Swiss Mycology Symposium 2025

27. June 2025

Swiss Federal Research Institute WSL, Zürcherstrasse 111, 8903 Birmensdorf, Englersaal

09:00 - 09:30 Arrival and Registration

Session 1: Fungal diversity, biogeography and evolution; chair Benjamin Dauphin

09:30 - 09:35 Welcome address; Martina Peter / Markus Künzler

09:35 - 09:55 **Ivan Skakov** (Uni Neuchâtel): Rapid mitochondrial genome structure evolution in the wheat pathogen *Zymoseptoria tritici* and beyond

09:55 - 10:15 **Ido Rog** (Uni Zürich): The increased environmental niche of dual-mycorrhizal woody species

10:15 - 10:35 **Fantin Mesny** (Uni Köln): Plant-pathogenic fungi evolved host-manipulating effectors from ancestral antimicrobial proteins

10:35 - 11:10 Coffee break

Session 2: Applied Mycology; chair Ludwig Beenken

11:10 - 11:30 **Lisa Cresp** (Uni Neuchâtel): Harnessing the Fungal Highway for Crop Protection: Isolation of Pathosystem-Specific Bacterial-Fungal Consortia

11:30 - 11:50 **James F. Smith** (Uni Fribourg): Biocontrol Partners in Action: Leveraging Bacterial and Fungal combinations to Protect Potatoes from Late Blight

11:50 - 12:10 **Tiago Carvalho** (EMPA): Foxfire: A Hybrid Living Material for Sustainable Illumination

12:10 - 12:50 **Keynote Talk by Claus Bässler** (Uni Bayreuth): Advancing Fungal Ecology and Conservation through Citizen Science and Experimental Forest Research

12:50 - 15:00 Lunch break in the canteen
Poster session with coffee break (Englersaal)

Session 3: Fungal interactions: from molecules to ecosystems; chair Carolina Cornejo

15:00 - 15:20	**Emma Alessandri** (ETH Zürich): The Unfolded Protein Response is involved in the antibacterial defense response of model mushroom *Coprinopsis cinerea*
15:20- 15:40	**Alannah Holderbusch** (ETH Zürich): Inducing novel endosymbioses in the filamentous fungus *Rhizopus microsporus*
15:40- 16:00	**Marine Louvet** (Uni Lausanne): Wor2 represses biofilm formation by downregulation of SCF1 and ALS4112
16:00 - 16:20	**Cecilia Panzetti** (Agroscope, Uni Neuchâtel): A new molecular detection method applied to barely seeds for quantifying *Ustilago nuda* and predicting their field infection levels
16:20 - 16:40	**Felix Zimmermann** (WSL): A native ectomycorrhizal fungus alters the internal clock-driven endogenous growth rhythm of Pedunculate oak
16:40	Closing remarks & farewell; Markus Künzler / Martina Peter

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ABSTRACTS OF THE ORAL PRESENTATIONS

Session 1

Rapid mitochondrial genome structure evolution in the wheat pathogen *Zymoseptoria tritici* and beyond

Ivan Skakov[1], Alice Feurtey[1, 2], Guido Puccetti[1] and Daniel Croll[1]

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Mitochondria play crucial roles in fungal cells serving as hubs for energy conversion. Despite the conservation of mitochondrial functions across the fungal tree of life, mitogenomes exhibit astonishing incidences of genome expansions and rearrangements among species. Genome expansions are best explained by selfish element proliferation, however, how such variation arises in its earliest stages (i.e. within species) remains largely unknown. Here, we address this question by establishing the largest intra-species survey of mitochondrial genomes focused on the major wheat pathogen *Zymoseptoria tritici*. We found that mitochondrial and nuclear population structures assessed for 2120 isolates were incongruent across the global distribution range. We systematically assembled mitochondrial genomes and validated major structural variants using long-read sequencing. We found that 97% of all mitochondria belong to five primary haplotypes distinguished mainly by two large insertions/deletions underpinning variation in mitogenomes by 18%. Selfish elements were absent from the mitochondria suggesting efficient purifying selection with the notable exception of a rare Eastern Europe haplotype encoding a GIY-YIG homing endonuclease. Assembling mitogenomes from closely related *Zymoseptoria* species revealed that the dynamics observed within the species expand to substantial interspecies variability in mitogenomes (44-60 kb) and essential gene content variation. The GIY-YIG homing endonuclease shows a sparse and patchy distribution in Ascomycetes with highly similar copies found in distant groups of fungi raising the possibility of horizontal transfer. In conjunction, our study shows how the extensive variability of mitogenomes has its origins within species. This facilitates mechanistic studies on how selfish element activity drives genome evolution.

The increased environmental niche of dual-mycorrhizal woody species

Ido Rog, David Lerner, S. Franz Bender, Marcel G.A. van der Heijden

University of Zürich and Agroscope

The presence and distribution of mycorrhizal symbionts can influence plant distribution through specific host-mycorrhiza symbiosis interactions. However, generalist hosts also exist, such as dual-mycorrhizal plants that form symbiotic associations to both ectomycorrhizal-fungi (EM) and arbuscular mycorrhizal-fungi (AM). Little is known about the effect of dual mycorrhization status on the hosts' global distribution and acclimation to specific environments. This study investigates the potential advantage of dual associations of more than 400 woody-genera spread at a global scale. We found that dual host woody-species occupy a broader geographical range and environmental niche space compared to those associating exclusively with either AM or EM. We show that

the increased geographic range and expanded environmental niche space is independent of phylogenetic architecture and evolutionary history of the woody-genera. Our results highlight the advantage of generalist host-microbe symbioses between woody-species and fungi to expand their range, and their potential role in colonizing dry climates.

