbial community. Each inoculation treatment was established either in the "home" or in the out-planting site’s "away" soil. The root colonizing communities of arbuscular mycorrhizal fungi (AMF) were described by Illumina sequencing three seasons after the establishment of the experiment.

Results and discussion. The inoculation treatment significantly affected the composition of the root-colonizing AMF community at three out of the four localities, the strength of the effect, relative to the effect of soil, depended on the locality. The combination of "away" soil and "home" microorganisms mostly lead to an intermediate community composition between the clearly distinct "home-home" and "away-away" communities. However, a strong effect of inoculation and absence of soil effects was also recorded at one locality.

Conclusion. These results show that a sympatric AMF community may retain long-term association with plants in allopatric soil-climatic conditions. The exact character, causes and consequences of compositional shifts in co-transplanted sympatric AMF communities are important topics for future research.

Key words: Arbuscular mycorrhiza, *Bouteloua gracilis*, co-adaptation, community composition, Illumina sequencing.

ID 245 - Revegetation technique changes root mycorrhizal communities: the advantage of direct seeding over transplanting tube-stock in riparian ecosystems

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Introduction. Riparian ecosystems are among the most degraded worldwide as they are subject to a range of human-mediated disturbances at different scales. As riparian vegetation plays a key role in maintaining waterway and landscape health, restoration often focuses on promoting riparian vegetation re-establishment. The role of below-ground processes and agents in this process of vegetation re-establishment is often overlooked even though agents like mycorrhizal fungi enhance seedling establishment and plant growth. We aimed to understand whether colonisation by fungi from the CMN and pool of local spores can be advantageous to the early phases of plant establishment during revegetation, and whether revegetation technique influences the extent of this potential colonisation, and so has the potential to enhance revegetation outcomes.

Methods. We examined colonisation rate and species composition of root fungal communities in direct seeded and tube-stock plants and compared them with local extant native vegetation in a retarding basin in Victoria, Australia, and modeled the relationship between root fungal community attributes and plant size.

Results and discussion. Results indicate that revegetation technique influence the colonisation rate, diversity and composition of root fungal communities. Moreover, greater fungal diversity and greater similarity of fungal communities to the mycobiota of native vegetation are positively related with growth of seeded plants but showed negative or little relationship to size of tube-stock plants.

Conclusion. High colonisation rates of all plant species studied, and relationships between fungal community characteristics and plant growth of seeded plants provide the first evidence of the potential importance of mycorrhizal associations for these plant species.

Key words: Direct seeding, revegetation, riparian, root colonisation, soil microbial community, tube-stock tran.

ID 14 - Arbuscular mycorrhizal fungi serve as keystone taxa for revegetation on Qinghai-Tibetan Plateau

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Introduction. Revegetation is widely used to enhance degraded topsoil recovery with the enhancements of soil nutrient accumulation and soil structure stabilization. Arbuscular mycorrhizal fungi (AMF) are important for the allocation of carbon into soil and the formation of soil aggregates. Thus, we hypothesized that AMF could construct more niches for other microbes during revegetation, making AMF keystone taxa of soil.

Methods. Soil fungal and bacterial communities were investigated under a revegetation experiment and correlation networks between soil fungi and bacteria were constructed. Simultaneously, the plant growth level, soil properties and structure, and soil microbial carbon decomposition abilities were measured.

Results and discussion. The results revealed that AMF were the most central fungi at the phylum (degree = 3), class (degree = 11), and family (degree = 15) levels. The reads number of AMF were positively correlated with both fungal ($R^2 = 0.431$, $P < 0.001$) and bacterial ($R^2 = 0.106$, $P = 0.044$) richness. Higher colonization of AMF in roots and/or more AMF extraradical mycelium and spores in soil indicated a better plant growth, more stable soil aggregates, and a higher carbon decomposition ratio.

Conclusion. Our results highlight that AMF are keystone taxa in revegetation, as they play significant roles in enhancing the recovery of the belowground microbiome diversity, soil structure stability, and nutrients cycling. The positive roles of AMF in revegetation support the application of AMF in ecosystem recovery.

Key words: carbon decomposition ability, correlation network, keystone taxa, revegetation, soil structure.

