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Celebrating the fifth edition of the International Symposium on Fungal Stress – ISFUS, a decade after its 2014 debut

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ABSTRACT

The Fifth International Symposium on Fungal Stress (ISFUS) brought together in Brazil many of the leaders in the field of fungal stress responses, from fourteen countries, for four days of outstanding science ranging from basic research to studies with agricultural, medical, industrial, and environmental significance. In addition to the excellent oral and poster presentations, the Symposium organisers ensured that all participants had ample opportunity to engage, socialise, and network to exchange ideas and share research. The conference was enhanced by the world-class venue near Iguazu Falls, probably the greatest natural phenomenon in South America.

1. Introduction

The International Symposium on Fungal Stress (ISFUS) proudly marks a decade since its inaugural meeting in 2014 (Rangel et al., 2015b). The study of fungal stress has flourished remarkably since then. Who would have anticipated that fungi, enduring some of nature's harshest challenges, would inspire such a dedicated scientific community? From modest beginnings, ISFUS has become a major success, showcasing that even the smallest organisms can have important stories of resilience worth celebrating (Alder-Rangel et al., 2018, 2020, 2023; Rangel and Alder-Rangel, 2020; Rangel et al., 2015a, 2015b). The five editions of ISFUS have brought together a total of 171 renowned speakers from 27 countries (Fig. 1A) from diverse areas of fungal stress research. In addition, the success and impact of ISFUS, particularly the publication of the Symposium articles in five special issues in reputable journals– *Current* Genetics, for the first edition, and *Fungal Biology*, for the second to fifth editions – further solidified the reputation of ISFUS.

Conceived and organised by Drauzio Eduardo Naretto Rangel and Alene Alder-Rangel, ISFUS has become a key gathering for scientists, researchers, and industry experts dedicated to understanding the multifaceted challenges fungi face in response to environmental stressors. With fungi playing critical roles across environmental ecosystems, agriculture, medicine, and industry, the insights gathered at ISFUS are instrumental for advancing knowledge on fungal resilience mechanisms, stress adaptation, and mitigation strategies. By fostering collaboration across disciplines, ISFUS enables participants to push the boundaries of fungal research, providing essential knowledge that addresses the demands of both fundamental and applied sciences.

Fungal stress research plays a critical role in developing new medications to combat pathogens affecting humans, animals, and plants. By understanding how fungi withstand stressful environments, scientists can identify pathways and compounds that may help in designing treatments against pathogenic fungi, especially those responsible for drug-resistant infections.

In the realm of biofuel production, studies of fungal stress have advanced new strategies for developing yeast strains that can tolerate high ethanol concentrations. Enhancing yeast resilience under stress improves bioethanol yields, paving the way for more efficient and sustainable fuel production. By highlighting such advancements, ISFUS underscores the potential of fungal biotechnology not only to contribute to renewable energy goals but also to support the development of industrial processes that are both economical and environmentally friendly (Rangel et al., 2018).

Furthermore, agriculture significantly benefits from fungal stress research, where the improvement of entomopathogenic fungi, such as *Metarhizium robertsii* and *Beauveria bassiana* aids in developing biocontrol solutions to manage insect pests (Rangel et al., 2018). Furthermore, stress-tolerant strains of *Trichoderma* are increasingly employed to control plant pathogens and promote crop health, leading to increased agricultural yields (Rangel et al., 2018). These advancements in fungal application for biocontrol and crop support were discussed at ISFUS, contributing to sustainable agricultural practices and enhancing global food security (Rangel et al., 2018).

ISFUS promotes the integration of emerging technologies and methodologies in fungal stress research, from genomic analysis to novel bioengineering tools. By bringing together experts from throughout the world, ISFUS helps shape future directions in fungal research, enabling developments that could profoundly impact agriculture, environmental science, medicine, and industrial processes.

For an insightful history about the origins of ISFUS, please refer to Rangel and Alder-Rangel (2020).

2. The Fifth International Symposium on Fungal Stress – a synopsis

In September 2024, the Fifth International Symposium on Fungal Stress (ISFUS-2024), led by Drauzio E.N. Rangel, Alene Alder-Rangel, and Joseph Heitman, was held at the Golden Park Hotel in Foz do Iguaçu (https://isfus2024.wordpress.com). Foz do Iguaçu is located at the junction where Brazil, Paraguay, and Argentina converge. The area is famous for the stunning Iguazu Falls, a magnificent set of waterfalls that span the border between Brazil and Argentina.

ISFUS-2024 featured thought-provoking science and ideas at the frontiers of understanding fungal responses to stress and how to harness this power for new technologies. The Symposium included stimulating talks from veteran and early-career scientists representing multiple countries, in addition to outstanding poster presentations. The 38 speakers were from 14 countries, including Argentina, Brazil, Canada, Chile, China, France, Germany, Ghana, Hungary, Israel, Italy, South Korea, Switzerland, and the USA (Fig. 1B). The Symposium featured an even balance of female and male speakers (Fig. 1C).

ISFUS-2024 provided a unique opportunity to learn about the breadth of fungal stress-response research in a positive and intimate atmosphere. Drauzio Rangel began the meeting by inviting all participants to form a large circle and join hands, creating a "fairy ring" (Fig. 2). He then asked everyone to bring their happiest, unconscious memories to the forefront of their minds and hearts and to transmit these memories, thoughts, and feelings to one another through intuition. This

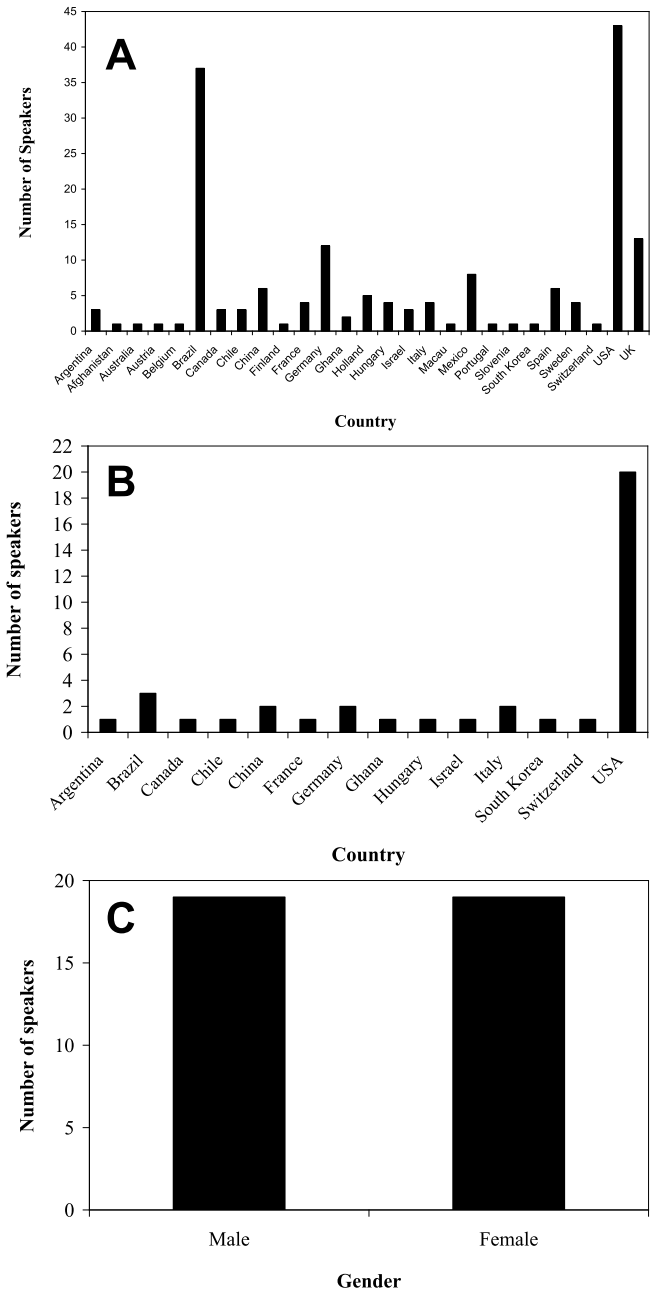

Fig. 1. (A) Number of speakers in all ISFUSs; (B) number of speakers at ISFUS-2024; and (C) gender of the speakers at ISFUS-2024.

collective exchange was meant to fill the auditorium with happiness, love, and peace. During the opening session and breaks, a series of beautiful images from world travel were displayed, accompanied by inspiring songs and words such as *determination, motivation, opportunity, curiosity, invigorated, collaboration, spectacular, exciting, generous, commitment, kindness, serendipity, spontaneous, endurance, commitment, honesty, perseverance, inspiration*, etc. At the conclusion of the opening ceremony, Drauzio invited everyone in the auditorium to contribute their thoughts on ISFUS to a large 50-year-old book that he discovered in the basement of his father's printing company. This book contains comments from participants of every ISFUS conference (Electronic Supplementary Material S1).

ISFUS created a space for scientists to connect, offering formal lecture sessions, followed by relaxed moments during meals and excursions. These unstructured times allowed for meaningful conversations, the exchange of ideas, and the opportunity to bond and get to know one another. All the speakers gathered for a group picture on the first day of the Symposium (Fig. 3). Six scientists from the US National Academy of Sciences illuminated ISFUS-2024 with their brilliant talks (Fig. 4). ISFUS-2024 also featured a book signing by Arturo Casadevall of his recent publication "What if Fungi Win?" (Fig. 5). The participants (Fig. 6) were able to recognise the speakers' pictures both on the two banners displayed near the stage (Fig. 7) and in the folders they received (Electronic Supplementary Material S2).

The meeting was supported by several prominent sponsors, including the American Society for Microbiology, the British Mycological Society, Elsevier, the Journal of Fungi, PLoS Pathogens, Zeiss, INFORS HT, Alder's English Services, and Inbioter – Institute of Biotechnology Rangel. ISFUS also received grant funding from the Coordination for the Improvement of Higher Education Personnel (CAPES) (Fig. 8).

Poster presentations at V ISFUS were crucial for participants to share their research, engage in meaningful discussions, and contribute to advancing knowledge, with 90 posters showcased during the event. The abstracts of all presentations can be perused in the Electronic Supplementary Material S3.

This special issue in *Fungal Biology*, titled *"Resilience in the Mycelial Network,"* presents a curated selection of approximately 17 articles that capture the Symposium's most significant contributions. It provides a multidisciplinary overview of fungal stress biology, spanning molecular biology, ecology, environmental science, agriculture, medical mycology, and biotechnology. The following are some examples of the articles published in the special issue (Acheampong et al., 2025; Kocsis et al., 2024; Medina and Rangel, 2025a, 2025b; Petrucci et al., 2025; Sarkar et al., 2025; Siebe et al., 2025; Stempinski et al., 2025; Zhang et al., 2025). The other articles are still in the process of review.

The scientific sessions focused on four topics: 1) Fungal stress in extreme environments and stress mechanisms and responses in fungi; 2) Fungal stress in medicine; 3) Fungal stress in industry and the environment; and 4) Fungal stress in agriculture.

2.1. *Fungal stress in extreme environments & Stress mechanisms and responses in fungi*

In this session, Deborah Bell-Pedersen discussed how the *Neurospora crassa* circadian clock controls levels of tRNA synthetases, which impact mRNA translation. Her lab discovered daily rhythms in Met misincorporation and its potential role in expanding the functional proteome. Jay C. Dunlap presented about light and circadian clock regulation in *Neurospora*, revealing new insights into the White Collar Complex and the roles of FRQ. Jason E. Stajich compared the genetic and phenotypic diversity in *Rhodotorula* yeast from extreme environments, linking genotype to phenotype. Minou Nowrousian has investigated the histone chaperone ASF1 in *Sordaria macrospora*, and she highlighted its importance in multicellular development and stress response. István Pócsi focused on stress responses and secondary metabolite production related to Atf1-AtfA orthologous transcription factors in fungi. Nir Osherov discussed how azole-priming in *Aspergillus fumigatus* leads to transient and stable resistance. Finally, Nichole A. Broderick explored polymicrobial interactions in the fly gut for stress management.

Deborah Bell-Pedersen – Texas A&M University, College Station, TX, USA. The *N. crassa* circadian clock controls daily rhythms in the levels of tRNA synthetases (RSs) that lead to rhythms in mRNA translation (Castillo et al., 2022a, 2022b). RSs also play a vital role in the accuracy (fidelity) of translation. For example, during oxidative stress, MetRS is phosphorylated by MAPKs. This led to methionylation of non-cognate tRNAs and reduced translation fidelity through Met misincorporation into polypeptides (Lee et al., 2014). Griffin Best, a graduate student in the Bell-Pedersen lab, discovered that under constant environmental conditions, the *N. crassa* circadian clock promotes daily rhythms in Met misincorporation during translation. Roughly 900 proteins were identified that contained rhythms in Met substitutions, and

Fig. 2. Speakers and participants holding hands to form a fairy ring and share happy moments at the opening ceremony. Credit: Saga Photography/Hidalgo Gomes.

experiments are currently underway to determine if this provides a mechanism to expand the functional proteome beyond what is encoded in the genome. Furthermore, during ageing, both translation accuracy and circadian amplitude decrease. The Bell-Pedersen lab discovered that compounds, which restore a youthful clock in old *N. crassa* cells, reduced translation errors, and significantly increased lifespan.

Jay C. Dunlap–Dartmouth Geisel School of Medicine, Hanover, NH, USA. Fungal stress responses regulate light and the circadian clock. *Neurospora* has been a salient model organism for understanding these aspects of regulation. In *Neurospora,* the White Collar Complex (WCC) serves as both the blue light photoreceptor and the Positive Element in the circadian feedback loop. In light, WCC binds to pLRE-like motifs in the genome to acutely regulate light-induced genes, including *frq*. In the dark, it binds C-box-like motifs that drive circadian expression of clock-controlled genes, including *frq,* which encodes the principle nucleating component of the circadian Negative Element complex. Before now, FRQ was thought to play a role in the clock only in the dark, but Dunlap showed that in the light, FRQ acts to keep WCC off the C-box, thereby silencing several thousand genes in the light. Preliminary cryo-EM structural data on the WCC were presented, as well as recent cell biological data showing that nuclear FRQ and WCC are not homogeneously distributed but rather exist as transient punctate bodies (Dunlap and Loros, 2017; Tariq et al., 2024).

Jason E. Stajich – University of California, Riverside, CA, USA. He presented a project to compare genetic and phenotypic diversity in the basidiomycete yeast *Rhodotorula* from a global collection of strains isolated from extreme and mesophilic environments that include Antarctica and the International Space Station (Coleine et al., 2020; Daudu et al., 2020). The project is generating new long-read reference genome sequences for several species to provide a foundation for pan-genome analysis to test for lineage differences among species and sub-populations. In addition, phenotypic screening of strains from different environments revealed that some have the capability of growing at 37 °C or above. The work demonstrated the broad ecological distribution of this yeast across human-built environments, as well as food, marine, soil, glacier, and dryland environments.