Plant-pathogenic fungi evolved host-manipulating effectors from ancestral antimicrobial proteins

Fantin Mesny

University of Cologne (Germany); Department of Plant and Microbial Biology, University of Zürich

Plant-pathogenic fungi secrete effector proteins that support plant tissue colonization by modulating host physiology. However, increasing evidence points to another crucial function of fungal effectors, namely in microbial antagonism. This antagonism supports host colonization by breaching the protective microbiota that plants assemble on their tissues. As only relatively few effectors with antimicrobial activities have been characterized, their occurrence throughout the fungal kingdom remains enigmatic. We developed AMAPEC, a highly accurate machine learning predictor to annotate candidate antimicrobials in fungal secretomes based on protein physicochemical properties. We predict that fungi secrete numerous antimicrobial proteins, regardless of their phylogeny and lifestyle. Given their remarkable conservation across phyla, antimicrobial effectors likely have ancient origins, predating the evolution of fungal symbioses with land plants. Therefore, we hypothesize that plant-pathogenic fungi evolved host-manipulating effectors from ancestral antimicrobial proteins. In line with this hypothesis, AMAPEC predicts antimicrobial activities for numerous effectors with known immunomodulatory functions. We experimentally validated this prediction for selected effectors and currently study the role of these effectors in microbial competition. Our findings shed a new light on the evolution of fungal effectors and their key roles in microbial antagonism and host colonization.

Session 2

Harnessing the Fungal Highway for Crop Protection: Isolation of Pathosystem-Specific Bacterial-Fungal Consortia

Lisa Cresp[1], Giulia Capella[2], Alexandra Kämpfer-Homsy[3], Edith Laux[3], Laure Jeandupeux[3], Jérémie Forney[4], Vincent Doimo[5], Victor Egger[6], Thomas Junier[1], , Ilona Palmieri[1], Empar Meyer[1], Melissa Cravero[1], Natacha Bodenhausen[2], Saskia Bindschedler[1]

[1] Laboratory of Microbiology, University of Neuchâtel (LAMUN), Neuchâtel; [2] Department of Soil Sciences, Research Institute of Organic Agriculture (FIBL), Frick; [3] Haute Ecole Arc (HE-Arc), University of Applied Sciences Western Switzerland, Neuchâtel; [4] Institute of Ethnology / Centre d'excellence et de compétence pour le développement de systèmes agroécologiques durables dans l'Arc jurassien dans un contexte de changement climatique (CEDD-Agro-Eco-Clim), University of Neuchâtel; [5] Office technique Maraîcher (OTM), Morges; [6] Fédération Rurale Interjurassienne (FRI), Courtemelon

Fungal diseases are a major threat to global agriculture, causing losses of 13% on average each year. Soil-borne pathogens are particularly problematic due to their broad

host range and their capability to survive for a long time without a host. Currently, synthetic fungicides remain the primary solution, but their extensive use contributes to resistance development and poses risks to human health and the environment. In this context, microbial biocontrol agents (mBCAs) represent a promising alternative. However, their effectiveness is often limited due to broad spectrum activity, reliance on single strains, and insufficient adaptation to soil heterogeneity.
In order to enhance the efficacy of mBCAs, we propose to use a combined bacterial-fungal inoculum building upon the fungal highway mechanism—employing fungi not only as BCAs but also as vectors for delivering beneficial bacteria. Furthermore, an encapsulation method is being developed to ensure a targeted delivery and sustained activity of the consortia. To ensure relevance and direct applicability to real-world farming systems, the project is built around a multidisciplinary team, bringing the LAMUN together with the FiBL for the agronomic expertise, the HE-Arc for the engineering expertise for formulation development, and regional stakeholders active in the agroecological field (CEDD-Agro-Eco-Clim, OTM, and FRI).
To identify compatible consortia, LAMUN is developing a high-throughput lab-scale method targeting pathosystem-specific isolates. To mimic soil complexity in vitro, a 3D-printed device enabling the use of in-tip seedlings is under development. This system allows controlled analysis of plant–mBCA–pathogen interactions in a spatially structured environment. Soil heterogeneity is mimicked using the Fungal Drops technique (Buffi et al. 2023), enabling observation of the fungal highway mechanism. Once optimized, this platform will be combined with microfluidics and microbial tagging for precise investigation of consortia dynamics.

Biocontrol Partners in Action: Leveraging Bacterial and Fungal combinations to Protect Potatoes from Late Blight

James F. Smith, Nicolas David Rappo, Floriane L'Haridon[1, 2], Mout De Vrieze, Laure Weisskopf[1, 2]

[1] Department of Biology, University of Fribourg; [2] Food Research and Innovation Center, University of Fribourg

As environmental and health concerns about broad-spectrum chemicals for crop treatment grow, research into sustainable biocontrol agents is advancing rapidly. Despite the global re-emergence of Phytophthora infestans, the cause of late blight in potatoes, no effective biocontrol agents have been developed. Although many bacterial strains show promise in labs, their results are rarely reproducible in field conditions. This study investigates how combining bacterial and fungal strains could provide better and more reliable protection against potato late blight compared to using bacteria alone. We created a diverse collection of bacterial strains from potato and grapevine microbiomes and screened their ability to inhibit oomycete development and prevent disease progression in planta using leaf disk assays, selecting a Pseudomonas, a Bacillus, and a Streptomyces as final candidates. In parallel, we selected and sequenced fungal strains from the potato microbiome showing anti-Phytophthora potential, many belonging to biocontrol-relevant genera. Results from both in planta and in vivo infection assays revealed that bacteria-fungi combinations perform better than bacteria or fungi alone. The performance of these combinations against other developmental stages of Phytophthora is currently being tested. Different application methods for fungi, such as drenching vs. foliar, and the use of fungal/bacterial co-cocultures compared to fungal

spores and bacterial cultures grown alone have been tested. Additional in vitro tests showed that the Pseudomonas strain migrates along the hyphae of the Trichoderma strain in an interaction known as fungal highways. This interaction will soon be tested in planta, which, if successful, may significantly improve the bacteria's ability to establish after field application.