ID 175 - Plant specific arbuscular mycorrhizal fungal species communities of important agricultural crops (Pequin pepper, soybean and orange) in the northeast Mexico

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Introduction. Arbuscular mycorrhizal fungi (AMF) are obligate symbionts of *ca*. 80% of land plants. Besides improving plant nutrition, they may significantly reduce drought stress, but their impact may differ depending on their host and environmental conditions. Pequin pepper, soybean and orange are important crops in the northeast of Mexico in arid areas exposed to drought conditions and their associated AMF community characterization may be relevant for sustainable management practices.

Methods. AMF species colonizing the roots of these different crops, from one location, were phylogenetically characterized by sequencing a 450 bp region of the large ribosomal rRNA gene with the MiSeq-Illumina platform followed by taxonomic affiliation based on an evolutionary placement algorithm (EPA).

Results and discussion. Twenty species from 13 different genera were detected. AMF community composition and relative read abundances of the AMF species were different in each crop. In Pequin pepper roots, several *Rhizophagus* species represented most of the community, being *Rhizophagus clarus* the most abundant. The soybean AMF community was dominated by *Rhizophaus irregularis* and *Funneliformis mosseae* and that of orange by species of *Dominikia*, with a set of species only found in this crop. Interestingly, sampling time and stage of plant development did not show a significant effect in the AMF community, but plant host-preference was shown as a significant factor shaping AMF communities.

Conclusion.The newly proposed ribosomal rDNA region and sequencing strategy combined with RAxML-EPA phylogenetic affiliation enabled the study of AMF communities at the species level. Unraveling AMF-host preferences will be important for the development of effective crop-specific biofertilizers.

Key words: Arbuscular mycorrhizal fungi species communities, DNA-based species identification, MiSeq-Illuminas.

ID 215 - Tight and flexible regulation of mycorrhizal formation and functioning through a gene-coexpression network module in diverse and fluctuating environments

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Introduction. Arbuscular mycorrhizal (AM) fungi form symbiotic associations with most families of land plants and improve phosphate (Pi) nutrition under diverse and fluctuating environments. In return, plants provide AM fungi with organic carbon derived from photosynthesis. Many genes responsible for AM formation and nutrient exchange have been identified, but the regulatory mechanism of AM functioning in the field is largely unknown.

Methods. We collected 251 maize root samples grown in the field across 24 plots in the United States and Japan. RNA-seq, followed by gene-coexpression network analysis using WGCNA R package, were conducted.

Results and discussion. We identified 19 coexpression modules, and in one of the modules the majority of AM-specific genes required for arbuscule development and nutrient exchange were enriched; e.g., those encoding the AM-inducible phosphate transporter Pht1;6, putative lipid exporter STR/STR2, enzymes involved in AM-specific lipid biosynthetic pathway FatM and RAM2, and proteins involved in periarbuscular membrane formation Vapyrin and Exo70I, namely, a ‘mycorrhizal module’. Eigengene values (principle component 1 scores) of the module, which is likely to represent the functional levels of mycorrhiza, were correlated positively with transcript abundances of AM fungal rDNA (biomass marker) and two fungal genes involved in Pi delivery and negatively with leaf-P concentrations.

Conclusion. These results suggest that relative expression levels of the genes in the mycorrhizal module are tightly regulated across environments, but their absolute expression levels are flexibly modulated in response to fungal abundance, functioning levels of the fungi, and plant nutrient status.

Key words: Arbuscular mycorrhiza, field transcriptomics, gene-coexpression network, maize.

ID 250 - Concept of mycorrhizal Potential applied to inoculants

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Introduction. All components of AM fungi are able to form new mycorrhizae in natural soils. These components, the spores (which sometime form inside the roots, but mostly in the soil), intra-radical vesicles and hyphae, and extra-radical hyphae, are collectively called 'propagules". The vigor and abundance in soil of these AM propagules determine the mycorrhizal potential of a soil. AM fungi's inoculants are sometime composed only of spores, but most often all parts of these fungi, i.e. spores, vesicles, and intra and extra radical hyphae, are present in commercial inoculants.

Methods. Based on the concept of MSI, we can determine the number of effective propagules in an inoculant.