Minou Nowrousian – Ruhr-University Bochum, Bochum, Germany. The histone chaperone ASF1 functions in multicellular development and in response to genotoxic stress in the filamentous ascomycete *S. macrospora*. Deletion of *asf1* in *S. macrospora* leads to sterility, a reduction of DNA methylation, and upregulation of genes that are usually weakly expressed in the wild type (Schumacher et al., 2018). Recent results showed that substitutions of amino acid V94 or truncations of the C-terminal tail of ASF1 abolish histone binding and do not complement the sterile phenotype. Δ*asf1* is sensitive to the DNA-damaging agent MMS, while complementation strains, even those with non-histone-binding variants, regain wild-type-like resistance, indicating that histone binding is required for multicellular development but

Fig. 3. Speakers of the V International Symposium on Fungal Stress (ISFUS) in 2024 held in Foz do Iguaçu, Paraná, Brazil. From left to right, Front row: Beatriz Casadevall-Broderick (USA), Nichole A. Broderick (USA), Arturo Casadevall (USA), Mary Tayal (USA), Joseph Heitman (USA), Drauzio E. N. Rangel (Brazil), Amanda E. A. Rangel (Brazil), Alene Alder-Rangel (USA), Sabrina Sarrocco (Italy). Second row: N. Louise Glass (USA), Minou Nowrousian (Germany), Consuelo Olivares-Yañez (Chile), Mia R. Maltz (USA), Vânia Aparecida Vicente (Brazil), Ling Lu (China), Mari Shinohara (USA), Joan W. Bennett (USA), Lucia Landi (Italy), Deborah Bell-Pedersen (USA). Third row: Jason E. Stajich (USA), Jay C. Dunlap (USA), Guilhem Janbon (France), István Pócsi (Hungary), Mavis A. Acheampong (Ghana), Xiaorong Lin (USA), Zachary A Lewis (USA), Asiya Gusa (USA), Salomé LeibundGut-Landmann (Switzerland), Yong-Sun Bahn (Republic of Korea). Fourth row: Chris Todd Hittinger (USA), Maurizio Del Poeta (USA), Claudio A. Masuda (Brazil), Nicolás Pedrini (Argentina), Charles M. Boone (Canada), Chaoyang Xue (USA), Gerhard Braus (Germany), Robert Blake Billmyre (USA), Michael C. Lorenz (USA). Credit: Saga Photography/Hidalgo Gomes.

Fig. 4. Members of the US National Academy of Sciences at ISFUS-2024, from left to right: Charles M. Boone (University of Toronto, Canada), Joseph Heitman (Duke University Medical Center, Durham, USA), Joan W. Bennett (Rutgers University, New Brunswick, New Jersey, USA), Jay C. Dunlap (Dartmouth Geisel School of Medicine, Hanover, NH, USA), N. Louise Glass (University of California, Berkeley CA, USA), and Arturo Casadevall (Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA). Credit: Minou Nowrousian.

not for response to genotoxic stress (Breuer et al., 2024a). Δ*asf1* shows a global decrease of the histone modification H3K56ac that might be mediated through the histone acetyltransferase RTT109 (Breuer et al., 2024b).

István Pócsi – University of Debrecen, Debrecen, Hungary. The orthologs of *Schizosaccharomyces pombe* Atf1 and *Aspergillus nidulans* AtfA transcription factors are important global transcriptional regulators in fungi, affecting nearly all aspects of fungal life, including vegetative growth, sexual and asexual sporulation, environmental stress responses, secondary metabolite production (*e.g.* mycotoxin), as well as virulence in pathogenic fungi (Leiter et al., 2021). Genome-wide gene expression analyses of the AtfA-mediated menadione (menadione sodium bisulfite, MSB; a chemical eliciting oxidative stress *via* generating superoxide anion radicals) stress response in *A. nidulans* revealed some genes putatively regulated by AtfA in both vegetative tissue and conidia in either unstressed or MSB-exposed cultures (Kocsis et al., 2023). Recent ChIP-seq studies performed in conidia harvested from unstressed and MSB-exposed cultures confirmed the presence of functionally active AtfA binding sites in the promoters of a large group of putatively AtfA-regulated genes.

Nir Osherov – Tel-Aviv University, Tel-Aviv, Israel. Prior exposures to stressful stimuli, such as antimicrobial drugs, can enhance the ability of pathogens to withstand re-exposure to the same or other stressors, a process called priming (Harish and Osherov, 2022). Specifically, Osherov's group made the intriguing observation that *A. fumigatus*, the most common fungal pathogen in humans, generates transiently azole-resistant conidia after exposure to subinhibitory concentrations of agricultural azole fungicides or medical triazoles. Notably, azole-priming of *A. fumigatus* conidia appears to be a stepping stone toward the acquisition of stable triazole resistance, as primed conidia form stably resistant colonies at high rates (Harish et al., 2022). RNA-seq and whole genome sequencing technologies were used to identify the

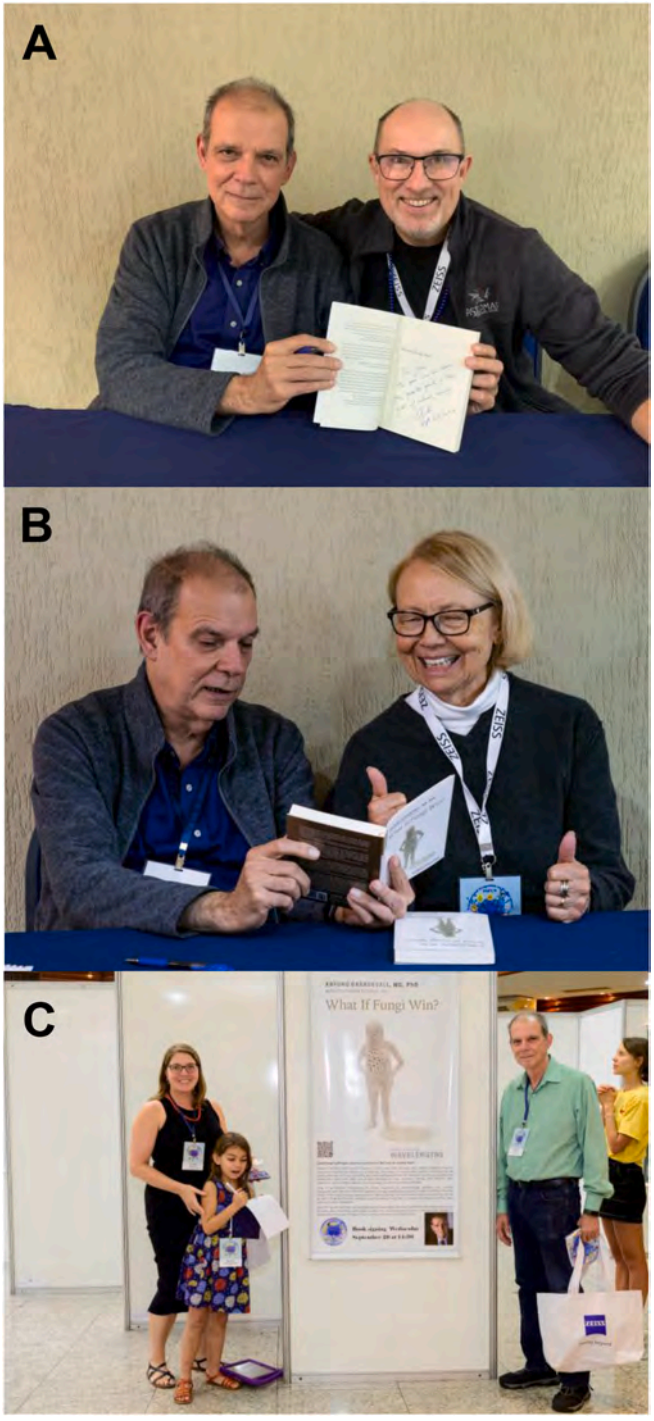

Fig. 5. Book signing with Arturo Casadevall. (A) Autographing the book for Joe Heitman, (B) Joan Bennett, and (C) Casadevall with his family.

mechanisms underlying the transient triazole priming effect and to define the genetic determinants of subsequent stable resistance development. Altogether, these studies have allowed characterisation of a novel biological phenomenon, triazole priming, with both basic-scientific interest and wide relevance to agricultural and medical issues related to the development of antifungal resistance.

Nichole A. Broderick – Johns Hopkins University, Baltimore, MD, USA. She focused on interactions between fungi and lactic acid and acetic acid bacteria of the *Drosophila* microbiome. Her lab has shown that mixed-species microbiome interactions influence *Drosophila* olfactory and egg-laying behaviours differently than individual members. *Drosophila* prefers yeast-bacteria co-cultures to the same microorganisms grown individually and then mixed (Fischer et al., 2017). This preference correlated with three emergent co-culture properties: ethanol catabolism, a distinct volatile profile, and yeast population decline. Similarly, interactions between lactic acid and acetic acid microbiome members reduced pathogen burden and improved fly survival during the invasion of enteric bacterial or fungal pathogens (Barron et al., 2024). These results highlight how emergent metabolites from different microbe–microbe interactions have important impacts on host fitness and physiology. Broderick's team is expanding these studies to include additional fungal pathogens and microbiome members to better understand how microbial interactions influence host fitness and physiology.

2.2. Fungal stress in medicine

Research presented by various scientists highlights different aspects of *Cryptococcus neoformans* and other fungal pathogens. Arturo Casadevall discussed the complexities in determining the structure of virulence factors, the polysaccharide capsule, and melanin of a pathogen. Asiya Gusa presented findings on how temperature-dependent movements of transposable elements influence genetic mutations in *Cryptococcus*, contributing to its adaptation and microevolution during infection. Chaoyang Xue focused on the role of inositol in fungal development, particularly its importance for *C. neoformans* to traverse the blood–brain barrier and cause meningitis. Maurizio Del Poeta reported promising clinical results of an acylhydrazone antifungal compound, D13, for treating sporotrichosis in cats. Joseph Heitman discussed a new mechanism of antifungal resistance in *Mucor circinelloides*, revealing both stable mutations and transient epigenetic changes that confer drug resistance. Salomé LeibundGut-Landmann discussed how the immune system maintains fungal homeostasis, particularly in the human oro-gastrointestinal tract, emphasising the role of T cells producing interleukin-17 in preventing *Candida albicans* from becoming pathogenic. Yong-Sun Bahn focused on *Candida auris*, a multidrug-resistant fungal pathogen, exploring the roles of key signalling pathways, such as Ras/cAMP/PKA and calcineurin, in stress response, drug resistance, and virulence. Guilhem Janbon's research on *C. neoformans* examined gene expression regulation via alternative transcription start sites, which help the fungus adapt to changing conditions. Mari Shinohara presented findings on the delayed microglial response in the brain during *Cryptococcus* infection, highlighting how this delay may contribute to the ability of the pathogen to establish infection. Michael Lorenz has explored the potential of a bacteriocin-derived peptide to combat fungal pathogens like *C. albicans* and *Cryptococcus*, showing its effectiveness without toxicity to mammalian cells. R. Blake Billmyre discussed the *C. neoformans* pan-genome and the use of transposon mutagenesis to predict gene essentiality and identify factors contributing to fluconazole susceptibility. Ling Lu's work on *A. fumigatus* highlights mechanisms of fungal persistence, tolerance, and resistance to antifungals, especially azoles. Xiaorong Lin has investigated the genetic basis of *C. neoformans* adaptation to host CO_2 levels, a key factor for its virulence. Erica J. Washington explored the trehalose biosynthesis pathway in fungal pathogens, focusing on its role in stress tolerance and virulence. To conclude, Claudio A. Masuda's work using *Saccharomyces cerevisiae* as a model provided insights into the molecular dysfunction caused by galactosemia, suggesting therapeutic avenues for the disease. Together, these studies advance the understanding of fungal virulence, adaptation, immune interaction, and treatment strategies for fungal infections.

Arturo Casadevall – Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA. The polysaccharide capsule and cell-wall-associated melanin are the two most important virulence factors for *C. neoformans*. Despite their importance, solving the structure of the capsule and melanin poses tremendous analytical challenges. The capsule is composed primarily of water, and dehydration collapses it

Fig. 6. Speakers and some participants in the auditorium at ISFUS-2024. Credit: Saga Photography/Hidalgo Gomes.

into fibrils that have little or no relevance to the hydrated structure. The capsular polysaccharide is a macromolecule that is heterodisperse, which means that it is too large for NMR to solve its structure. In contrast, melanin is insoluble and amorphous, such that the structure of any naturally occurring melanin has not been solved. Hence, the structure of the capsule and melanin must be approached by indirect means. Dynamic light scattering has shown that the capsular polysaccharide is branched, with a dense core, suggesting that it is a dendrimer (Cordero et al., 2011). Capsular polysaccharide is synthesised intracellularly and shipped to the outside of the cell in vesicles, where it presumably undergoes extracellular assembly into the capsule (Casadevall et al., 2019). Similarly, melanin is synthesised in melanosomes and shipped to the cell wall, where it is covalently linked to chitin and other polysaccharides (Camacho et al., 2019).

Asiya Gusa – Duke University Medical Center, Durham, NC, USA. She described temperature-dependent mobility of several newly identified transposable elements (TEs) in clinical isolates of the disease-causing yeast *C. neoformans*. This work was followed by foundational studies, which demonstrated that heat stress-stimulated TE movements in *Cryptococcus deneoformans*, a closely related species, are a major driver of mutations in this yeast at human body temperature *in vitro* and in a murine model of infection (Gusa et al., 2020, 2023). Gusa proposed that heat stress-stimulated TE mutations, with the ability to disrupt or alter gene function, could be an important mechanism for rapid adaptation of *Cryptococcus* in the environment and for microevolution during human infection. Her team is utilising experimental evolution and comparative genomics approaches to investigate how stress-stimulated TE mutations contribute to the evolution of pathogenic traits, such as increased thermal tolerance and drug resistance in environmental fungi.

Chaoyang Xue – Rutgers Biomedical and Health Sciences, Newark, NJ, USA. His findings elucidate the role of the host inositol sensing and utilisation by *C. neoformans* in fungal development and virulence. *C. neoformans* is the most common cause of fungal meningitis. However, the mechanism whereby *C. neoformans* causes meningitis remains poorly understood. His group found that inositol, an abundant metabolite in the brain, promotes fungal traversal of the blood–brain barrier (BBB) and plays a critical role in host–pathogen interactions during infection of the central nervous system (CNS). The *C. neoformans* genome contains an expanded inositol transporter gene family, and it can utilise the inositol stores of its plant niches to complete its sexual cycle (Xue et al., 2007). *C. neoformans* is probably uniquely adapted to thrive in the inositol-rich environment of the CNS and to utilise inositol-dependent pathways for pathogenesis. His group's data show that both inositol transporters and the inositol catabolic pathway are required for inositol utilisation, not only as a metabolite but also as a substrate for polysaccharide production. Mutants lacking two major inositol transporters exhibited defects in fungal pathogenicity, including during brain infection (Liu et al., 2013). Results demonstrate that inositol can promote formation of a unique capsule structure enriched in an M3 mannosyl triad structure reporter group that can help the fungus evade the host immune response (Wang et al., 2021). He employs fungal mutagenesis analysis, enzymatic assays, and polysaccharide structural analysis to help define inositol sensing and metabolic pathways required for modifying fungal cell surface structure. His group also used an *in vitro* model of the human BBB and animal infection models of cryptococcosis to characterise the mechanisms of inositol-mediated promotion of *Cryptococcus* CNS infection.