Foxfire: A Hybrid Living Material for Sustainable Illumination

Tiago Carvalho

Eidgenössische Materialprüfungs- und Forschungsanstalt (EMPA), St. Gallen

Bioluminescent fungi have fascinated scientists and storytellers alike for centuries, yet the controlled production of glowing wood has remained elusive. In this work, we present a method to engineer a hybrid living material by colonizing balsa wood with the white rot fungus *Desarmillaria tabescens*. This fungus selectively degrades lignin, triggering the caffeic acid cycle and the biosynthesis of luciferin, resulting in autonomous, visible light emission.
Wood blocks were incubated in a 3% microfibrillated cellulose medium, with or without 4% malt extract, for 1 to 4 months. Bioluminescence was activated by air exposure and peaked after 3 months of incubation, particularly in samples without malt. Moisture content between 700–1200% and the presence of oxygen were essential for optimal glow. Rehydration after drying could reinitiate light emission, confirming the dynamic dependence on environmental conditions.
Spectroscopic and structural analyses (FTIR, microscopy, XRD) confirmed that cellulose integrity is maintained while lignin and hemicellulose are selectively broken down. Comparative studies with non-lignified PETG demonstrated that lignin is essential for sustained bioluminescence. These results mark a significant step toward standardizing bioluminescent wood as a functional, reproducible, and sustainable material.
This research aims to pave the way for applications in ambient lighting, eco-design, biosensing, and education, offering a glimpse into a future where hybrid living materials illuminate our world.

Keynote Talk

Advancing Fungal Ecology and Conservation through Citizen Science and Experimental Forest Research

Claus Bässler

Uni Bayreuth, Faculty of Biology, Chemistry & Earth Sciences, Biology, Ecology of Fungi

This presentation addresses two key aspects of applied mycology with relevance for fungal ecology and conservation. First, it highlights the potential of citizen science data and other open-access mycological sources to investigate fungal diversity patterns at broad spatial scales. Despite the limitations in spatial and temporal resolution compared to plant and animal datasets, these resources offer valuable insights. A particular focus will be placed on how fruit body traits in fungal communities respond to environmental variability across landscapes. The second part of the talk presents findings from forest experiments aimed at disentangling the drivers of wood-inhabiting fungal diversity. Specifically, the influence of dead wood characteristics and forest

microclimate—shaped by management practices and disturbance regimes—will be discussed. The presentation draws on a broad spectrum of observational and experimental data across multiple scales to identify key determinants of fungal diversity, with the goal of informing more effective conservation and forest management strategies.

Session 3

The Unfolded Protein Response is involved in the antibacterial defense response of model mushroom *Coprinopsis cinerea*

Emma Alessandri, Judyta Welman, Markus Künzler

Institute of Microbiology, ETH Zürich

Fungi and bacteria often share the same ecological niches, which can lead to competition for limited resources such as space and nutrients. The saprophytic mushroom *Coprinopsis cinerea* responds to antagonistic bacteria with the significant overexpression of secreted molecules, such as the lysozyme LYS1 targeting peptidoglycans in the bacterial cell wall.
Interestingly, the lys1 gene is also strongly induced by dithiothreitol (DTT), a reducing agent and inhibitor of protein folding in the endoplasmic reticulum (ER). DTT is a well-established elicitor of the unfolded protein response (UPR), a central regulatory pathway required for ER homeostasis. The UPR is conserved across eukaryotes and activated by the key transcription factor HAC1. The HAC1 mRNA harbours an intron, which is spliced out by the ER-localized endoribonuclease sensor IRE1 upon accumulation of misfolded proteins. Only following this unconventional splicing event, the HAC1 mRNA is translated into a functional protein and the UPR consequently upregulated.
Comparative transcriptomic analysis further revealed that DTT does not only induce lys1 but also several other genes encoding antibacterial effectors in *C. cinerea*. Our findings indicate a functional connection between antibacterial defense and the UPR in *C. cinerea*. To elucidate this connection, we first identified the HAC1 homolog of *C. cinerea* and characterized the unconventional intron borders. We then quantified and compared HAC1 mRNA splicing in response to either DTT or bacteria. Finally, we treated *C. cinerea* with bacteria or DTT and the known UPR inhibitor 4μ8C to investigate the effect of the latter on lys1 expression. The significant downregulation of lys1 in the presence of 4μ8C suggests that the UPR might not only overlap with but also be required for antibacterial defense. We will confirm this hypothesis by monitoring the induction of antibacterial defense genes in hac1 null mutants of *C. cinerea*.