Results and discussion. Because field and greenhouse soil conditions are likely to differ from those in the standardized test, the amount of AM propagules in commercial inoculants are expressed in 'Unit of Potential Mycorhization' (UPM), where: U = Unit, a propagule of any type able to initiate AM formation in a host plant's root. P = Potential, since the development of the symbiosis depends on different factors (soil, plant, agricultural practices, competition with other soil borne microorganisms, etc.). M = Mycorrhizal, since the inoculum is able to synthesize new mycorrhizae in association with plant roots depending on factors previously cited.

Conclusion. The UPM concept may also be applied to express the amount of 'active ingredients' on the label of commercial for AM and ectomycorrhizal inoculants.

Key words: Inoculants, potential, unit.

ID 266 - Evaluation of the performance of MALDI-TOF-MS biotyping to identify Gigasporaceae

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Introduction. High precision and accuracy are crucial both for new species recognition and for routine identification of arbuscular mycorrhizal fungi (AMF, Glomeromycota). The identification of AMF is challenging due to limited morphological characters often obscured by homoplasy. So far, the amplification, cloning and sequencing of the 18S-ITS-28S region of the nuclear ribosome is the most reliable approach to identify species within AMF. Nevertheless, the entire molecular process is time-consuming and can be relatively expensive for routine identification. Here we compare the identification of species from the Gigasporaceae using MALDI-TOF mass spectrometry to sanger sequencing of the 18S-ITS-28S nuclear region.

Methods. A total of 20 in vivo cultures representing five genera and 14 species were targeted. These isolates were maintained by the Canadian Collection of AMF (CCAMF) and the International Bank of Glomeromycota (BEG). For each strain, spores were isolated from soil and spore proteins were extracted to produce the MALDI-TOF mass spectra. Total genomic DNA was isolated and the 18S-ITS-28S region amplified, cloned and sequenced. Here, we show that MALDI-TOF-MS proteomic-based biotyping is a highly efficient to identify species within Gigasporaceae.

Results and discussion. All isolates showed a unique proteome profile. This method was able to separate closely related isolates (under species level), which was not possible with Sanger sequencing of the 18S-ITS-28S nuclear region. However, phylogenetic relationships were not reliably recovered by proteomic profiles, as shown in the rDNA phylogeny.

Conclusion. AMF identification by MALDI biotyping is fast, accurate and inexpensive and it represents a promising avenue for “routine” quality control of culture collections and of commercial biofertilizers.

Key words: Gigasporaceae, MALDI-TOF-MS biotyping, Sanger sequencing, species identification.

ID 282 - Simple and convenient observation methods of mycorrhizal fungi by a newly developed portable fluorescence microscope using mycorrhizal fungus-detection fluorescence reagent

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Introduction. The standard procedure (Philips and Hayman, 1970) to observe arbuscular mycorrhizal fungal (AMF) root colonization is cumbersome, and various light microscopical techniques are required to clearly distinguish between AMF and root tissues.

Methods. Therefore, we developed a new reagent to detect a specific 24 kDa protein related to mycorrhizal symbiosis (patent pending). The 24 kDa protein has been reported to exist in various mycorrhizal fungi (Ishii et al. 1999; Matsubara et al. 2012; Matsubara and Ishii, 2014; Ishii and Amanai, in press). Furthermore, we developed a new type of fluorescence microscope (Joint development with Soma Optics, Ltd.) (Ishii and Amanai, in press).

Results and discussion. In this ICOM, the author presents simple and convenient observation methods of mycorrhizal fungi in various kinds of roots, soils and artificial media, by using both the portable fluorescence microscope and the fluorescence reagent. Rootlets of various plants were cut in 1-2 cm from the apex, and 8 µl of the fluorescence reagent was dropped onto each root. Immediately, mycorrhizal root colonization was observed at wavelength of 472 nm using the portable fluorescence microscope, and were taken with a cell phone camera or a CMOS camera. The presence and dynamics of mycorrhizal fungi in soils and cultural media were observed by using the aforementioned fluorescence microscope with a diluted fluorescence reagent. As a result, the presence and dynamics of mycorrhizal fungi were observed conveniently and clearly in all cases.

Conclusions. This observation methods will greatly contribute to the studies on the function and utilization of mycorrhizal fungi.