Maurizio Del Poeta – Stony Brook University, Long Island, NY, USA. The first clinical study of a new acylhydrazone antifungal compound (D13) was done in cats affected by sporotrichosis (Dib Ferreira Gremiao et al., 2024). Current antifungal agents have limited clinical efficacy. They are poorly fungicidal in the host, occasionally toxic, and increasingly ineffective due to emerging resistance. Del Poeta's laboratory researches the development of innovative antifungal agents (Haranahalli et al., 2019; Lazzarini et al., 2018, 2020). In this meeting, he presented data on the antifungal efficacy of the acylhydrazone D13 *in vitro* and during a clinical study. *In vitro*, D13 is highly efficacious against both planktonic cells and biofilms formed by *Sporothrix brasiliensis*. Importantly, when D13 was administered (as a compassionate drug) in combination with itraconazole (ITC), with or without potassium iodide, in ten cats with sporotrichosis refractory to the standard of care with ITC, improvement or total clinical cure was achieved in five cases after 12 weeks of treatment. Minimal abnormal laboratory tests, *e.g.*, elevation of alanine aminotransferase, were observed in four cats during the treatment and returned to normal levels within a week upon ending the treatment. Because D13 performed better than ITC in reducing biofilm formation in the cat claw, it suggests that transmission of the fungus from animal to animal or/and from animal to human may be reduced. Although highly encouraging, a larger and randomised controlled study is required to evaluate the effectiveness and the safety of this new and exciting acylhydrazone to be used alone or/and in combination with ITC for the treatment of feline sporotrichosis.

Joseph Heitman – Duke University Medical Center, Durham, NC, USA. His group discovered a new mechanism conferring antifungal drug resistance in the human fungal pathogen *M. circinelloides* (Calo et al., 2014). Spontaneous resistance to the antifungal drug FK506 was found to evolve via two distinct mechanisms (Calo et al., 2014; Lee et al., 2013, 2015). One mechanism involves Mendelian mutations conferring stable, irreversible drug resistance; the other occurs via an epigenetic RNA interference (RNAi)-mediated pathway resulting in unstable, transient drug resistance. The peptidyl-prolyl isomerase FKBP12 interacts with FK506, forming a complex that inhibits the protein phosphatase

Fig. 7. The Meet the Speakers poster for the V International Symposium on Fungal Stress.

Fig. 8. Sponsors and stands (A) Zeiss stand (B) Infors HT stand at ISFUS-2024.

calcineurin. Calcineurin inhibition by FK506 blocks *M. circinelloides* dimorphic transition to hyphae and enforces growth as yeasts (Lee et al., 2013). In some FK506-resistant isolates, mutations in the *fkbA* gene encoding FKBP12 or the calcineurin *cnbR* or *cnaA* genes confer FK506 resistance and restore hyphal growth. In other resistant isolates, no mutations are found in the known drug targets. Instead, RNAi has been triggered to silence the *fkbA* gene, yielding drug-resistant epimutants. FK506-resistant epimutants readily revert to drug sensitivity in the absence of FK506. The establishment of epimutants is accompanied by the generation of abundant small RNAs targeting the FKBP12 gene and requires some known RNAi pathway components, whereas others are dispensable. Surprisingly, epimutants occur at a higher frequency and are more stable in mutants lacking RNA-dependent RNA polymerase 1 or 3 (Rdrp1/3) or the RNaseIII-like protein R3B2, revealing some RNAi components inhibit epimutation (Calo et al., 2017). These findings have been generalised to show that epimutations occur in three species of *Mucor* and identify epimutations in the *pyrF* or *pyrG* genes conferring 5-fluoroorotic acid (5-FOA) resistance (Chang et al., 2019; Perez-Arques et al., 2024).

Salomé LeibundGut-Landmann – University of Zurich, Zurich, Switzerland. Preserving microbial homeostasis is essential for the host to benefit from the host-beneficial functions of commensal fungi such as

Fig. 9. Group picture of the awardees from Elsevier Ward, the American Society for Microbiology Award, and the PLoS Pathogens Award. Right to left: Monise Fazolin Petrucelli, Emily Mesquita da Silva, Elias Barbosa da Silva-Junior, Siebe Pierson, João Neves-da-Rocha, Adrián Adolfo Álvarez Padilla, Bruno Montanari Borges, Mavis A. Acheampong, Amanda E.A. Rangel, Drauzio E.N. Rangel, Joseph Heitman, Renan E. A. Piraine, Alejandra Goity, and Alene Alder-Rangel. Credit: Saga Photography/Hidalgo Gomes.

C. albicans. The immune system, and interleukin-17 (IL-17)-producing T cells in particular, are indispensable for preventing this normally harmless yeast from converting into a pathogen that can cause fatal infections in humans (Scheffold et al., 2020). These Th17 cells reside locally in the colonised tissue and respond in an antigen-specific manner to *C. albicans* (Kirchner and LeibundGut-Landmann, 2021). During commensalism, this occurred without inflammation. In turn, *C. albicans* evades the IL-17 immune stress to which it is continuously exposed at the host interface by means of a transcriptional adaptative response.

Yong-Sun Bahn – Yonsei University, Seoul, South Korea. *C. auris* is an emerging multidrug-resistant fungal pathogen with high mortality rates, possibly linked to global warming. Despite growing attention, the signalling pathways governing stress responses, drug resistance, and virulence in *C. auris* still need to be explored. This study focuses on the roles of the Ras/cAMP/PKA and calcineurin pathways, which are essential for virulence and drug resistance in other fungi. The cAMP/PKA pathway regulates growth, morphogenesis, stress responses, secreted aspartyl protease production, melanin deposition on the cell surface, drug resistance, and virulence, with hyperactivation surprisingly reducing *C. auris* systemic virulence (Kim et al., 2021; Kim et al., 2023b, 2023a). The calcineurin pathway also plays critical roles in stress responses and drug resistance, with *CRZ1* deletion exhibiting resistance to echinocandins, while *cna1*Δ and *cnb1*Δ show sensitivity (Cha et al., 2025). A genome-wide functional survey of transcription factors is underway to further explore these pathobiological pathways in *C. auris*.

Guilhem Janbon – Institut Pasteur, Paris, France. *Cryptococcus* yeasts, recognised as critical pathogens by the WHO, cause over 200,000 deaths globally each year. These fungi are naturally found in the environment but can colonise the human body, requiring them to adapt to a variety of conditions by modulating gene expression. In recent research, Janbon's team applied TSS-Seq and 3′UTR-Seq in *C. neoformans*, complementing traditional RNA-Seq to map gene boundaries and identify alternative transcription start sites (TSSs). This analysis revealed numerous TSS clusters linked to coding genes, many modulated by growth conditions. Some alternative TSSs are within the 5′UTR, influencing gene expression by altering UTR length, while others affect the N-terminal sequence of the protein, impacting subcellular targeting. Through screening TF mutants, they discovered a transcription factor, Tur1, which governs most alternative TSS usage during growth-phase transitions. Their findings indicate that TSS regulation, beyond traditional gene expression control, supports adaptation by diversifying lncRNA and protein localisation (Dang et al., 2024).

Mari Shinohara – Duke University Medical School, Durham, NC, USA. *C. neoformans* infections often start in the lungs and can spread to the brain, leading to cryptococcal meningoencephalitis (CM). In a chronic infection model, we observed rapid systemic dissemination of *Cryptococcus*, yet full microglial response in the brain was delayed by up to two weeks – unlike the immediate response of alveolar macrophages in the lungs. Single-cell RNA sequencing indicated that microglial activation is primarily driven by interferon-gamma (IFNγ) from $CD4^+$ T cells. This delay is attributed to the time required for T cells to be activated and infiltrate the brain, potentially allowing *Cryptococcus* to establish infection more effectively. Current investigations focus on identifying signals that prompt T cell infiltration into the brain and understanding how microglia shape CM outcomes, providing insights into *Cryptococcus* pathogenesis in the central nervous system (Reyes and Shinohara, 2022).

Michael C. Lorenz – University of Texas McGovern Medical School, Houston, TX, USA. Competition within the human microbiota is a largely untapped source of antimicrobial compounds. *C. albicans* and *Enterococcus faecalis* occupy overlapping niches, and these species mutually antagonise each other's virulence. The effect on *C. albicans* is mediated by a secreted bacteriocin, and we used structural data to identify a 12aa peptide as necessary and sufficient for the antifungal activity. This peptide is protective at sub-nanomolar concentrations in a *Caenorhabditis elegans* infection assay and reduces *C. albicans* burdens in rodent oral, systemic, and catheter infection models in both therapeutic and prophylactic modalities. It is also active against azole-resistant

Fig. 10. Amanda E.A. Rangel and Drauzio E.N. Rangel delivering the Elsevier award to (A) right to left: Adrián Adolfo Álvarez Padilla from Universidade Federal de São Paulo, SP, São Paulo, Brazil, Siebe Pierson from Universität Innsbruck, Tyrol, Austria, and João Neves-da-Rocha, from Universidade de São Paulo, Ribeirão Preto, SP, Brazil. Credit: Saga Photography/Hidalgo Gomes.

C. auris and *C. albicans* strains, as well as *Cryptococcus* species. However, this peptide is not toxic to mammalian cells nor, surprisingly, fungal cells. The mechanism of action is not fully resolved, but it acts at the cell surface to inhibit adhesion and biofilm formation. This is a promising new antifungal approach (Graham et al., 2017; Guha et al., 2024).

R. Blake Billmyre – University of Georgia, Athens, GA, USA. Pangenomics, which recognises and captures gene content variation between individuals within a species, has been spearheaded recently in fungi, primarily within the *Aspergillus* community (Barber et al., 2021; Lofgren et al., 2022). Billmyre shared preliminary data for a *C. neoformans* pan-genome that suggests substantial variation in gene content both between individual isolates and molecular types within the *C. neoformans* species. He also described his lab's recent development of a transposon mutagenesis sequencing (TN-seq) toolset for *C. neoformans* (Billmyre et al., 2024). TN-seq enables genome-wide prediction of gene essentiality as well as functional genomic screens. Because this approach generates very high densities of transposon inserts, TN-seq can often identify regulatory mutations that perturb but do not eliminate gene function, enabling assays of essential gene functions. His data for fluconazole selections of TN-seq libraries suggest that genes involved in essential mitochondrial functions are important for fluconazole susceptibility.

Ling Lu – Nanjing Normal University, Nanjing, China. She presented work on antifungal persistence, tolerance, and resistance in *A. fumigatus*. During antifungal treatment, pathogens may evolve resistance within the host, leading to treatment failure. Antifungal drug resistance arises by multiple mechanisms, and how *A. fumigatus* isolates develop resistance or tolerance has not been fully addressed. Amongst these

Fig. 11. Drauzio E.N. Rangel and Amanda E.A. Rangel delivering the American Society for Microbiology awards to students and early-career mycologists. The gold award went to (A) Alejandra Goity from the Pontificia Universidad Católica de Chile, Santiago, Chile. The silver awards went to (B) Monise Fazolin Petrucelli from the Universidade de São Paulo, Ribeirão Preto, SP, Brazil; (C) to Bruno Montanari Borges from the Universidade Federal de São Paulo, São José dos Campos, SP, Brazil; (D) to Emily Mesquita da Silva from Brock University, St. Catharines, ON, Canada; (E) to Elias Barbosa da Silva-Junior from the Universidade Federal do Rio de Janeiro, RJ, Brazil; (F) and to Renan E. A. Piraine form the Universidade de São Paulo, Ribeirão Preto, SP, Brazil. Credit: Saga Photography/Hidalgo Gomes.

mechanisms, the most common mechanism of *A. fumigatus* azole resistance is mutations in the gene encoding the target protein Cyp51A; however, azole-resistant isolates with wild-type *cyp*51As have emerged. In comparison, drug tolerance in these strains is caused by a diminished response to azoles, probably by activating fungal stress-response pathways to adapt to the presence of drugs. Moreover, treatment failure is also common in patients infected with azole-susceptible isolates, which may be caused by persistent isolates in which only a small fraction of the isogenic population survives and grows at low rates. Therefore, the identification of the resistance mechanism is essential for the development of novel methods for prompt diagnosis and efficacious pharmacotherapy (Chen et al., 2024; Zhu et al., 2023, 2024).

Xiaorong Lin – University of Georgia, Athens, GA, USA. She discussed the molecular bases for cryptococcal CO_2 tolerance. *C. neoformans* is a ubiquitous soil fungus and opportunistic pathogen. Its pathogenicity relies on its adaptation to the host CO_2 level, which is ~125-fold higher than in ambient air. Her group found that while clinical isolates are CO_2-tolerant, many environmental isolates are CO_2-sensitive. They employed multiple approaches to identify the genetic bases responsible for CO_2 tolerance, including quantitative trait loci mapping of progeny derived from a cross between a clinical and an environmental isolate, experimental evolution of CO_2-sensitive natural isolates, and a genetic screen of gene deletion mutants in a CO_2-tolerant strain (Chadwick et al., 2022; Chadwick et al., 2024; Ristow et al.,

Fig. 12. Amanda Estella Alder Rangel (12 years old), Alene Alder-Rangel, and Drauzio E.N. Rangel delivering the PLoS Pathogens award, which was open to early-career mycologists. The award was received by Mavis Agyeiwaa Acheampong, who is a Senior Lecturer at the University of Ghana and studies entomopathogenic fungi as biological control agents against insect pests in Ghana. Credit: Saga Photography/Hidalgo Gomes.

2023). They discovered that CO_2 tolerance is a key virulence factor, CO_2 tolerance can be evolved *in vitro* and during infection, and post-transcriptional regulation is critical for cryptococcal adaptation to CO_2. Their findings highlight the underappreciated importance of CO_2 tolerance in cryptococcal ability to cause disease.

Erica J. Washington – Duke University Medical Center, Durham, NC, USA. The trehalose biosynthesis pathway is important in mediating cellular responses to stress. Her group aims to understand the contribution of the trehalose biosynthesis pathway to thermotolerance and virulence in fungal pathogens, with the goal of developing antifungal drugs that target this critical pathway. The trehalose biosynthesis pathway in fungal pathogens consists of two major enzymes, Tps1 and Tps2 (Rangel, 2011; Thammahong et al., 2017). Cryo-electron microscopy was utilised to determine the homo-tetrameric structure of Tps1 from *C. neoformans* (Washington et al., 2024). This structure, as well as others, has enabled her laboratory and collaborators to take a structure-based approach to developing an antifungal drug that inhibits Tps1 activity (Miao et al., 2025; Washington et al., 2024). A high-throughput screen was used to identify potential compounds that inhibit Tps1 activity and fungal growth (Miao et al., 2025). Currently, her laboratory is investigating complexes of lead compounds bound to Tps1 using X-ray crystallography and cryo-electron microscopy. They will also pursue the development of Tps2 inhibitors.