Inducing novel endosymbioses in the filamentous fungus *Rhizopus microsporus*

Alannah Holderbusch, Thomas Gassler, Gabriel H. Giger, Benedikt Jäger, Julia A. Vorholt

Institute of Microbiology, ETH Zürich

Endosymbioses are widespread in nature, often giving rise to new metabolic capabilities in the host cell and allowing them to inhabit more diverse environments. However, the process of how these intricate partnerships is established remains poorly understood and difficult to extrapolate from far-evolved endosymbiotic relationships. In the field of intracellular endosymbioses, the mucoromycete *Rhizopus microsporus* is emerging as a

model system as this species comprises both endobacteria-harbouring and endobacteria-free strains. Previous work has established a fluidic force microscopy (FluidFM) approach for implantation of bacteria into the cytosol of *R. microsporus*, bypassing the requirement for self-directed bacterial entry. The introduction of bacteria pre-adapted to an intrahyphal lifestyle led to a compatible interaction with their new fungal host. Both partners resumed growth and vertical inheritance of bacteria was achieved through asexual sporulation. In contrast, the implantation of free-living bacteria further distant from natural endobacterial strains led to different interaction outcomes and resulted in the termination of the novel endosymbiotic relationship in subsequent generations. Our live-cell observations across six distinct bacterial strains revealed various outcomes, with some strains successfully multiplying and spreading through the fungal hyphae while others failed to establish. The findings indicate that the fungal immune system, a lack of directed transport along the growing hyphae, and the incompatibility of growth rates of both partners each play a role in the initial encounter and the potential for stabilization of the endosymbiosis. This works demonstrates the potential that synthetic endosymbiotic systems hold in examining the onset of these interactions and to identify the elements required for stable endosymbioses to occur. A better understanding of these processes could pave the way towards endosymbioses with metabolically beneficial partners such as carbon- and nitrogen-fixing bacteria.

Wor2 represses biofilm formation by downregulation of SCF1 and ALS4112

Marine Louvet[1], Jizhou Li[1,2], Daniel Bachmann[1], Dominique Sanglard[1], Frédéric Lamoth[1,2]

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Background: *Candida auris* is an emerging fungal pathogen of concern due to its multidrug resistance and ability to cause nosocomial outbreaks. A significant feature of *C. auris* is its ability to adhere to abiotic surfaces and to be transmitted between patients via medical devices. Two adhesins, Scf1 and Als4112, have been identified for their role in adhesion in *C. auris*. In this study, we characterized a zinc-cluster transcription factor Wor2 (B9J08_002136), for its role in biofilm formation and regulation of Scf1 and Als4112.
Methods: We constructed two WOR2 mutants in the wild-type strain IV.1: WOR2HA (hyperactivation of WOR2) and wor2Δ (deletion of WOR2). Biofilm formation was assessed using crystal violet assay. The downstream effectors of Wor2 were investigated by RNA sequencing, comparing WOR2HA to IV.1. Expression of genes potentially regulated by Wor2 was validated by reverse transcriptase qPCR. The function of Wor2-regulated genes was further examined through their overexpression under the control of the ADH1 promoter at their native loci.
Results: Compared to the IV.1 strain, WOR2HA reduced biofilm formation while wor2Δ increased biofilm formation. RNA sequencing comparing WO2HA to IV.1 revealed two adhesins significantly downregulated: ALS4112 and SCF1. We then confirmed the overexpression of both ALS4112 and SCF1 in wor2Δ compared to IV.1 by RT-qPCR. Next, we overexpressed ALS4112 and SCF1 in the WOR2HA background and observed that ALS4112 overexpression restored biofilm formation while SCF1 overexpression had no significant impact compared to the parental strain.
Conclusion: In this study, we identified for the first time the role of Wor2 in biofilm formation in *C. auris*. Our findings suggest that Wor2 could inhibit biofilm formation,

possibly by repressing ALS4112 and SCF1 expression. Further studies are needed to understand the role of Wor2 in host cell interactions and in vivo virulence.

A new molecular detection method applied to barely seeds for quantifying *Ustilago nuda* and predicting their field infection levels

Cecilia Panzetti[1,2], Eveline Jenny[3], Irene Bänziger[3], Andreas Kägi[3], Susanne Vogelgsang[3], Thomas Hebeisen[4], Peter Büttner[5], Daniel Croll[2], Franco Widmer[1], Karen E. Sullam[1]

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Seed health testing is used to avoid sowing seeds with problematic levels of plant pathogens. The detection of seedborne pathogens located in the embryo, such as *Ustilago nuda* – the causative agent of loose smut in barley (*Hordeum vulgare*) – is challenging. Loose smut is only visible once teliospores replace the barley inflorescence, and a smutted ear develops. Current methods for detecting *U. nuda* infections, the visual analysis of extracted seed embryos or field inspections of plants used for seed production, are laborious and often unreliable. We developed a multiplex qPCR protocol targeting *U. nuda* and *H. vulgare* DNA in milled seed samples to detect infected seed. To ensure that each sample accurately represented a seed lot, we evaluated key parameters, including the number of milled seeds per sample and the amount of seed flour used for the DNA extraction. Additionally, we tested the DNA variation within and between milled seed batches. Naturally infected seed lots with different levels of *U. nuda* were analyzed with our newly developed qPCR method and the inspection of extracted embryos. The same seed lots were then grown over two field seasons; the average number of smutted ears observed in the field served as the reference to evaluate the qPCR method's and the embryo test's performance. The qPCR results, normalized by the ratio of *U. nuda* to *H. vulgare* DNA copies, showed a stronger correlation with field infection levels than the embryo test results. Compared to embryo test, our qPCR method discriminated more accurately between seed lots with infection levels above and below the field tolerance threshold. Overall, our qPCR method provides a reliable alternative to the current seed health testing method. Its integration with field observations can contribute to avoid sowing infected seed lots, ultimately reducing the reliance on prophylactic synthetic seed treatments while ensuring yield quality.