Key words: Mycorrhizal fungi, mycorrhizal fungus-detection fluorescence reagent, new observation methods, Porta.

ID 296 - Web interface of arbuscular mycorrhizal fungal and bacterial classification pipeline

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Introduction. Arbuscular Mycorrhizal (AM) fungi form symbiotic associations with most land plants and interact with a wide range of soil microorganisms. We have been developing the user-friendly web interface ‘Arbuscular Mycorrhizal Fungi and Bacteria classification pipeline’ for rapid identification of fungi (including AM fungi) and bacteria from raw-sequence reads.

Methods. The fungal reference database consists of the sequences of divergent D2 region of LSU including 524 AM fungal OTUs and 82,082 non-glomeromycotinan sequences obtained from 34 and 5 agricultural field across Japan and North America, respectively. The bacterial reference database consists of the sequences of 7,292 type strains and 300,706 sequences of V3-V4 regions of SSU.

Results and discussion. In the fungi mode of pipeline, users input fastq files of either paired-end (PE) or single-end reads generated by Illumina MiSeq. The pipeline connects PE reads and assigns to either AM fungal OTUs or non-glomeromycotinan fungal sequences through BLASTN searches against the database, and generates two OTU tables, ‘AM fungi assigned’ and ‘Other fungi assigned.’ Distinct characteristics of this pipeline is that each user can manage a private reference database, namely, user can construct their own database and add new OTUs/sequences found in 'unassigned reads' to the database. Since this pipeline provides the fixed OTU as an output, users can apply the obtained results for comparison between the independent experiments.

Conclusion. This system would be applicable for the community analysis based different regions of ribosomal DNA and internal transcribed spacer regions. Currently, the ‘Arbuscular Mycorrhizal fungal and bacterial classification pipeline’ is freely available under http://amfungi.kazusa.or.jp.

Key words: Arbuscular Mycorrhizal, bacteria, classification, database, NGS, pipeline.

ID 258 - Analysis of mycorrhizal associations of the invasive plant Brazilian pepper tree (*Schinus terebinthifolius*) in South Florida

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Introduction. Multiple invasive plants employ mycorrhizal networks to enhance their establishment and inhibition of other native plants in their non-native location. Little is known however, about the mycorrhizal status of the most destructive invasive plant in Florida – Brazilian pepper tree (*Schinus terebinthfiolius*).

Methods. To gain an insight into its mycorrhizal associations, the rhizobiome of *Schinus* and two Florida native plants (*Hamelia patens* and *Bidens alba*) across six locations in Florida was examined. A small greenhouse study was also conducted to assess the AM infectivity of *Schinus* and another Florida native *Magnolia virginiana*. AM from the roots of all plants was characterized by spore morphotyping and infectivity measured by light microscopy. Sequence analysis (ITS2) was done with extracted DNA from lateral roots/rhizosphere of *Schinus* (n = 52) and *H. patens* (n = 37).

Results and discussion. The total population and infectivity of AMF associated with *Schinus* were two-three folds greater than that of the native plants growing on the same site and in the greenhouse study, with *Glomus* and *Rhizophagus* spp. being most prevalent. By contrast, the most prevalent AMF in the rhizosphere of the Florida native plants, *Acaulospora* spp. (29%) was reduced (9%) under *Schinus* rhizosphere. Analysis of the ITS2 sequences revealed that *Schinus* rhizosphere had a high prevalence of EM fungi (76.5%) compared to the native *H. patens* (2.6%), with the species *Lactifluus hygrophoroides* being the most prevalent (61.5%).

Conclusions. *S. terebinthifolius* could serve as a model plant for studying other mycorrhizal invasive plant species aiding in deciphering the role of mycorrhiza in plant invasion.

Key words: Arbuscular mycorrhiza, Brazilian pepper tree, ectomycorrhizal, invasive plants, rhizobiome.

ID 246 - Can the arbuscular mychorrizal fungi (AMF) limit the absorption and translocation of cadmium in cocoa (*Theobroma cacao*) plants?