Claudio Akio Masuda –Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil. Using *S. cerevisiae* as a model, his work shows that the accumulation of galactose-1-phosphate – a hallmark of the human disease classic galactosemia – causes dysfunction in the endoplasmic reticulum, mitochondria, and phosphate homeostasis (Machado et al., 2024; Machado et al., 2017; Pimentel et al., 2022). His work also highlights the relevance of sphingolipids for the adaptation to this stressful condition (Pimentel et al., 2022). These results advance the understanding of the molecular pathophysiology and suggest potential therapeutic avenues for the treatment of classic galactosemia.

2.3. Fungal stress in industry and the environment

This session explored fungal stress mechanisms and their industrial and environmental applications. Charles M. Boone discussed genetic interactions in yeast, highlighting how large-scale studies map genetic networks and their potential in human disease research. Chris Todd Hittinger presented the Y1000+ Project, which sequenced over 1100 yeast genomes, revealing insights into metabolic pathways and stress tolerance. Xin-Qing Zhao focused on the epigenetic regulation of yeast stress tolerance, particularly the role of the histone methyltransferase Set5 and the Ino80 chromatin remodeller in enhancing resilience under stress for developing robust industrial strains. N. Louise Glass explored the immune-like response in *N. crassa*, showing how regulated cell death governs fungal interactions. Mia R. Maltz discussed microbial inoculation in degraded landscapes, highlighting how disturbances like volcanic eruptions and wildfires affect fungal diversity. Finally, Vânia Aparecida Vicente presented on *Cladophialophora exuberans*, a black yeast with the potential for bioremediation in contaminated environments. This session emphasised the critical roles of fungi in stress tolerance and environmental remediation.

Charles M. Boone – University of Toronto, Toronto, ON, Canada. This presentation centred on how genetic interactions (GIs) influence phenotypic expression. Large-scale studies in yeast have tested almost all 18 million gene pairs for GIs and generated a global genetic interaction map for this organism (Costanzo et al., 2016). Different types of GIs can be quantified, including negative interactions, such as synthetic lethality, and positive interactions, which include genetic suppression. Using a CRISPR-based approach (Varland et al., 2023), a genome-scale, GI network was constructed for a human cell line, HAP1, mapping ~90, 000 negative and positive GIs for ~200 functionally diverse query genes. Systematic comparative analyses showed that the general principles and topology of genetic networks are conserved from yeast to human cells. The potential for identifying GIs in humans as disease gene modifiers, from UK Biobank data (https://www.ukbiobank.ac.uk), was briefly explored.

Chris Todd Hittinger – University of Wisconsin–Madison, Madison, WI, USA. The Y1000+ Project (http://y1000plus.org) has sequenced, analysed, and published the genomes of nearly every known yeast species of the subphylum Saccharomycotina, spanning more than 400 million years of evolution. This dataset includes genome sequences for 1154 yeasts, high-throughput quantitative growth rate data in 24 carbon and nitrogen sources, and a new hierarchical ecological ontology for studying isolation sources (Opulente et al., 2024). Machine learning and phylogenetic analyses showed that differences in the number of carbon sources a yeast could utilise stemmed from intrinsic gene content differences in specific metabolic pathways but found little evidence of tradeoffs. Hittinger also reported the transcriptomic identification of a candidate alternative *GAL*actose utilisation pathway previously inferred through machine learning and biochemical assays (Harrison et al., 2024). Applying machine learning to a new reactive oxygen species tolerance dataset implicated reductase and mannosyltransferase gene families, which were experimentally validated (Aranguiz et al., 2024).

Xin-Qing Zhao – Shanghai Jiao Tong University, Shanghai, China. She discussed the progress on yeast stress tolerance mechanisms and the applications of stress-tolerant yeast strains for production of ethanol fuel and succinic acid. Her group examined the beneficial effects of overexpressing the histone H4 methyltransferase Set5 on yeast stress tolerance. Further proteomic studies revealed that elevated Set5 expression

Fig. 13. Poster session at ISFUS-2024. Participants engaging in and enjoying discussions about the posters during the coffee break, and at the end of the poster session, they are content as they returned to the auditorium.

under stress conditions leads to higher expression levels of protein kinase Rim15 and the chromatin remodeller Ino80. Ino80 is a key component in the INO80 chromatin remodelling complex. Multi-omics studies revealed that under long-term stress conditions, Ino80 plays novel roles in regulating nitrogen metabolism, and its expression regulates yeast tolerance to multiple stressors. Specifically, several genes related to nitrogen catabolite repression (NCR) were proven to be directly regulated by Ino80, and one of the NCR genes, *GDH2*, was found to be a novel target to engineer yeast stress tolerance. The reported epigenetic control of stress-related metabolism is significant for developing robust strains for industrial applications (Yuan et al., 2024; Zeng et al., 2024; Zhang et al., 2024).

N. Louise Glass – University of California, Berkeley, CA, USA. The model filamentous fungus, *N. crassa* is used to explore fungal trigger allorecognition and regulated cell death (RCD). RCD serves as a defence mechanism against mycoparasitism, genome exploitation, and deleterious cytoplasmic elements. Functional analyses of fungal RCD loci revealed that they have similarities to proteins involved in innate immunity in animals, including Nod-like receptor proteins PLP-1 (Gonçalves et al., 2020) and a functional homolog of mammalian gasdermin (Daskalov et al., 2020), an executioner protein involved in pyroptosis. The fungal gasdermin homolog, RCD-1, forms oligomers in *N. crassa* (Daskalov et al., 2020), and recent cryo-EM studies showed that RCD-1 forms heterooligomeric membrane pores (Li et al., 2024), a unique structure for the gasdermin family of pore proteins. These studies revealed that filamentous fungi have an innate immune system that operates during allorecognition and regulates the outcome of fungal–fungal interactions. The discovery of fungal innate immunity also suggests that these systems may be important for interactions with other organisms in the environment.

Fig. 14. Journal of Fungi Award, from left to right, Drauzio E.N. Rangel, Alene Alder-Rangel, Renan Santini Barbosa (Universidade Federal de São Paulo, SP, Brazil); Júlia Sant'Ana (Universidade Federal do Rio Grande do Sul, Porto Alegre, RG, Brazil); Hyunjin Cha (Yonsei University, Seoul, Republic of Korea); Paola A. Ramos Irizarry (Duke University, Durham, NC, USA); Isabella Bresciani (Pontificia Universidad Católica de Chile, Santiago, Chile); Amanda E.A. Rangel, and Joseph Heitman. Credit: Minou Nowrousian.

Fig. 15. Volunteers at ISFUS-2024. From left to right: Mary Tayal (USA), Cleyde D. Massingue (Mozambique), Miri Osherov (Israel), Alene Alder-Rangel (USA), Eduardo I. Buendia Huerta (Mexico), Amanda E.A. Rangel (Brazil), and Drauzio E.N. Rangel (Brazil).

Mia R. Maltz – University of Connecticut, Storrs, CT, USA. Microbial inoculation into degraded landscapes and experimental field sites holds promise when disturbance-based selective microbial mortality has resulted in losses of microbial groups or individual taxa, changing the structure and functioning of microbial communities (Shade, 2023). The type and severity of the disturbance may lead to varying levels of selective mortality, which then would require different types of active or passive interventions to achieve pre-disturbance levels of taxa richness, functioning, composition, or diversity. For instance, following the volcanic eruption of Mount St. Helens, small mammals were introduced to the pumice plain that dug into the tephra and introduced arbuscular mycorrhizal spores and N-fixing bacteria that supported ecological succession in this depauperate volcanic landscape (Maltz et al., 2024). Additionally, when fire affects landscapes, it matters whether the fire is a low-intensity prescribed fire versus a high-intensity wildfire. Fungal taxa richness may increase after low-intensity controlled burns, while fungal richness may decline after severe wildfires.

Vânia Aparecida Vicente – Federal University of Paraná, Curitiba, Brazil. *C. exuberans* is a new candidate for hydrocarbon and bioremediation of heavy metal-polluted habitats. *C. exuberans* is a black yeast from the Chaetothyriales order that can degrade aromatic and xenobiotic compounds, such as benzene, toluene, ethylbenzene, and xylene (Nascimento et al., 2017). The final assembly of its whole genome sequence comprised 660 contigs and a 37.5 Mb genome size (GCA_030068005). Genomic evaluations comparing with sibling species, including clinical and environmental strains, focused on genes and pathways related to aromatic carbon, heavy metal tolerance, bioremediation of lead and copper, and the presence of metal homeostasis genes (Silva et al., 2023). This study contributes to a better understanding of the mechanisms used in the adaptation to extreme conditions and remediation of environments contaminated with high concentrations of lead and copper.

2.4. Fungal stress in agriculture

In the final session, researchers presented diverse studies on fungal biology and stress responses applied to agriculture. Zachary A. Lewis discussed the role of Polycomb Repressive Complex 2 in *N. crassa*, revealing how it governs development under stress by regulating key transitions and ensuring environmental conditions are met. Sabrina Sarrocco highlighted the role of killer proteins in competition between *Fusarium graminearum* and other fungi, showing how their expression varies depending on the opposing species. Gerhard Braus focused on stress responses in fungi such as *A. fumigatus* and *Verticillium dahliae*, discussing transcription factors that enable stress adaptation and infection processes. Mavis A. Acheampong shared insights on biocontrol agents in Ghana, noting the promising results of indigenous fungal isolates against crop pests. Lucia Landi explored the use of atmospheric cold plasma to control fungal growth, particularly on *Aspergillus chevalieri*. Joan W. Bennett presented research on fungal volatile organic compounds, focusing on the toxic effects of 1-octen-3-ol. Nicolás Pedrini discussed dual RNA-seq for studying fungal stress in entomopathogens and their insect hosts. Consuelo Olivares-Yañez described the transcriptional response of *Trichoderma atroviride* in mycoparasitism with *Botrytis cinerea*, revealing key genes involved in this interaction. Alene Alder-Rangel provided a scientometric overview of fungal stress research, emphasising the growth of studies and the importance of collaboration through ISFUS. Finally, Drauzio Eduardo Naretto Rangel concluded with an intriguing study on how Reiki-induced priming enhanced stress tolerance in *Metarhizium robertsii* conidia, suggesting fungi may possess a form of memory for stress responses.

Zachary A. Lewis – University of Georgia, Athens, GA, USA. Sexual development and meiosis are well-known responses to nutritional stress in fungi, but the mechanisms that control proper development remain poorly understood. Polycomb Repressive Complex 2 (PRC2) is a chromatin modifier that establishes large domains of silent chromatin by methylating histone H3. Approximately 7 % of *N. crassa* genes are repressed by PRC2 (Ferraro et al., 2021; Kamei et al., 2021). New data show that PRC2 represses the mycelia-to-perithecia transition, acting as a developmental checkpoint to ensure that key conditions, such as nutritional stress and mating partner availability, are met before development proceeds. In other work, a genetic screen was performed to identify regulators of PRC2 (Courtney et al., 2020). This revealed that histone deacetylase-1 (HAD-1) is required for proper control of PRC2. HDA-1-deficient cells undergo progressive epigenome instability over hundreds of nuclear divisions, indicating that histone deacetylase-1 is a key guardian of the epigenome.

Sabrina Sarrocco – Università di Pisa, Pisa, Italy. Killer proteins (KPs) play a role in the inter-specific competitive interactions of *F. graminearum* – one of the main causal agents of Fusarium head blight on wheat – with other plant pathogenic *Fusarium* species or the biocontrol agent *Trichoderma gamsii* T6085 (Zapparata et al., 2021). KPs are present in several Ascomycota species, including those belonging to the *Fusarium* genus. In *F. graminearum,* the clustered *Fgkp4l-1, Fgkp4l-2,*

Fig. 16. Pre-symposium excursion to the Brazilian side of the Iguaçu waterfalls. (A) Excursion to the Bird Park. (B) Minou Nowrousian, István Pócsi, Yoko Yashiroda, and Xiaorong Lin the Bird Park. (C) Claudio A. Masuda, Mari Shinohara, and Jay C. Dunlap at the Iguaçu National Park. (D) Mavis A. Acheampong and Salomé LeibundGut-Landmann getting soaked by the waterfall. (E) Asiya Gusa, Anna Lehmann, Erica J. Washington, Paola Ramos Irizarry, Joseph Heitman, Joan W. Bennett, Zachary Lewis, N. Louise Glass, Chaoyang Xue, R. Blake Billmyre, and Michael C. Lorenz enjoying the Iguaçu Falls.

and *Fgkp4l-3* genes encode for monomeric, while *Fgkp4l-4* encodes for a heterodimeric KP4Ls (LP4-like). When in the presence of other plant pathogenic Fusaria, an upregulation of the clustered *Fgkp4l* genes is observed both in dual cultures and on spikes. Conversely, the *Fgkp4l-4* gene is up-regulated when competing with *T. gamsii* T6085 *in vitro* and *in vivo* (Vicente et al., 2022). Results herewith support the hypothesis that KPs can be involved in *F. graminearum* inter-specific interactions, with the clustered *Fgkp4l-1, -2,* and *-3* genes and the *Fgkp4l-4* gene expressed in different ways, depending on the interacting species (Petrucci et al., 2025).

Gerhard Braus – Georg August University Göttingen, Göttingen, Germany. Fungal stress can be caused at the cellular level by aggregated proteins interfering with degradation pathways (Galka et al., 2024). Fungi must anticipate and respond to external biotic or abiotic stress stimuli interfering with growth or development. Fungi also experience multiple stresses in host cells during pathogenic interactions. Adaptation to these stresses requires specific genetic networks controlled by various transcription factors. The opportunistic human pathogen *A. fumigatus* carries in its genome a large group of genes for C_6-Zn_2 DNA-binding Zinc cluster transcription factors. Induction of corresponding genes provides not only protective oxidative stress responses but also adaptation to various antifungal drugs (Sasse et al., 2023). Fungal plant pathogens

Fig. 17. Post-symposium excursion to the Itaipú hydroelectric power plant and catamaran cruise. (A) Group at the Buddhist temple in Foz de Iguaçu on the way back from Itaipú. Standing left to right: Alene Alder-Rangel, Soojin Yu, Yujin Lee, Hyunjin Cha, Yuanwei Zhang, Ling Lu, Xiaorong Lin, István Pócsi, Ningning Liu, Lucia Landi, Chaoyang Xue, Joseph Heitman, Joan W. Bennett, Nir Osherov. Kneeling: Minou Nowrousian, Yong-Sun Bahn, Jay C. Dunlap, Deborah Bell-Pedersen, N. Louise Glass, Drauzio E.N. Rangel, Mary Tayal, Yoko Yashiroda, Clemencia C. Lopez, Mari Shinohara, and Salomé LeibundGut-Landmann. (B) Korean students Yujin Lee, Hyunjin Cha, and Soojin Yu at the Buddhist temple. (C) István Pócsi on the catamaran. (D) Alene Alder-Rangel, István Pócsi, Miri Osherov, Nir Osherov, Deborah Bell-Pedersen, and Gerhard Braus enjoying the catamaran. (E) Drauzio E.N. Rangel and Joseph Heitman wearing navy captain hats.

such as *V. dahliae* can colonise the vascular system and enter plants through their roots. This requires sequential activation of different transcription factors, which control distinct infection steps from root adhesion to entry through the plant into the xylem until the later phases of the disease (Maurus et al., 2023).