A native ectomycorrhizal fungus alters the internal clock-driven endogenous growth rhythm of Pedunculate oak

Felix Zimmermann

Swiss Federal Research Institute WSL, Birmensdorf

Pedunculate oak (*Quercus robur* L.), a long-lived forest tree species, forms symbiotic relationships with ectomycorrhizal fungi (EMF), which can promote nutrient uptake, stress resilience, and growth. Like other tropical and temperate tree species, Pedunculate oak exhibits endogenous rhythmic growth (ERG), a trait conferring the ability to alternate root and shoot flushes as well as growth cessation as response to changing environmental conditions. However, effects of different EMF species on ERG

dynamics remain largely unknown. Here, we investigated the impact of two EMF species—*Piloderma croceum*, a non-native fungus previously shown to promote growth, and *Cenococcum geophilum*, a native species with broad ecological range—on growth performance, biomass allocation, and ERG patterns in a clonal oak system (clone DF159). By combining in-vitro measured data with Bayesian modelling, our results show that *P. croceum* accelerates plant development across growth stages, without disrupting the endogenous growth rhythm. In contrast, *C. geophilum*, while showing high mycorrhization rates, led to reduced biomass accumulation and lengthened development through the ERG stages, especially by prolonging the root flush. Co-inoculation revealed a competitive advantage of *C. geophilum* in root colonization, yet growth responses resembled those of the control. Our findings demonstrate that EMF species exert species-specific effects on both biomass production and temporal development of plants, underscoring the functional importance of EMF in shaping host development. Understanding these interactions provides new insights into the functional diversity of ectomycorrhizal symbiosis and can therefore inform forest management strategies aimed at enhancing resilience in oak-dominated ecosystems under rapidly changing climatic conditions.

POSTER ABSTRACTS (IN ALPHABETICAL ORDER)

Kingdom-Wide Tranposable Element Dynamics and Impacts on Fungal Genome Evolution

Tobias Baril, Clément Gilbert, Daniel Croll

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Transposable elements (TEs) are abundant, diverse, and persistent features of eukaryotic genomes. Growing evidence shows they can drive host adaptation, raising a fundamental question: To what extent is the complexity of eukaryotic life shaped by TE activity?
Fungi represent an ideal system to study TE-host dynamics. With exceptional diversity in ecology, life history, and morphology, fungi are amenable to large-scale comparative analyses and facilitate systematic investigation of TE diversity and dynamics across broad phylogenetic distances.
We analyse 4,309 genome assemblies across the fungal kingdom in a controlled phylogenetic framework to explore why TE abundance and diversity vary so widely across species. Our work addresses four key questions: (i) How do host life histories shape TE landscapes across fungal genomes? (ii) How do host defense systems limit TE activity, and how does their variation impact genome evolution? (iii) How diverse are TE landscapes across fungi, and how quickly do novel TE families emerge? (iv) How essential is horizontal transposon transfer (HTT) for the long-term spread and persistence of TEs?

From seed to storage: disease management in organic beetroot production to reduce food waste

Alessio Bernasconi[1], Tobias Härri[3], Carlo Gamper Cardinali[2], Martin Koller[4], Nadine Peter[1], Pascale Flury[5], Hans-Jakob Schärer[1]

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The market for organic agriculture is rapidly growing. In Switzerland, the production of organic Beetroot is particularly renowned. However, their storage until spring has become increasingly difficult in recent years, and losses due to post-harvest rots can lead to over 50 % by March. Consequently, most organic beetroots sold in spring need to be imported if the previous season was poor. The causes of the various storage rots in beetroot are currently unclear, and therefore there are few measures to prevent them in organic production. Pathogen infections causing storage rots in beetroot, but also in other long-stored vegetables, can occur via the seed, in the field, or post-harvest. Understanding the process of infection is, therefore, critical to find preventive solutions. Here, we present the results of a three-year project aiming at reducing post-harvest losses in organic beetroot production. In a combination of on-farm field experiments and laboratory analyses, we aimed to elucidate the causes of storage rots in organic beetroot and develop measures to improve storability. Analysis of stored beetroot in 2021, 2022 and 2023 revealed *Phoma betae*, *Fusarium* sp. and *Plectosphaerella* sp. as predominant pathogens in Switzerland. *Plectosphaerella* sp. was never identified before on beetroot. *Mortierella*, *Mucor* and *Alternaria* were found to be additional causative agents of storage rots. Seeds analysis highlighted the same pathogen identified on the rotting tuber (*Alternaria* sp., *Phoma betae* and *Fusarium* sp.), suggesting that the possible cause may come directly from the seeds. Different measures, such as steam sterilization of the seed, the use of biocontrol products in the field and before storage, or processing and cooling methods after harvest, as well as cultivar differences were investigated. Various measures were found to affect seed health, seedling emergence, leaf health, and the quality of beetroot after storage.