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Introduction. Colombia is one of the top ten countries with the highest production of cocoa. Along with other Latin American countries produces about 70% of the world's fine cocoa. One of the main crop limitations is the plant high capacity to absorb cadmium, reducing the product harmlessness and makes it very difficult to fulfill international quality standards. AGROSAVIA, has been evaluating potential strategies to reduce the absorption of cadmium in cocoa plants, one of them is the use of AMF. The main objective of this study was evaluated the effectiveness of the inoculation with AMF on the cadmium translocation, to the different organs of the cocoa pattern (PA12).

Methods. We evaluate three AMF strains, *Glomus intraradices*, *Glomus macrocarpum*, and a native inoculum (formed by spores communities isolated from cocoa soils), under five cadmium levels (0, 6, 12, 18 and 24 mg.kg-1) and an absolute control. We measure plant development, AMF root colonization and a nutrient and cadmium content in plant organs.

Results and discussion. We analyzed the information statistically by a multifactor analysis and Tukey’s comparison test, finding that the AMF inoculation can limit in an average of 15%, the metal absorption and translocation to the different organs of the cocoa plant.

Conclusion. AMF also can promote the absorption of essential nutrients.

Key words: Cadmium, cocoa, heavy metals, mychorriza.

ID 317 - Richness of arbuscular mycorrhizal fungi in two contrasting orchards of *Persea americana* within an ecological Reserve

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Introduction. The land use change has led to the loss of diversity of the arbuscular mycorrhizal fungi (AMF) and decreasing their ecosystem services. For example, avocado production in Nayarit, Mexico is increasing, so the cultivation areas are expanding towards the State Ecology Reserve Sierra de San Juan, located in the municipality of Xalisco, Nayarit. This study aimed to know the diversity of AMF of two contrasting orchards of avocado inside the Reserve. Both orchards differ in their nutritional management (orchard 1: O1= without nutritional management and orchard 2: O2= with nutritional management).

Methods. AMF propagation was carried out in trap plants (*Festuca rubra, Cynodan dactylan, Lolium perenne*). DNA extraction from roots and spores was carried out with DNAzol^{TM} according to the manufacturer. The gDNA was used to perform the molecular identification by the nested PCR technique, with the primers suggested by Krüger *et al*. 2009. A third PCR was performed using the ITS generalist primers to sequencing in the Illumina's Miseq platform. Sequencing and Bioinformatics were performance in the Institute of Biotechnology, UNAM.

Results and discussion. Alpha diversity in O2 was greater compared to O1 (16 *vs* 11 species respectively). Nevertheless, according to the Jaccard similarity index, the species shared in the plots are similar in 80%. It is important to say that nine species have not been reported before for avocado orchards in Mexico (*Ambispora fennica, Acaulospora entreriana, Diversispora aurantia, Cetraspora nodosa, Claroideoglomus luteum, Funneliformis mosseae, Rhizophagus proliferum, Redeckera megalocarpus, Paraglomus occultum*).

Conclusion. Our preliminary results suggested that land use change in the avocado orchards did not affect the richness of AMF. However, analyses deeper are necessary.

Key words: Avocado orchards, land use change, Nayarit.

ID 247 - Quantifying Arbuscular Mycorrhiza (AM) propagules in the semi-finished or finished formulated product: A proposed method towards quality compliance

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Introduction. Currently AM products are being quantified on the basis of number of spores/gram. AM fungi colonize the roots of the plants and produces spores (inside the roots as well as outside the root) after 2-3 months. The propagules in AM thus include spores inside as well as outside roots, infective hyphae, vesicles etc. thus its quantification is undervalued with current methodology, if the product contains the sheared root fragments.

Methods. Blending methodology to extract propagules from the root fragments in the product has been optimized. An average of 80% of the propagules inside the roots has been successfully extracted. Determination of total propagules after this blending method, which are quantifiable and thus does not have the inherent inaccuracy discussed above. For the rest 20% unrecovered propagules, quantification methodology has been developed based on the total root segments/g and the percentage of the length of root segments containing AM structures.

Results and discussion. From the examination of 10 samples, each with 100 randomly selected sheared root segments, this estimation of AM quantification was found to be more accurate than the determination of the AM fungal based on spores without blending. It was no more time consuming.

Conclusion. It is proposed that, for the sake of quality compliance, this procedure be adopted as a standard method.

Keywords: Blending, methodology, quantification.

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