Mavis A. Acheampong – University of Ghana, Accra, Ghana. Since the 2000s, the use of indigenous and exotic entomopathogenic fungal isolates have been studied as biocontrol agents of key insect pests of several crops in Ghana including cocoa [*Distantiella theobromae* and *Sahlbergella singularis* (Hemiptera: Miridae)], mango [*Bactrocera dorsalis* (Diptera: Tephritidae)], maize [*Spodoptera frugiperda* (Lepidoptera: Noctuidae), *Prostephanus truncatus* (Coleoptera: Bostrichidae), *Sitophilus*

Fig. 18. Post-symposium excursion to Argentina. Group at the Argentinian Iguazu National Park: Xin-Qing Zhao, Zachary A Lewis, Drauzio E.N. Rangel, Mary Tayal, N. Louise Glass, Lucia Landi, Clemencia C. Lopez, István Pócsi, Alene Alder-Rangel, R. Blake Billmyre, Chaoyang Xue, Gerhard Braus, Charles M. Boone, Susanna Braus-Stromeyer, Joan W. Bennett, Anna Lehmann, Mari Shinohara, Amanda E.A. Rangel, Barbara Sztok, Salomé LeibundGut-Landmann, Joseph Heitman, Minou Nowrousian.

zeamais (Coleoptera: Curculionidae)], cabbage [*Plutella xylostella* (Lepidoptera: Plutellidae)], and pepper [*Thaumatotibia leucotreta* (Lepidoptera: Tortricidae)]. She highlighted the lessons, challenges, and opportunities of these control agents, acknowledging that even though efficacy studies against the aforementioned pests have been largely done under laboratory conditions (Acheampong et al., 2023), the few field trials with some isolates have been extremely positive (Luke et al., 2023); warranting their commercialisation.

Lucia Landi – Università Politecnica delle Marche, Ancona, Italy. The inactivation of filamentous fungi by non-thermal processing techniques to obtain food safety is a challenge for the food industry. Her group evaluated the effectiveness of atmospheric cold plasma (CAP) technology at low (CAP-O3) and high (CAP-NOx) power densities in reducing fungal growth and spore germination of *A. chevalieri*, a strain isolated from sun-dried tomatoes (Molina-Hernandez et al., 2023b). CAP-NOx treatment significantly decreased both conidial germination and mycelial growth. Fluorescent dyes confirmed that CAP treatment damaged cell membranes in the surface layers of the mycelium. Cell death was correlated with the generation of reactive oxygen and nitrogen species, changes in membrane potential, accumulation of intracellular Ca2+, and damage to nuclear DNA. Surviving cells responded to CAP by modulating the expression of key genes involved in stress response, aligned with the accumulation of glutathione, trehalose, glycerol, and chitin (Molina-Hernandez et al., 2023a). CAP-NOx treatment altered *A. chevalieri* volatilome profile, indicating shifts in lipid metabolism.

Joan W. Bennett – Rutgers University, New Brunswick, NJ, USA. Volatile organic compounds (VOCs) are low molecular weight compounds that easily vaporise. The most common fungal VOC is 1-octen-3-ol, which displays many physiological activities and has been described as a semiochemical (Jaddaoui et al., 2023). Bennett's laboratory has used genetic models to develop toxicological assays and shown that low concentrations of gas phase 1-octen-3-ol induce apoptotic, inflammatory, and neurotoxic effects in wild-type *Drosophila melanogaster* (Inamdar et al., 2020). Surprisingly, when volatiles emitted by growing *A. fumigatus* cultures or vapours of 1-octen-3-ol were tested against *Drosophila* flies carrying a mutation in the Toll pathway, the flies were resistant to the toxicological response seen in wild-type flies (Almaliki et al., 2023). In the future, Bennett hopes to have laid the groundwork for fungal biologists to pay more attention to the smell compounds associated with their experiments on fungal stress.

Nicolás Pedrini – Instituto de Investigaciones Bioquímicas de La Plata, La Plata, Argentina. Dual RNA-seq is a useful technique for studying fungal stress during interactions between entomopathogens and their hosts. Fungus–insect interactions are known to drive pathogenic cycles that typically culminate in host mortality (Pedrini, 2018); however, these fungi can also establish endophytic relationships with plants, protecting the host plant against insect herbivores (Vega et al., 2009). Pedrini summarised several dual RNA-seq findings from these interacting systems, identifying oxidative stress-related genes in the entomopathogenic fungus *Beauveria bassiana* within the model insect *Tribolium castaneum* during pathogenesis, immune-related genes in the insect host that are induced in response to fungal infection (Mannino et al., 2023), and photosynthesis-related genes that are activated in plants hosting the fungus as an endophyte.

Consuelo Olivares-Yañez – Centro de Genómica y Bioinformática

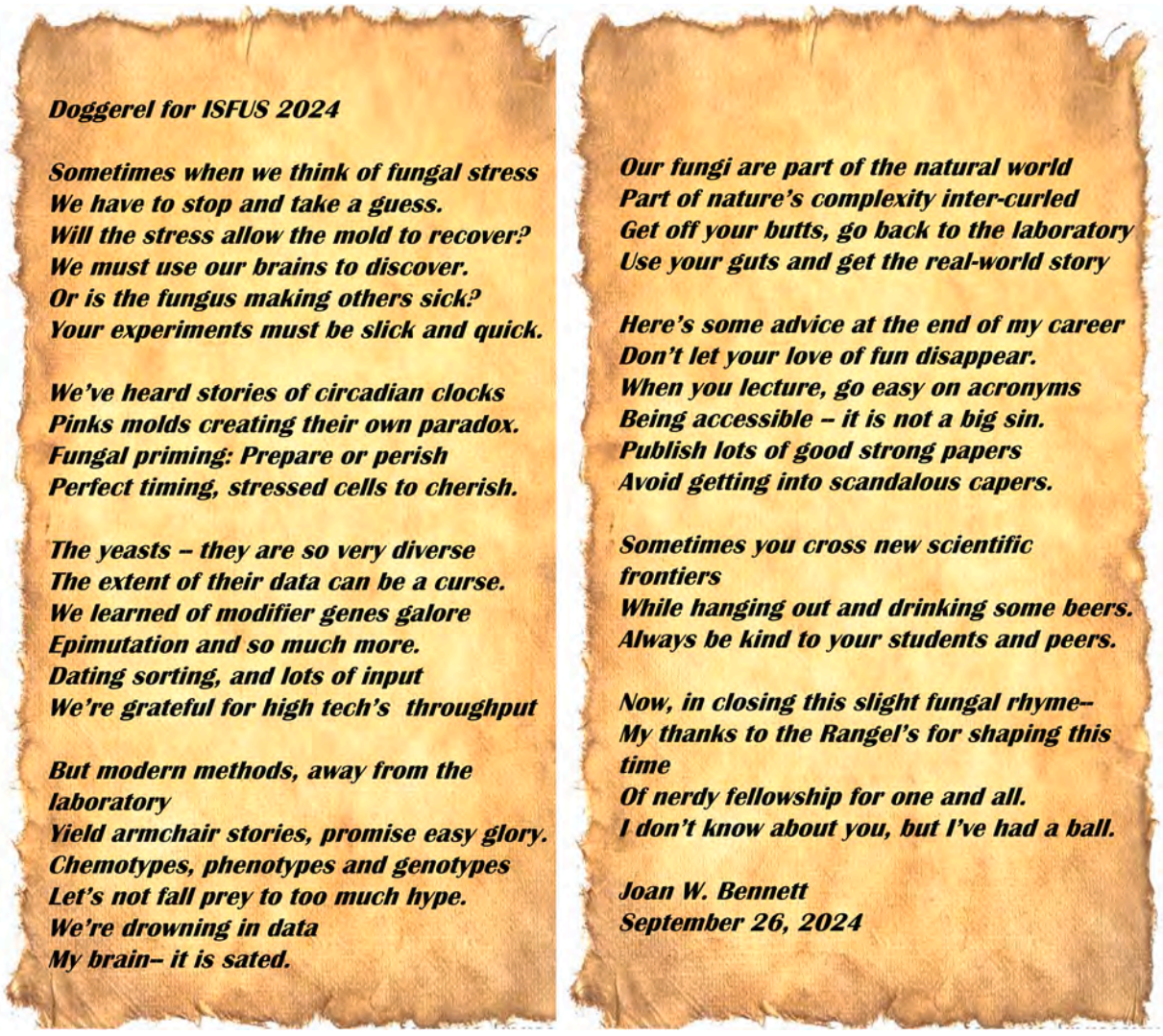

Fig. 19. Poem written by Joan W. Bennett, a member of the US National Academy of Sciences.

Universidad Mayor, Santiago, Chile and Millennium Institute for Integrative Biology (iBio), Santiago, Chile. She employed a systems biology approach based on gene regulatory networks to study the transcriptional response in the mycoparasitic process between the biocontrol fungus *T. atroviride* and the plant pathogen *B. cinerea* (Olivares-Yañez et al., 2025). Her group identified key transcription factors involved in the response of *B. cinerea* to attacks by *T. atroviride* (Olivares-Yanez et al., 2021). Mutant strains of these transcription factors showed increased sensitivity to *Trichoderma* mycoparasitism. Furthermore, using the same strategy, transcription factors were identified from *T. atroviride* as crucial for mycoparasitism. Mutant strains of these transcription factors had a reduced capacity to the mycoparasitised *B. cinerea*, while overexpression led to a faster process. Additionally, when the supernatant from these cultures was used to inhibit *B. cinerea* germination, the overexpression strains exhibited higher inhibition of *B. cinerea* growth.

Alene Alder-Rangel – Alder's English Services, São José dos Campos, SP, Brazil. For an overview of research on fungal stress tolerance, she conducted a scientometric review on fungi important in agriculture, industry, and the environment, but excluded medically important fungi. The Web of Science was used to search for relevant articles, and after electronic and manual sorting, a total of 3126 articles were analysed. Publications on fungal stress have increased significantly in the last 30 years. This research evaluated articles from 87 countries published in 558 different journals. Scientists from China and the US have conducted the most studies. Of the 498 different fungi studied, the most studied were *B. bassiana, Saccharomyces cerevisiae, Aspergillus nidulans, and A. niger*. Many of the top researchers analysed in this study have already presented at ISFUS. In conclusion, the review found that the studies on fungal stress are diverse and ISFUS has been instrumental in bringing scientists together for collaboration.

Drauzio Eduardo Naretto Rangel – INBIOTER - Institute of Biotechnology Rangel, Itatiba, SP, Brazil. The last presentation of the Symposium was entitled "Reiki-induced priming responsiveness in *M. robertsii* conidia." Fungi can store "priming" experiences as a memory, helping them respond to future stress, and this memory can be passed to the first generation of offspring. The fungus *M. robertsii* has four different levels of priming from very low conidial stress tolerance to very high conidial stress tolerance (Licona-Juárez et al., 2023; Rangel, 2024; Rangel et al., 2004, 2008, Rangel, 2011, 2012, 2015c). Rangel and his group have tested eleven conditions that induce priming in *M. robertsii* in which conidia become more tolerant to osmotic stress, oxidative stress, heat, and UV-B radiation than conidia produced on rich medium PDA without any apparent stress (Rangel, 2024). Fungi can learn, recognise, and adapt their responses based on environmental stimuli. However, could other types of stimuli affect conidial tolerance to stress conditions? His PhD student Ilkilene T.C. Oliveira employed her extensive experience with Reiki to determine if this alternative medicine technique produced priming in *M. robertsii.* In Reiki, "universal energy"

is supposedly transferred through the palms of the practitioner to the patient to encourage emotional or physical healing. Remarkably, *M. robertsii* conidia produced after Reiki during mycelial growth were significantly more heat tolerant, and more tolerant to osmotic stress and UV-B radiation than the control that did not receive Reiki. The experiments for heat were repeated in a different setting and verified the increase in heat tolerance of conidia produced after Reiki.

3. Awards

This meeting offered more awards to participants than previous ISFUSs. The awards were generously sponsored by Elsevier and the British Mycological Society, the American Society for Microbiology (ASM), PLoS Pathogens, and the Journal of Fungi. Drauzio Rangel, Alene Alder-Rangel, and their daughter Amanda Estella Alder Rangel (12 years old) presented them. Most of the awards required candidates to apply prior to the Symposium. These awards were announced at the opening ceremony on Monday morning. Then, the winners made oral presentations on the following days (Fig. 9).

For the **Elsevier** award, students had to submit a full manuscript ready for publication. Seven students applied, and two bronze and one silver were awarded. A bronze award was given to **Adrián Adolfo Álvarez Padilla**, originally from Colombia and a doctoral student of Marcelo Afonso Vallim at the Universidade Federal de São Paulo, in the city of São Paulo, Brazil. His article focused on the expression of the *GPP2* gene in *C. neoformans*. Also receiving a bronze, **Siebe Pierson** is a PhD student at the Universität Innsbruck, Tyrol, Austria, and he submitted an article about the antioxidant defences of *Trichoderma asperellum*. The silver award was given to **João Neves-da-Rocha**, who is a PhD student in genetics at the Universidade de São Paulo, Ribeirão Preto, SP, Brazil. His major professor is Nilce Maria Martinez Rossi, and his article focused on proteostasis and competition for rare tRNAs to define translation kinetics for the integrated stress response of *Saccharomyces cerevisiae* (Fig. 10).

The **American Society for Microbiology** Award was open to students and early-career mycologists. The application consisted of a letter of application, abstract, career narrative, list of work, statement of plans, and proof of enrolment or PhD diploma. Eight worthy candidates applied, and five silver and one gold awards were presented. The gold award went to **Alejandra Goity** (Fig. 11A), a postdoctoral fellow in the laboratory of Luis F. Larrondo at the Pontificia Universidad Católica de Chile, Santiago, Chile, and she presented a study identifying novel transcription factors involved in plant cell wall deconstruction by *N. crassa*. The silver awards went to **Monise Fazolin Petrucelli** (Fig. 11B), who is a postdoctoral researcher in the Fungi Genetics and Molecular Biology Laboratory at the Universidade de São Paulo, Ribeirão Preto, SP, Brazil, and her work focuses on the transcription factor StuA of oxidative stress-response genes in *Trichophyton rubrum*. **Bruno Montanari Borges** (Fig. 11C) recently completed his PhD in Biotechnology at the Universidade Federal de São Paulo, São José dos Campos, SP, Brazil, under Flávio Vieira Loures, and his research is about *Paracoccidioides brasiliesis*. **Emily Mesquita da Silva** (Fig. 11D) completed her PhD at the Universidade Federal Rural do Rio de Janeiro, UFRRJ, Brazil, and was a postdoctoral fellow with Michael J. Bidochka at Brock University, St. Catharines, ON, Canada. She studied untargeted secondary metabolites of *M. robertsii* under stress conditions. **Elias Barbosa da Silva-Junior** (Fig. 11E) is from the Universidade Federal do Rio de Janeiro, RJ, Brazil, and he has researched how the lack of TLR9 exacerbates ocular impairment and visual loss during systemic *Cryptococcus gattii* infection. **Renan E. A. Piraine** (Fig. 11F) received his degrees from the Universidade Federal de Pelotas and is currently a postdoctoral fellow with Fausto Almeida at the Universidade de São Paulo, Ribeirão Preto, SP, Brazil, with Fausto Almeida studying how extracellular vesicles from *Candida* and *Cryptococcus* induce specific responses (Fig. 11).