Phylogenetic and morphological evidence reveal overlooked diversity in Swiss populations of *Sticta* (Lobariaceae)

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In this study, we investigated the taxonomic relationships within Swiss populations of the *Sticta fuliginosa* species complex, a group of cyanolichens with isidiate thalli that inhabit moist, forested habitats. These lichens are important indicators of forest ecosystem health and are listed as endangered in Switzerland. Recent studies have revealed that this complex is highly diverse, comprising a greater number of taxa than traditionally recognized. However, its diversity has not yet been investigated in Switzerland.
Sampling included both the well-known localities previously attributed to *Sticta fuliginosa* and newly discovered localities along the Doubs River. Phylogenetic analyses

based on concatenated ITS, LSU, and mtSSU markers revealed that, contrary to previous expectations, *Sticta fuliginosa* is entirely absent from Switzerland. Our results strongly suggest that all currently known Swiss records attributed to *Sticta fuliginosa* in fact belong to *Sticta fuliginoides*. Thus, Swiss populations comprise *Sticta sylvatica*, previously reported in the region, as well as two newly recorded taxa: *Sticta fuliginoides* and a member of the *Sticta torii* group, previously known only from North America. The latter is described as a new subspecies, *Sticta arenosella* ssp. *toriioides*, based on its morphological and phylogenetic affinities with two North American taxa. We also provide the first description of apothecia in *Sticta fuliginoides*.
Overall, our results demonstrate that even in relatively small and well-studied regions such as Switzerland, a considerable diversity of lichenized fungi remains to be discovered and taxonomically resolved. These findings highlight the importance of integrating multilocus phylogenetic inference with morphological analyses to clarify species boundaries in lichens.

Interactive effects of drought and arbuscular mycorrhizal fungi on plant resistance to leaf herbivores

Giulia Capella [1], Sheharyar Khan* [1], Natacha Bodenhausen[2], Christelle Robert[1]

[1] Lab. of Chemical Ecology, Institute of Plant Sciences, University of Bern; [2] Department of Soil Sciences, Research Institute of Organic Agriculture FiBL, Frick

Food security is increasingly threatened by the rising global food demand and the adverse effects of climate change, including drought and altered herbivore dynamics. Arbuscular mycorrhizal fungi (AMF) have emerged as a potential solution to enhance crop resilience, but their interactions with drought and herbivory remain poorly understood.
We aimed to understand how AMF colonization affects maize (*Zea mays*) growth, chemical defense, and herbivore performance under drought stress. We conducted a semi-field experiment and two controlled growth chamber assays to evaluate maize growth, metabolism, and herbivore performance. Three soil moisture levels and AMF inoculation served as treatments in the semi-field experiment. In the growth-chamber assays, herbivory by *Spodoptera exigua* larvae was used as third treatment.
In the semi-field experiment, drought significantly reduced maize shoot height, biomass, and chlorophyll content, while AMF colonization increased cob length and number, indicating improved reproductive success across soil moisture levels. Natural herbivore pressure in the field was low and did not differ between treatments. In the growth chamber assays, drought increased herbivore performance, but this effect was mitigated by AMF colonization. Drought also elevated benzoxazinoid levels in roots and leaves, while AMF mitigated the effect in roots.
These results suggest that drought increases herbivore susceptibility, possibly due to altered plant nutritional quality, but that AMF can counteract this effect. Overall, our results show that drought negatively affects maize growth and metabolism, while AMF enhances reproductive success and modulates plant defense mechanisms.

Genetic variation among progeny shapes symbiosis in a basidiomycete with poplar

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Forest trees rely on ectomycorrhizal (ECM) fungi for acquiring scarce resources such as water and nutrients. However, the molecular mechanisms governing ECM traits remain inadequately understood, particularly the role of intraspecific fungal variation in root-tip colonisation and trophic interactions. This study examined six ECM traits using *Pisolithus microcarpus*, an ECM fungus capable of forming ECM rootlets in poplar. A collection of 40 sibling monokaryons and their parental dikaryon was analysed through genome and transcriptome sequencing to examine quantitative trait loci, gene expression, and mating-type loci. These findings revealed a pronounced phenotypic continuum in poplar root colonisation by sibling monokaryons, ranging from incompatible to fully compatible strains. Genetic recombination among monokaryons was demonstrated, and genomic regions potentially involved in ECM-fungal traits were identified. Transcriptomic analysis revealed greater differentiation of transcriptomic profiles between fungal strains than between fungal tissues, and uncovered tissue-specific functional responses for ECM and free-living mycelia. Poplar exhibited distinct transcriptomic responses when interacting with different sibling monokaryons and the parental dikaryon. Allele sorting at 11 mating-type loci confirmed the species' heterothallic tetrapolar system. This study advances understanding of the genetic and transcriptomic mechanisms underlying ECM symbioses, highlighting intraspecific fungal diversity's role in forest ecosystem functioning.

***Verticillium* spp. – an improved generic TaqMan qPCR application for pathogen detection**

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Several species of the soil-born fungus of the genus *Verticillium* are involved in leaf wilting and vascular bundle browning in more than 200 plant species, including many cultivated plants. An infestation significantly reduces the quality and the market value of the harvest. The aim of this project is to screen the occurrence of *Verticillium* spp. especially in potato tuber, as the responsible pathogen for the potato tuber vascular tissue browning syndrome is not yet clear. Since all *Verticillium* spp. leads to the same symptoms, it is not necessary to determine the species of *Verticillium* in diagnostics. Therefore, we have developed an improved generic TaqMan qPCR method that allowing us to identify as many *Verticillium* spp. as possible simultaneously in plant tissue.