The **PLoS Pathogens** Award was open to early-career mycologists. The application consisted of a letter of application, abstract, career narrative, list of work, and statement of plans. The award was received by **Mavis Agyeiwaa Acheampong,** who is a Senior Lecturer at the University of Ghana. She studies entomopathogenic fungi as biological control agents against insect pests in Ghana (Fig. 12).

The **Journal of Fungi** awards recognised the best poster presentations and were handed out on the last day of the Symposium. Of the 90 posters presented at ISFUS (Fig. 13), 38 were eligible for the competition and judged by the international speakers at ISFUS. The students, who must be the first authors, presented their work to the judges during the poster sessions. The quality of the posters was outstanding; therefore, five gold awards were given for posters with scores above 90 %. **Júlia Sant'Ana** is an undergraduate at the Universidade Federal do Rio Grande do Sul, Porto Alegre, RG, Brazil, and she presented a poster about the expression of stress and infection-related proteins of *Metarhizium anisopliae* using an *in vitro* model of cattle tick infection. **Renan Santini Barbosa**, a graduate student at the Universidade Federal de São Paulo, SP, Brazil, presented a fast methodology for photoinduction and detection of mycosporine and mycosporine-like amino acids in yeasts. **Paola A. Ramos Irizarry** is a PhD student at Duke University, Durham, NC, USA; she researched how heat adaptation modifies the genetic landscape and pathogenicity in *C. deneoformans*. **Isabella Bresciani** studies at the Pontificia Universidad Católica de Chile, Santiago, Chile, and she presented about heat shock, oxidative stress survival, and thermotolerance evolution in *N. crassa* populations. The highest poster score was achieved by **Hyunjin Cha** from Yonsei University, Seoul, Republic of Korea, for her study about transcription factor networks in *C. auris* (Fig. 14).

On behalf of the entire organising team, we want to extend our deepest gratitude to the volunteers for their dedication and hard work during ISFUS-2024. Their enthusiasm, support, and commitment played an integral role in making this event a success (Fig. 15).

4. Excursions

Besides the high-quality science, the location attracted many people to ISFUS-2024. The nearby natural and technological wonders not only offered breathtaking views but also provided a refreshing contrast to the intense scientific discussions during the Symposium. Three excursions were available to speakers and participants before and after the Symposium.

The pre-meeting tour to Iguaçu National Park was fully booked with 53 adventurers. The first stop of the day was the Parque das Aves, which features a variety of different species of colourful Brazilian birds in large aviaries. Next came the hike along the Brazilian side of the Iguaçu River until the magnificent waterfalls (Fig. 16). The stunning display of nature's power was truly inspiring and a reminder of the delicate balance of ecosystems. After eating lunch and almost losing István Pócsi, the group took the Macuco Safari Boat Adventure for a refreshingly cold bath as the motorboats went multiple times under the spray of a

waterfall (Fig. 16).

The day after the Symposium featured a tour of the Itaipú dam, one of the world's largest hydroelectric plants, located on the border between Brazil and Paraguay. On the way back to the hotel, the bus stopped at the Buddhist temple (Fig. 17). Later, everyone enjoyed dinner and the sunset on a catamaran boat on the Paraná River along the border between Brazil, Argentina, and Paraguay.

The final excursion was across the border to Argentina (Fig. 18). The Argentinian Park had metal-grill walkways built over stretches of the river upstream of the waterfalls, and at some points, the walkways extended right to the edges of the falls. People were bedazzled by the multiple rainbows, rushing river water, exotic birds, various butterflies, and monkeys. The tour was capped off by an excellent dinner, including Tango dancing (Bennett, 2024).

The excursions offered during ISFUS provided an opportunity to form bonds and build relationships in the most unlikely way. This experience was akin to a child's summer camp and will undoubtedly lead to long-lasting collaborations among the scientists who attended ISFUS 2024.

5. Closing ceremony

As Drauzio tends to get emotional during the closing ceremony, he delegated the closing statement to Joseph Heitman, who encouraged everyone to come to the next ISFUS. Joan Bennett wrote another poem (Fig. 19) and read it as part of the closing ceremony of ISFUS-2024. Given the great success of this meeting, plans are already well underway for the VI International Symposium on Fungal Stress (ISFUS) to be held on September 21–27, 2026 (https://isfus2026.wordpress.com).

6. Conclusion

ISFUS continues to serve as an exceptional platform for exchanging groundbreaking research on fungal biology, with a strong focus on stress responses. The presentations highlighted the profound impact of stress adaptation mechanisms in industrial, agricultural, and medicinal fungi. What stands out is the collaborative spirit fostered here, bringing together leading experts and early-career scientists from across the globe. The level of discussion, especially around innovative approaches and emerging technologies in fungal research, was truly inspiring. The Symposium's dedication to advancing the understanding of fungal stress responses will undoubtedly lead to future breakthroughs.

CRediT authorship contribution statement

Alene Alder-Rangel: Conceptualization, Data curation, Funding acquisition, Investigation, Writing – original draft, Writing – review & editing, Formal analysis, Methodology, Project administration, Resources, Supervision, Validation, Visualization. **Amanda E.A. Rangel:** Writing – review & editing. **Arturo Casadevall:** Writing – review & editing. **Asiya Gusa:** Writing – review & editing. **Chaoyang Xue:** Writing – review & editing. **Charles M. Boone:** Writing – review & editing. **Chris Todd Hittinger:** Writing – review & editing. **Claudio A. Masuda:** Writing – review & editing. **Consuelo Olivares-Yañez:** Writing – review & editing. **Deborah Bell-Pedersen:** Writing – review & editing. **Erica J. Washington:** Writing – review & editing. **Gerhard Braus:** Writing – review & editing. **Guilhem Janbon:** Writing – review & editing. **István Pócsi:** Writing – review & editing. **Jason E. Stajich:** Writing – review & editing. **Jay C. Dunlap:** Writing – review & editing. **Joan W. Bennett:** Writing – review & editing. **Joseph Heitman:** Writing – review & editing. **Ling Lu:** Writing – review & editing. **Lucia Landi:** Writing – review & editing. **Mari L. Shinohara:** Writing – review & editing. **Maurizio Del Poeta:** Writing – review & editing. **Mavis A. Acheampong:** Writing – review & editing. **Mia R. Maltz:** Writing – review & editing. **Michael C. Lorenz:** Writing – review & editing. **Minou Nowrousian:** Writing – review & editing. **N. Louise Glass:** Writing – review & editing. **Nichole A. Broderick:** Writing – review & editing. **Nicolás Pedrini:** Writing – review & editing. **Nir Osherov:** Writing – review & editing. **R. Blake Billmyre:** Writing – review & editing. **Sabrina Sarrocco:** Writing – review & editing. **Salomé LeibundGut-Landmann:** Writing – review & editing. **Vânia Aparecida Vicente:** Writing – review & editing. **Xiaorong Lin:** Writing – review & editing. **Xin-Qing Zhao:** Writing – review & editing. **Yong-Sun Bahn:** Writing – review & editing. **Zachary A. Lewis:** Writing – review & editing. **Drauzio E.N. Rangel:** Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Supervision, Visualization, Writing – original draft, Writing – review & editing, Resources, Validation.

Dedication

The last author, Drauzio Eduardo Naretto Rangel, dedicates this work to his mother, Maria Hilda Naretto Rangel. She was born on February 17, 1936, and passed away on January 19, 2025, while this manuscript was being written. Maria Hilda was born in her grandmother's house in Itatiba, State of São Paulo, Brazil, but she was raised in the city of São Paulo. She studied until primary school and began working at nine years old in her father's general store and then in her mother's knitting factory until her mother's death on May 1, 1955, when she was 19 years old. The next year, she married Drauzio Taveiros Rangel on September 8, 1956, when she was 20 years old. Maria Hilda, Drauzio, and their two sons lived in a small, one-bedroom house behind her father's house for 11 years. The success of their typographical printing company eventually enabled the rental of a larger family home. When D. E. N. R. was 9 years old and was living behind his grandfather's house, he showed an interest in science, so his parents gave him a small microscope, which is still in the author's office. Three years later, they also gave science kits that were sold weekly inside a foam box at the newspaper stand. At this time (the 1970s), the author's father bought weekly issues about science, history, arts, religion, etc., at the newspaper stand and collated these to form several encyclopaedias. Despite their lack of formal education, Maria Hilda and Drausio enthusiastically read these, stimulating similar interest in their sons. After 20 years of marriage and motherhood, Maria Hilda finally had the opportunity to complete high school. They also encouraged and supported their sons to obtain a university education. By this time (1980s), their printing company had grown to more than 30 employees. D. E. N. R. wishes to express his deepest gratitude to her. The picture below was taken at her country house (https://sitioterradosol.wordpress.com) in the city of Itatiba, state of São Paulo, Brazil. Sadly, Drauzio Taveiros Rangel passed a few months after the first ISFUS in 2014 (Rangel et al., 2015c), and Maria Hilda Rangel passed a few months after the ISFUS-2024.

Declaration of competing interest

The manuscript has been prepared in accordance with the formatting guidelines for *Fungal Biology*. The work is not under consideration for publication in any form elsewhere. The manuscript does not infringe any personal or other copyright or property rights and has been approved for publication by all authors. Dr. Maurizio Del Poeta, M.D., is a Co-Founder and Chief Scientific Officer (CSO) of MicroRid Technologies Inc. The goal of MicroRid Technologies Inc. is to develop new antifungal agents for therapeutic use. All other authors declare that they have no conflicting interests.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.funbio.2025.101590.

References

Acheampong, M.A., Cornelius, E.W., Eziah, V.Y., Fening, K.O., Ofori, K., Storm, C., Jessop, N., Luke, B., Moore, D., Clottey, V.A., Potin, O., Grammare, P., 2023. Efficacy of *Beauveria bassiana* against adults of *Prostephanus truncatus* (horn), *Sitophilus zeamais* motschulsky and *Teretrius nigrescens* Lewis in stored maize. Afr. Entomol. 31. https://doi.org/10.17159/2254-8854/2023/a11734.

Acheampong, M.A., Pupin, B., Dias, L.P., Santos, M.P., Bernardes, L.O., Pinheiro, M.S., Ferreira, P.C., Mikaelyan, A., Medina, H.R., Alder-Rangel, A., Rangel, D.E.N., 2025. Physiological stress tolerance responses of the dung decomposer fungus *Mucor circinelloides*. Fungal Biol. 129, 101575. https://doi.org/10.1016/j.funbio.2025.101575.

Alder-Rangel, A., Bailão, A.M., da Cunha, A.F., Soares, C.M.A., Wang, C., Bonatto, D., Dadachova, E., Hakalehto, E., Eleutherio, E.C.A., Fernandes, E.K.K., Braus, G.H., Braga, G.Ú.L., Goldman, G.H., Malavazi, I., Hallsworth, J.E., Takemoto, J.Y., Fuller, K., Selbmann, L., Corrochano, L.M., Bertolini, M.C., Schmoll, M., Pedrini, N., Loera, O., Finlay, R.D., Peralta, R.M., Rangel, D.E.N., 2018. The second international symposium on fungal stress: ISFUS. Fungal Biol. 122, 386–399. https://doi.org/10.1016/j.funbio.2017.10.011.

Alder-Rangel, A., Bailão, A.M., Herrera-Estrella, A., Rangel, A.E.A., Gácser, A., Gasch, A. P., Campos, C.B.L., Peters, C., Camelim, F., Verde, F., Gadd, G.M., Braus, G., Eisermann, I., Quinn, J., Latgé, J.-P., Aguirre, J., Bennett, J.W., Heitman, J., Nosanchuk, J.D., Partida-Martínez, L.P., Bassilana, M., Acheampong, M.A., Riquelme, M., Feldbrügge, M., Keller, N.P., Keyhani, N.O., Gunde-Cimerman, N., Nascimento, R., Arkowitz, R.A., Mouriño-Pérez, R.R., Naz, S.A., Avery, S.V., Basso, T.O., Terpitz, U., Lin, X., Rangel, D.E.N., 2023. The IV international symposium on fungal stress and the XIII international fungal biology conference. Fungal Biol. 127, 1157–1179. https://doi.org/10.1016/j.funbio.2023.04.006.

Alder-Rangel, A., Idnurm, A., Brand, A.C., Brown, A.J.P., Gorbushina, A., Kelliher, C.M., Campos, C.B., Levin, D.E., Bell-Pedersen, D., Dadachova, E., Bauer, F.F., Gadd, G.M., Braus, G.H., Braga, G.Ú.L., Brancini, G.T.P., Walker, G.M., Druzhinina, I., Pócsi, I., Dijksterhuis, J., Aguirre, J., Hallsworth, J.E., Schumacher, J., Wong, K.H., Selbmann, L., Corrochano, L.M., Kupiec, M., Momany, M., Molin, M., Requena, N., Yarden, O., Cordero, R.J.B., Fischer, R., Pascon, R.C., Mancinelli, R.L., Emri, T., Basso, T.O., Rangel, D.E.N., 2020. The third international symposium on fungal stress – ISFUS. Fungal Biol. 124, 235–252. https://doi.org/10.1016/j.funbio.2020.02.007.

Almaliki, H.S., Niu, M., Keller, N.P., Yin, G., Bennett, J.W., 2023. Mutational analysis of *Aspergillus fumigatus* volatile oxylipins in a *Drosophila* eclosion assay. J. Fungi. 9. https://doi.org/10.3390/jof9040402.