Induced endosymbiosis between *Rhizopus microsporus* and *Ralstonia pickettii* indicates a shift from antagonism to commensalism

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Endosymbioses represent complex and dynamic relationships between organisms that may involve pathogenic phases during their emergence. Here, we used fluidic force microscopy (FluidFM) to induce cell-in-cell interactions between the opportunistic pathogen *Ralstonia pickettii* and a non-endosymbiotic strain of *Rhizopus microsporus* to probe the unstable early phase of endosymbiosis. The intracellular presence of *R. pickettii* affected host fitness and induced immune responses. Despite these effects, successful vertical transmission of the *R. pickettii* to next generation of the fungus enabled adaptation of the merged system by positive selection. Adaptation effects were observed at the phenotypic and transcriptional level. High-throughput imaging showed that the adapted system accepts a higher bacterial load inside viable spores on the cost of fungal growth rate. A change in transcriptomic profiles between early and late adaptation resembled a shift from pathogenic antagonism to commensalism, as eidenced by reduced expression of genes involved in cell wall remodeling and altered reactive oxygen metabolism, both hallmarks of fungal defense. Our work provides insights into the early processes of endosymbiosis and highlights the dynamics between pathogenic response and commensal coexistence, reflected by increased host resilience.

Speckle Spectroscopy for Mycelium Network Characterization

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Mycelium, the intricate fungal network beneath our soils, exhibits a multiscale structure that continuously adapts to changing external demands. Understanding and harnessing the dynamic properties of this system is essential for developing novel functional materials with tailored characteristics suitable for a wide range of applications, including packaging, construction and textiles. In this study, we demonstrate the impact of different hyphal systems on the scattering properties of fungal mycelium, a factor that significantly affects light propagation within such a turbid medium thereby influencing its optical properties. Using speckle spectroscopy, we aim to link changes in the network topology to its light-matter interaction. Our findings offer novel insights on the optical transport properties of mycelium showcasing the predominance of different scattering mechanisms within the systems.

Foliar fungal endophytes in broadleaf trees along urbanisation gradients: a pan-european study

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In contrast to natural sites, urban environments are characterized by fragmented habitats, modified microclimates (e.g., increased heat and drought), high levels of pollution, and a higher prevalence of non-native tree species. These conditions can influence urban trees and their associated microbiota. Among the microbiota, foliar fungal endophytes play an important role, as some can enhance host resilience to stress, while others may act as latent pathogens, especially in weakened hosts. Urbanisation may alter endophyte communities directly or indirectly, via stress-induced changes in their hosts, potentially reducing their diversity and favouring generalists over specialists, and pathogens over mutualists. Despite their significance, foliar endophytes in urban trees remain poorly understood, with most research limited to culturable fungi, a few tree species, and small geographic areas.
This study investigates foliar fungal endophytes along rural-urban gradients across approximately 40 European cities, using high-throughput sequencing technologies. We focus on three common broadleaf genera—*Quercus*, *Acer*, and *Fraxinus*—including both native and non-native species at each location. Sampling is carried out in collaboration with members of the COST Action CA20132 Urban Tree Guard. Within each city, trees are selected across areas with increasing levels of impervious surface density, representing different degrees of urbanisation.
In addition to sequencing, data on tree morphology, health status, and local tree diversity are collected using a standardized field protocol. These will be supplemented with open-access climate and land cover data to explore the drivers of endophyte community composition and diversity.
This large-scale study will provide new insights into how urbanisation may shape microbial communities in trees and the potential consequences for urban tree health and associated biodiversity. Ultimately, the results will contribute to developing strategies to mitigate the impacts of urbanisation and support the conservation of urban forest ecological functions.

Exploration of novel mechanisms of azole resistance in Candida auris

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Candida auris is a pathogenic yeast of particular concern because of its ability to cause nosocomial outbreaks of invasive candidiasis (IC) and to develop resistance to all current antifungal drug classes. Most *C. auris* clinical isolates are resistant to fluconazole, an azole drug that is used for the treatment of IC. Azole resistance may arise from diverse mechanisms, such as mutations of the target gene (ERG11) or upregulation of efflux pumps via gain of function mutations of the transcription factors TAC1 and/or MRR1. To explore novel mechanisms of azole resistance in *C. auris*, we

applied an in vitro evolutionary protocol to induce azole resistance in a TAC1A/TAC1B/MRR1 triple deletion strain. Azole-resistant isolates without ERG11 mutations were further analyzed. In addition to a whole chromosome aneuploidy of chromosome 5, amino-acid substitutions were recovered in the transcription factor Upc2 (N592S, L499F), the ubiquitin ligase complex consisting of Ubr2 (P708T, H1275P) and Mub1 (Y765*) and the mitochondrial protein Mrs7 (D293H). Genetic introduction of these mutations in an azole-susceptible wild-type *C. auris* isolate of clade IV resulted in significantly decreased azole susceptibility. Real-time reverse transcription PCR analyses allowed to assess the link between these mutated proteins and some known modulators of azole resistance, such as Erg11, the efflux pumps Cdr1 and Mdr1 or the transcription factor Rpn4. In conclusion, this work provides further insights in the complex and multiple pathways of azole resistance of *C. auris*. Further analyses would be warranted to assess their respective role in azole resistance of clinical isolates.

Genetic dissection of the chemical defense of ink cap mushroom *Coprinopsis cinerea* against fungivorous nematodes

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Fungivorous nematodes are ecologically significant predators of fungal mycelium. The chemical defense of the coprophilic mushroom Coprinopsis cinerea against these predators includes both a constitutive (autonomous) and an inducible part. Latter part is manifested by the production of a series of nematotoxic intracellular proteins in the vegetative mycelium of this fungus upon attack by the stylet-harbouring fungivorous nematode Aphelenchus avenae. Interestingly, this inducible chemical defense response can propagate along specific hyphae both acropetally and basipetally. The signalling pathways responsible for triggering this inducible anti-nematode defense response and the nature of signals mediating its propagation remain unclear. Moreover, the physiological relevance of the constitutive and inducible chemical defense of C. cinerea against fungivorous nematodes has not been assessed.
Recently, we tested the vegetative mycelia of a series of monokaryotic and dikaryotic C. cinerea strains for their susceptibility to grazing by A. avenae. We found nematode populations thrive rapidly on some strains, while on others, nematodes struggle to propagate. To unravel the genetic basis of the difference between permissive and prohibitive strain, we have crossed a permissive and a prohibitive strain, isolated 123 F1 progenies, and performed phenotyping. We will apply bulk segregant analysis (BSA) with and without backcrossing of single progenies to the parents to identify the gene loci associate with the permissive phenotype. The results of this study will hopefully reveal the signalling pathways involved in the defense response of C. cinerea against A. avenae and demonstrate that this response is physiologically relevant for the fungus.

No effect of pesticides on rhizosphere fungal diversity and community composition

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Pesticide use has continued to rise worldwide as a primary strategy for crop protection. However, this reliance on chemical inputs comes at a significant cost. Pesticides are known to harm the environment, contaminating soil and water and disrupting ecosystems. In particular, they can damage soil microbial communities, which are essential for maintaining soil health and fertility. Beyond environmental concerns, pesticides also pose risks to human health. Agricultural workers are directly exposed during application, often facing increased risks of acute poisoning and long-term health issues. Consumers, too, may be affected through pesticide residues on food, raising concerns about chronic exposure and its potential links to health problems. These consequences highlight the need to reduce pesticide dependence and promote safer, more sustainable practices.

We report the findings of one year of a field study assessing the effect of seed treatment on key agronomic parameters and bacterial and fungal rhizosphere composition. The research is conducted in collaboration with farmers who intend to decrease the usage of pesticides on their farms. We compared pesticides and alternative treatments, such as Thermoseed, to untreated wheat seeds. Cereal monitoring occurred at the time of emergence, the winter after seeding, and at harvest. Long-read PacBio Revio sequencing was utilized to characterize the diversity and composition of the fungal rhizosphere communities.

The results show no significant improvement of the agronomic parameters between treated and untreated seeds regarding emergence, Septoria leaf blotch, yield, or protein quality. In addition, our sequencing data show no significant impact of seed treatment on alpha diversity. Moreover, the fungal community composition was not affected by seed treatment but was shaped primarily through soil properties. These findings support the viability of farming strategies that eliminate seed treatments without compromising yield or microbial health, reinforcing the potential for more sustainable and environmentally conscious cereal production.

A pangenome analysis of structural variants and transposable elements across *Candida albicans*

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The human fungal pathogen *Candida albicans* represents a major challenge on global health, largely due to its rapid evolution of antifungal drug resistance. Beyond point mutations, structural variants (SVs) are an important but understudied source of adaptation. To comprehensively investigate SVs across clinical isolates of *C. albicans*, we conducted long read sequencing and genome-wide SV analysis in distantly related clinical isolates. Our work included a new, comprehensive analysis of transposable element (TE) composition, location and diversity. Our findings reveal that SVs and TEs

are distributed genome-wide and are frequently located close to coding sequences. We found TE polymorphism between clinical isolates, including indication of recent TE activity. Most SVs are uniquely present in only one clinical isolate and often are heterozygous. SVs and TEs thus likely impact gene and allele-specific expression and represent a significant source of intra-species genetic variation. We identified multiple, distinct SVs and TEs at the centromeres of Chromosome 4 and Chromosome 5, including inversions and transposon polymorphisms. These two chromosomes are often aneuploid in drug resistant clinical isolates and can form isochromosome structures with breakpoints near the centromere. Our work shows the importance of genome plasticity in *C. albicans* and identifies SVs and TEs as key contributors. The widespread heterozygosity of these variants further suggests that genomic rearrangements may drive phenotypic diversity, which in turn could facilitate adaptation to changing environments in the host and during antifungal therapy.

Molecular dissection of the septal pore apparatus of agaricomycete *Coprinopsis cinerea*

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Vegetative mycelia of agaricomycetes can be exceptionally large and long-lived. The hyphae of these fungi are compartmentalized by cross-walls (septa) containing pores with thickened cell walls (dolipores) and sophisticated cap structures, referred hereafter as septal pore apparatus. This apparatus ensures that nutrients and signals are distributed between the hyphal compartments via cytoplasmic bulk flow. Like in ascomycetes, the apparatus can also block cytoplasmic bulk flow between compartments by septal pore plugging e.g. as a response to hyphal damage and maybe also internal cues. Since the septal pore apparatus ultimately controls the cytoplasmic bulk flow in a fungal mycelium, it is an essential organelle for multicellular fungi. In contrast to multicellular ascomycetes, however, very little is known about the molecular composition of the septal pore apparatus and the mechanism of septal pore plugging in multicellular basidiomycetes. We set out to determine the function, the structure and the protein composition of the septal pore apparatus in the model agaricomycete *Coprinopsis cinerea* using a combination of microscopic, genetic and biochemical approaches. These findings will contribute to our understanding of cytoplasmic bulk flow dynamics within coenocytic systems.

K LAB

Nils Thomann

K LAB, Zürich

K LAB is non-profit community lab in Zürich (CH) run by a passionate group of mycologists and citizen scientists. Our members explore the remarkable capabilities of mycelium and its various applications. Join our community lab to unlock the full potential of mycelium!