Aranguiz, K., Horianopoulos, L.C., Elkin, L., Abá, K.S., Wrobel, R.L., Shiu, S.-H., Rokas, A., Hittinger, C.T., 2024. Machine learning reveals genes impacting oxidative

stress resistance across yeasts. bioRxiv, 607963. https://doi.org/10.1101/2024.08.14.607963.
Barron, A.J., Agrawal, S., Lesperance, D.N.A., Doucette, J., Calle, S., Broderick, N.A., 2024. Microbiome-derived acidity protects against microbial invasion in *Drosophila*. Cell Rep. 43, 114087. https://doi.org/10.1016/j.celrep.2024.114087.
Bennett, J.W., 2024. Report on the International Symposium on Fungal Stress (ISFUS) 2024, Inoculum. Mycological Society of America, Madison, WI, pp. 20–24.
Breuer, J., Busche, T., Kalinowski, J., Nowrousian, M., 2024a. Histone binding of ASF1 is required for fruiting body development but not for genome stability in the filamentous fungus *Sordaria macrospora*. mBio 15, e0289602823. https://doi.org/10.1128/mbio.02896-23.
Breuer, J., Ferreira, D.E.A., Kramer, M., Bollermann, J., Nowrousian, M., 2024b. Functional Analysis of Chromatin-Associated Proteins in Sordaria Macrospora Reveals Similar Roles for RTT109 and ASF1 in Development and DNA Damage Response. G3 (Bethesda). https://doi.org/10.1093/g3journal/jkae019.
Calo, S., Nicolás, F.E., Lee, S.C., Vila, A., Cervantes, M., Torres-Martinez, S., Ruiz-Vazquez, R.M., Cardenas, M.E., Heitman, J., 2017. A non-canonical RNA degradation pathway suppresses RNAi-dependent epimutations in the human fungal pathogen *Mucor circinelloides*. PLoS Genet. 13, e1006686.
Calo, S., Shertz-Wall, C., Lee, S.C., Bastidas, R.J., Nicolás, F.E., Granek, J.A., Mieczkowski, P., Torres-Martínez, S., Ruiz-Vázquez, R.M., Cardenas, M.E., Heitman, J., 2014. Antifungal drug resistance evoked via RNAi-dependent epimutations. Nature 513, 555–558. https://doi.org/10.1038/nature13575.
Camacho, E., Vij, R., Chrissian, C., Prados-Rosales, R., Gil, D., O'Meally, R.N., Cordero, R.J.B., Cole, R.N., McCaffery, J.M., Stark, R.E., Casadevall, A., 2019. The structural unit of melanin in the cell wall of the fungal pathogen *Cryptococcus neoformans*. J. Biol. Chem. 294, 10471–10489. https://doi.org/10.1074/jbc.RA119.008684.
Casadevall, A., Coelho, C., Cordero, R.J.B., Dragotakes, Q., Jung, E., Vij, R., Wear, M.P., 2019. The capsule of *Cryptococcus neoformans*. Virulence 10, 822–831. https://doi.org/10.1080/21505594.2018.1431087.
Castillo, K.D., Chapa, E.D., Lamb, T.M., Gangopadhyay, M., Bell-Pedersen, D., 2022a. Circadian clock control of tRNA synthetases in *Neurospora crassa*. F1000Research 11, 1556. https://doi.org/10.12688/f1000research.125351.2.
Castillo, K.D., Wu, C., Ding, Z., Lopez-Garcia, O.K., Rowlinson, E., Sachs, M.S., Bell-Pedersen, D., 2022b. A circadian clock translational control mechanism targets specific mRNAs to cytoplasmic messenger ribonucleoprotein granules. Cell Rep. 41, 111879. https://doi.org/10.1016/j.celrep.2022.111879.
Cha, H., Won, D., Kang, S., Kim, E.-S., Lee, K.-A., Lee, W.-J., Lee, K.-T., Bahn, Y.-S., 2025. The calcineurin pathway regulates extreme thermotolerance, cell membrane and wall integrity, antifungal resistance, and virulence in *Candida auris*. bioRxiv 2025, 631159. https://doi.org/10.1101/2025.01.02.631159.
Chang, Z., Billmyre, R.B., Lee, S.C., Heitman, J., 2019. Broad antifungal resistance mediated by RNAi-dependent epimutation in the basal human fungal pathogen *Mucor circinelloides*. PLoS Genet. 15, e1007957. https://doi.org/10.1371/journal.pgen.1007957.
Chadwick, BJ, Pham, T, Xie, X, Ristow, LC, Krysan, DJ, Lin, X, 2022. The RAM signaling pathway links morphology, thermotolerance, and CO(2) tolerance in the global fungal pathogen *Cryptococcus neoformans*. Elife 11. https://doi.org/10.7554/eLife.82563. Epub 2022/11/24.
Chadwick, BJ, Ristow, LC, Xie, X, Krysan, DJ, Lin, X, 2024. Discovery of CO(2) tolerance genes associated with virulence in the fungal pathogen *Cryptococcus neoformans*. Nat Microbiol 9 (10), 2684–2695. https://doi.org/10.1038/s41564-024-01792-w. Epub 20240904.
Chen, S., Zhu, G., Lin, H., Guo, J., Deng, S., Wu, W., Goldman Gustavo, H., Lu, L., Zhang, Y., 2024. Variability in competitive fitness among environmental and clinical azole-resistant *Aspergillus fumigatus* isolates. mBio 15, e0026300224. https://doi.org/10.1128/mbio.00263-24.
Coleine, C., Masonjones, S., Onofri, S., Selbmann, L., Stajich, J.E., 2020. Draft genome sequence of the yeast *Rhodotorula* sp. strain CCFEE 5036, isolated from McMurdo Dry Valleys, Antarctica. Microbiol. Resour. Announc. 9. https://doi.org/10.1128/MRA.00020-20.
Cordero, R.J., Frases, S., Guimaraes, A.J., Rivera, J., Casadevall, A., 2011. Evidence for branching in cryptococcal capsular polysaccharides and consequences on its biological activity. Mol. Microbiol. 79, 1101–1117. https://doi.org/10.1111/j.1365-2958.2010.07511.x.
Costanzo, M., VanderSluis, B., Koch, E.N., Baryshnikova, A., Pons, C., Tan, G., Wang, W., Usaj, M., Hanchard, J., Lee, S.D., Pelechano, V., Styles, E.B., Billmann, M., van Leeuwen, J., van Dyk, N., Lin, Z.Y., Kuzmin, E., Nelson, J., Piotrowski, J.S., Srikumar, T., Bahr, S., Chen, Y., Deshpande, R., Kurat, C.F., Li, S.C., Li, Z., Usaj, M. M., Okada, H., Pascoe, N., San Luis, B.J., Sharifpoor, S., Shuteriqi, E., Simpkins, S.W., Snider, J., Suresh, H.G., Tan, Y., Zhu, H., Malod-Dognin, N., Janjic, V., Przulj, N., Troyanskaya, O.G., Stagljar, I., Xia, T., Ohya, Y., Gingras, A.C., Raught, B., Boutros, M., Steinmetz, L.M., Moore, C.L., Rosebrock, A.P., Caudy, A.A., Myers, C.L., Andrews, B., Boone, C., 2016. A global genetic interaction network maps a wiring diagram of cellular function. Science 353. https://doi.org/10.1126/science.aaf1420.
Courtney, A.J., Kamei, M., Ferraro, A.R., Gai, K., He, Q., Honda, S., Lewis, Z.A., 2020. Normal Patterns of Histone H3K27 Methylation Require the Histone Variant H2A.Z in Neurospora crassa. Genetics 216, 51–66.
Dang, T.T.V., Maufrais, C., Colin, J., Moyrand, F., Mouyna, I., Coppée, J.-Y., Onyishi, C. U., Lipecka, J., Guerrera, I.C., May, R.C., Janbon, G., 2024. Alternative TSS use is widespread in *Cryptococcus* fungi in response to environmental cues and regulated genome-wide by the transcription factor Tur 1. PLoS. Biol. 22, e3002724.
Daskalov, A, Mitchell, PS, Sandstrom, A, Vance, RE, Glass, NL, 2020. Molecular characterization of a fungal gasdermin-like protein. Proc. Natl. Acad. Sci. U S A 117 (31), 18600–18607. https://doi.org/10.1073/pnas.2004876117.
Daudu, R., Parker, C.W., Singh, N.K., Wood, J.M., Debieu, M., O'Hara, N.B., Mason, C.E., Venkateswaran, K., 2020. Draft genome sequences of *Rhodotorula mucilaginosa* strains isolated from the International Space Station. Microbiol. Resour. Announc. 9. https://doi.org/10.1128/MRA.00570-20.
Dib Ferreira Gremiao, I., Pereira-Oliveira, G.R., Pereira, S.A., Correa, M.L., Borba-Santos, L.P., Vicosa, A.L., Garg, A., Haranahalli, K., Dasilva, D., Pereira de Sa, N., Matos, G.S., Silva, V., Lazzarini, C., Fernandes, C.M., Miranda, K., Artunduaga Bonilla, J.J., Nunes, A.L., Nimrichter, L., Ojima, I., Mallamo, J., McCarthy, J.B., Del Poeta, M., 2024. Combination therapy of itraconazole and an acylhydrazone derivative (D13) for the treatment of sporotrichosis in cats. Microbiol. Spectr. 12, e0396723. https://doi.org/10.1128/spectrum.03967-23.
Dunlap, J.C., Loros, J.J., 2017. Making time: conservation of biological clocks from fungi to animals. Microbiol. Spectr. 5 (10). https://doi.org/10.1128/microbiolspec.FUNK-0039-2016.
Ferraro, A.R., Ameri, A.J., Lu, Z., Kamei, M., Schmitz, R.J., Lewis, Z.A., 2021. Chromatin accessibility profiling in Neurospora crassa reveals molecular features associated with accessible and inaccessible chromatin. BMC genomics 22, 459.
Fischer, C.N., Trautman, E.P., Crawford, J.M., Stabb, E.V., Handelsman, J., Broderick, N. A., 2017. Metabolite exchange between microbiome members produces compounds that influence *Drosophila* behavior. Elife 6, e18855. https://doi.org/10.7554/eLife.18855.
Galka, D., Ali, T.T., Bast, A., Niederleithinger, M., Gerhardt, E., Motosugi, R., Sakata, E., Knop, M., Outeiro, T.F., Popova, B., Braus, G.H., 2024. Inhibition of 26S proteasome activity by α-synuclein is mediated by the proteasomal chaperone Rpn14/PAAF1. Aging Cell 23, e14128. https://doi.org/10.1111/acel.14128.
Gonçalves, AP, Heller, J, Rico-Ramírez, AM, Daskalov, A, Rosenfield, G, Glass, NL, 2020. Conflict, competition, and cooperation regulate social interactions in filamentous fungi. Annu Rev Microbiol 74, 693–712. https://doi.org/10.1146/annurev-micro-012420-080905.
Gusa, A., Williams, J.D., Cho, J.-E., Averette, A.F., Sun, S., Shouse, E.M., Heitman, J., Alspaugh, J.A., Jinks-Robertson, S., 2020. Transposon mobilization in the human fungal pathogen *Cryptococcus* is mutagenic during infection and promotes drug resistance in vitro. Proc. Natl. Acad. Sci. 117, 9973–9980. https://doi.org/10.1073/pnas.2001451117.
Gusa, A., Yadav, V., Roth, C., Williams, J.D., Shouse, E.M., Magwene, P., Heitman, J., Jinks-Robertson, S., 2023. Genome-wide analysis of heat stress-stimulated transposon mobility in the human fungal pathogen *Cryptococcus deneoformans*. Proc. Natl. Acad. Sci. U. S. A. 120, e2209831120. https://doi.org/10.1073/pnas.2209831120.
Haranahalli, K., Lazzarini, C., Sun, Y., Zambito, J., Pathiranage, S., McCarthy, J.B., Mallamo, J., Del Poeta, M., Ojima, I., 2019. SAR studies on aromatic acylhydrazone-based inhibitors of fungal sphingolipid synthesis as next-generation antifungal agents. J. Med. Chem. 62, 8249–8273. https://doi.org/10.1021/acs.jmedchem.9b01004.
Harish, E., Osherov, N., 2022. Fungal priming: prepare or perish. J. Fungi. 8. https://doi.org/10.3390/jof8050448.
Harish, E., Sarkar, A., Handelman, M., Abo Kandil, A., Shadkchan, Y., Wurster, S., Kontoyiannis Dimitrios, P., Osherov, N., 2022. Triazole priming as an adaptive response and gateway to resistance in *Aspergillus fumigatus*. Antimicrob. Agents Chemother. 66, e0045800422. https://doi.org/10.1128/aac.00458-22.
Harrison, M.-C., Ubbelohde, E.J., LaBella, A.L., Opulente, D.A., Wolters, J.F., Zhou, X., Shen, X.-X., Groenewald, M., Hittinger, C.T., Rokas, A., 2024. Machine learning enables identification of an alternative yeast galactose utilization pathway. Proc. Natl. Acad. Sci. 121, e2315314121. https://doi.org/10.1073/pnas.2315314121.
Inamdar, A.A., Morath, S., Bennett, J.W., 2020. Fungal volatile organic compounds: more than just a funky smell? Annu. Rev. Microbiol. 74, 101–116. https://doi.org/10.1146/annurev-micro-012420-080428.
Jaddaoui, I.E., Rangel, D.E.N., Bennett, J.W., 2023. Fungal volatiles have physiological properties. Fungal Biol. 127, 1231–1240. https://doi.org/10.1016/j.funbio.2023.03.005.
Kamei, M., Ameri, A.J., Ferraro, A.R., Bar-Peled, Y., Zhao, F., Ethridge, C.L., Lail, K., Amirebrahimi, M., Lipzen, A., Ng, V., Grigoriev, I.V., Schmitz, R.J., Liu, Y., Lewis, Z. A., 2021. IMITATION SWITCH is required for normal chromatin structure and gene repression in PRC2 target domains. Proc Natl Acad Sci U S A 118.
Kim, J.-S., Lee, K.-T., Bahn, Y.-S., 2023a. Deciphering the regulatory mechanisms of the cAMP/protein kinase A pathway and their roles in the pathogenicity of *Candida auris*. Microbiol. Spectr. 11, e0215202123. https://doi.org/10.1128/spectrum.02152-23.
Kim, J.-S., Lee, K.-T., Bahn, Y.-S., 2023b. Secreted aspartyl protease 3 regulated by the Ras/cAMP/PKA pathway promotes the virulence of *Candida auris*. Front. Cell. Infect. Microbiol. 13–2023. https://doi.org/10.3389/fcimb.2023.1257897.
Kim, J.S., Lee, K.T., Lee, M.H., Cheong, E., Bahn, Y.S., 2021. Adenylyl cyclase and protein kinase A play redundant and distinct roles in growth, differentiation, antifungal drug resistance, and pathogenicity of *Candida auris*. mBio 12, e0272921. https://doi.org/10.1128/mBio.02729-21.
Kirchner, F.R., LeibundGut-Landmann, S., 2021. Tissue-resident memory Th17 cells maintain stable fungal commensalism in the oral mucosa. Mucosal Immunol. 14, 455–467. https://doi.org/10.1038/s41385-020-0327-1.
Kocsis, B., Boldizsár, I., Kovács, G.M., Nagy, T., Gyémánt, G., Csillag, K., Pócsi, I., Leiter, É., 2024. Could the transcription factor AtnN coordinating the aspercryptin secondary metabolite gene cluster in *Aspergillus nidulans* be a global regulator? Fungal Biol. 128, 2311–2316. https://doi.org/10.1016/j.funbio.2024.11.006.
Kocsis, B., Lee, M.-K., Antal, K., Yu, J.-H., Pócsi, I., Leiter, É., Emri, T., 2023. Genome-wide gene expression analyses of the AtfA/AtfB-mediated menadione stress response in *Aspergillus nidulans*. Cells 12, 463. https://doi.org/10.3390/cells12030463.

Lazzarini, C., Haranahalli, K., McCarthy, J.B., Mallamo, J., Ojima, I., Poeta, M.D., 2020. Preclinical evaluation of acylhydrazone SB-AF-1002 as a novel broad-spectrum antifungal agent. Antimicrob Agents Ch 64. https://doi.org/10.1128/aac.00946-20.

Lazzarini, C., Haranahalli, K., Rieger, R., Ananthula, H.K., Desai, P.B., Ashbaugh, A., Linke, M.J., Cushion, M.T., Ruzsicska, B., Haley, J., Ojima, I., Poeta, M.D., 2018. Acylhydrazones as antifungal agents targeting the synthesis of fungal sphingolipids. Antimicrob Agents Ch 62. https://doi.org/10.1128/aac.00156-18.

Lee, J.Y., Kim, D.G., Kim, B.G., Yang, W.S., Hong, J., Kang, T., Oh, Y.S., Kim, K.R., Han, B.W., Hwang, B.J., Kang, B.S., Kang, M.S., Kim, M.H., Kwon, N.H., Kim, S., 2014. Promiscuous methionyl-tRNA synthetase mediates adaptive mistranslation to protect cells against oxidative stress. J. Cell Sci. 127, 4234–4245. https://doi.org/10.1242/jcs.152470.

Lee, S.C., Li, A., Calo, S., Heitman, J., 2013. Calcineurin plays key roles in the dimorphic transition and virulence of the human pathogenic zygomycete *Mucor circinelloides*. PLoS Pathog. 9, e1003625. https://doi.org/10.1371/journal.ppat.1003625.

Lee, S.C., Li, A., Calo, S., Inoue, M., Tonthat, N.K., Bain, J.M., Louw, J., Shinohara, M.L., Erwig, L.P., Schumacher, M.A., Ko, D.C., Heitman, J., 2015. Calcineurin orchestrates dimorphic transitions, antifungal drug responses and host-pathogen interactions of the pathogenic mucoralean fungus *Mucor circinelloides*. Mol. Microbiol. 97, 844–865. https://doi.org/10.1111/mmi.13071.

Leiter, É., Emri, T., Pákozdi, K., Hornok, L., Pócsi, I., 2021. The impact of bZIP Atf1ortholog global regulators in fungi. Appl. Microbiol. Biotechnol. 105, 5769–5783. https://doi.org/10.1007/s00253-021-11431-7.

Li, Y, Hou, Y, Sun, Q, Zeng, H, Meng, F, Tian, X, He, Q, Shao, F, Ding, J, 2024. Cleavage-independent activation of ancient eukaryotic gasdermins and structural mechanisms. Science 384 (6697), adm9190. https://doi.org/10.1126/science.adm9190.

Licona-Juárez, K.C., Bezerra, A.V.S., Oliveira, I.T.C., Massingue, C.D., Medina, H.R., Rangel, D.E.N., 2023. Congo red induces trans-priming to UV-B radiation in *Metarhizium robertsii*. Fungal Biol. 127, 1544–1550. https://doi.org/10.1016/j.funbio.2023.06.005.

Liu, T.-B., Kim, J.-C., Wang, Y., Toffaletti, D.L., Eugenin, E., Perfect, J.R., Kim, K.J., Xue, C., 2013. Brain inositol is a novel stimulator for promoting *Cryptococcus* penetration of the blood-brain barrier. PLoS Pathog. 9, e1003247.

Luke, B., Acheampong, M.A., Rangel, D.E.N., Cornelius, E.W., Asante, S.K., Nboyine, J.A., Eziah, V.Y., Fening, K.O., Storm, C., Jessop, N., Clottey, V.A., Potin, O., Tyson, C., Moore, D., Mikaelyan, A., 2023. The use of *Beauveria bassiana* for the control of the larger grain borer, *Prostephanus truncatus*, in stored maize: semi-field trials in Ghana. Fungal Biol. https://doi.org/10.1016/j.funbio.2023.08.004.

Machado, C.M., de-Souza-Ferreira, E., Silva, G.F.S., Pimentel, F.S.A., De-Souza, E.A., Silva-Rodrigues, T., Gandara, A.C.P., Zeidler, J.D., Fernandes-Siqueira, L.O., De-Queiroz, A.L.F.V., Andrade-Silva, L., Victória-Martins, K., Fernandes-Carvalho, C., Chini, E.N., Passos, J.F., Da Poian, A.T., Montero-Lomelí, M., Galina, A., Masuda, C. A., 2024. Galactose-1-phosphate inhibits cytochrome c oxidase and causes mitochondrial dysfunction in classic galactosemia. Biochim Biophys Acta Mol Basis Dis 1870. https://doi.org/10.1016/j.bbadis.2024.167340.

Machado, C.M., De-Souza, E.A., De-Queiroz, A.L.F.V., Pimentel, F.S.A., Silva, G.F.S., Gomes, F.M., Montero-Lomelí, M., Masuda, C.A., 2017. The galactose-induced decrease in phosphate levels leads to toxicity in yeast models of galactosemia. Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease 1863, 1403–1409. https://doi.org/10.1016/j.bbadis.2017.02.014.

Maltz, M.R., Allen, M.F., Phillips, M.L., Hernandez, R.R., Shulman, H.B., Freund, L., Andrews, L.V., Botthoff, J.K., Aronson, E.L., 2024. Microbial community structure in recovering forests of Mount St. Helens. Fronti. Microbio. 3. https://doi.org/10.3389/frmbi.2024.1399416.

Mannino, M.C., Davyt-Colo, B., Huarte-Bonnet, C., Diambra, L., Pedrini, N., 2023. Transcriptomic landscape of the interaction between the entomopathogenic fungus *Beauveria bassiana* and its tolerant host *Tribolium castaneum* revealed by dual RNA-seq. Sci. Rep. 13, 16506. https://doi.org/10.1038/s41598-023-43889-y.

Maurus, I., Harting, R., Herrfurth, C., Starke, J., Nagel, A., Mohnike, L., Chen, Y.-Y., Schmitt, K., Bastakis, E., Süß, M.T., Leonard, M., Heimel, K., Valerius, O., Feussner, I., Kronstad, J.W., Braus, G.H., 2023. *Verticillium dahliae* Vta3 promotes ELV1 virulence factor gene expression in xylem sap, but tames Mtf1-mediated late stages of fungus-plant interactions and microsclerotia formation. PLoS Pathog. 19, e1011100.

Medina, H.R., Rangel, D.E.N., 2025a. Light enhances the production of conidia and influences their hydrophobicity in *Tolypocladium inflatum*. Fungal Biol. 129, 101483. https://doi.org/10.1016/j.funbio.2024.07.005.

Medina, H.R., Rangel, D.E.N., 2025b. *Metarhizium acridum* exhibits a different conidial hydrophobicity than other insect-pathogenic fungi. Fungal Biol. 129, 101547. https://doi.org/10.1016/j.funbio.2025.101547.

Miao, Y., Yadav, V., Shadrick, W., Liu, J., Jenner, A.R., Gee, C., Schäfer, M., Perfect, J.R., Lee, R.E., Brennan, R.G., Washington, E.J., 2025. Inhibitors of trehalose-6-phosphate synthase activity in fungal pathogens compromise thermal tolerance pathways. bioRxiv 2025. https://doi.org/10.1101/2025.03.07.642065, 2003.2007.642065.

Molina-Hernandez, J.B., Landi, L., De Flaviis, R., Laika, J., Romanazzi, G., Chaves-Lopez, C., 2023a. Understanding the mechanisms of action of atmospheric cold plasma towards the mitigation of the stress induced in molds: the case of *Aspergillus chevalieri*. Innov. Food Sci. Emerg. Technol. 90, 103492. https://doi.org/10.1016/j.ifset.2023.103492.

Molina-Hernandez, J.B., Tappi, S., Gherardi, M., de Flaviis, R., Laika, J., Peralta-Ruiz, Y. Y., Paparella, A., Chaves-López, C., 2023b. Cold atmospheric plasma treatments trigger changes in sun-dried tomatoes mycobiota by modifying the spore surface structure and hydrophobicity. Food Control 145, 109453. https://doi.org/10.1016/j.foodcont.2022.109453.

Nascimento, M.M.F., Vicente, V.A., Bittencourt, J.V.M., Gelinski, J.M.L., Prenafeta-Boldu, F.X., Romero-Guiza, M., Fornari, G., Gomes, R.R., Santos, G.D., Gerrits Van Den Ende, A.H.G., de Azevedo, C., De Hoog, G.S., 2017. Diversity of opportunistic black fungi on babassu coconut shells, a rich source of esters and hydrocarbons. Fungal. Biol. 121, 488–500. https://doi.org/10.1016/j.funbio.2017.01.006.

Olivares-Yañez, C., Arias-Inostroza, N., Polanco, R., Canessa, P., 2025. Mycoparasitic transcription factor 1 (BcMTF1) participates in the *Botrytis cinerea* response against *Trichoderma atroviride*. iScience 28, 111783. https://doi.org/10.1016/j.isci.2025.111783.

Olivares-Yanez, C., Sanchez, E., Perez-Lara, G., Seguel, A., Camejo, P.Y., Larrondo, L.F., Vidal, E.A., Canessa, P., 2021. A comprehensive transcription factor and DNA-binding motif resource for the construction of gene regulatory networks in *Botrytis cinerea* and *Trichoderma atroviride*. Comput. Struct. Biotechnol. J. 19, 6212–6228. https://doi.org/10.1016/j.csbj.2021.11.012.

Opulente, D.A., LaBella, A.L., Harrison, M.-C., Wolters, J.F., Liu, C., Li, Y., Kominek, J., Steenwyk, J.L., Stoneman, H.R., VanDenAvond, J., Miller, C.R., Langdon, Q.K., Silva, M., Gonçalves, C., Ubbelohde, E.J., Li, Y., Buh, K.V., Jarzyna, M., Haase, M.A. B., Rosa, C.A., Čcadež, N., Libkind, D., DeVirgilio, J.H., Hulfachor, A.B., Kurtzman, C.P., Sampaio, J.P., Gonçalves, P., Zhou, X., Shen, X.-X., Groenewald, M., Rokas, A., Hittinger, C.T., 2024. Genomic factors shape carbon and nitrogen metabolic niche breadth across Saccharomycotina yeasts. Science 384, eadj4503. https://doi.org/10.1126/science.adj4503.

Pedrini, N., 2018. Molecular interactions between entomopathogenic fungi (Hypocreales) and their insect host: perspectives from stressful cuticle and hemolymph battlefields and the potential of dual RNA sequencing for future studies. Fungal Biol. 122, 538–545. https://doi.org/10.1016/j.funbio.2017.10.003.

Perez-Arques, C., Navarro-Mendoza, M.I., Xu, Z., Walther, G., Heitman, J., 2024. RNAi epimutations conferring antifungal drug resistance are inheritable. bioRxiv. https://doi.org/10.1101/2024.10.15.618540.

Petrucci, A., Vicente, I., Cesarini, M., Susca, A., Sarrocco, S., Vannacci, G., 2025. *Fusarium graminearum* regulates kp4l genes, encoding killer toxins, during competitive interaction with other plant pathogenic *Fusarium* species. Fungal Biol. 129, 101569. https://doi.org/10.1016/j.funbio.2025.101569.

Pimentel, F.S.A., Machado, C.M., De-Souza, E.A., Fernandes, C.M., De-Queiroz, A.L.F.V., Silva, G.F.S., Del Poeta, M., Montero-Lomeli, M., Masuda, C.A., 2022. Sphingolipid depletion suppresses UPR activation and promotes galactose hypersensitivity in yeast models of classic galactosemia. Biochim Biophys Acta Mol Basis Dis 1863, 1403–1409. https://doi.org/10.1016/j.bbadis.2017.02.014.

Rangel, D.E.N., 2011. Stress induced cross-protection against environmental challenges on prokaryotic and eukaryotic microbes. World J. Microbiol. Biotechnol. 27, 1281–1296. https://doi.org/10.1007/s11274-010-0584-3.

Rangel, D.E.N., 2024. How *Metarhizium robertsii*'s mycelial consciousness gets its conidia Zen-ready for stress. In: Rangel, D.E.N. (Ed.), Advances in Applied Microbiology. Academic Press, London, pp. 1–33.

Rangel, D.E.N., Alder-Rangel, A., 2020. History of the international symposium on fungal stress – ISFUS, a dream come true. Fungal Biol. 124, 525–535. https://doi.org/10.1016/j.funbio.2020.02.004.

Rangel, D.E.N., Alder-Rangel, A., Dadachova, E., Finlay, R.D., Dijksterhuis, J., Braga, G. Ú.L., Corrochano, L.M., Hallsworth, J.E., 2015a. The international symposium on fungal stress: ISFUS. Curr. Genom. 61, 479–487. https://doi.org/10.1007/s00294-015-0501-2.

Rangel, D.E.N., Alder-Rangel, A., Dadachova, E., Finlay, R.D., Kupiec, M., Dijksterhuis, J., Braga, G.Ú.L., Corrochano, L.M., Hallsworth, J.E., 2015b. Fungal stress biology: a preface to the Fungal Stress Responses special edition. Curr. Genom. 61, 231–238. https://doi.org/10.1007/s00294-015-0500-3.

Rangel, D.E.N., Anderson, A.J., Roberts, D.W., 2008. Evaluating physical and nutritional stress during mycelial growth as inducers of tolerance to heat and UV-B radiation in *Metarhizium anisopliae* conidia. Mycol. Res. 112, 1362–1372. https://doi.org/10.1016/j.mycres.2008.04.013.

Rangel, D.E.N., Braga, G.Ú.L., Fernandes, É.K.K., Keyser, C.A., Hallsworth, J.E., Roberts, D.W., 2015c. Stress tolerance and virulence of insect-pathogenic fungi are determined by environmental conditions during conidial formation. Curr. Genom. 61, 383–404. https://doi.org/10.1007/s00294-015-0477-y.

Rangel, D.E.N., Braga, G.Ú.L., Flint, S.D., Anderson, A.J., Roberts, D.W., 2004. Variations in UV-B tolerance and germination speed of *Metarhizium anisopliae* conidia produced on artificial and natural substrates. J. Invertebr. Pathol. 87, 77–83. https://doi.org/10.1016/j.jip.2004.06.007.

Rangel, D.E.N., Fernandes, E.K.K., Anderson, A.J., Roberts, D.W., 2012. Culture of *Metarhizium robertsii* on salicylic-acid supplemented medium induces increased conidial thermotolerance. Fungal Biol. 116, 438–442.

Rangel, D.E.N., Finlay, R.D., Hallsworth, J.E., Dadachova, E., Gadd, G.M., 2018. Fungal strategies for dealing with environmental and agricultural stress. Fungal Biol. 122, 602–612. https://doi.org/10.1016/j.funbio.2018.02.002.

Ristow, LC, Jezewski, AJ, Chadwick, BJ, Stamnes, MA, Lin, X, Krysan, DJ, 2023. *Cryptococcus neoformans* adapts to the host environment through TOR-mediated remodeling of phospholipid asymmetry. Nature Communications 14 (1), 6587. https://doi.org/10.1038/s41467-023-42318-y. Epub 20231018.

Reyes, E.Y., Shinohara, M.L., 2022. Host immune responses in the central nervous system during fungal infections. Immunol. Rev. 311, 50–74. https://doi.org/10.1111/imr.13101.

Sarkar, A., Rangel, D.E.N., Osherov, N., 2025. Leading developments in basic research on aspergillosis and mucormycosis. Fungal Biol., 101574 https://doi.org/10.1016/j.funbio.2025.101574.

Sasse, C., Bastakis, E., Bakti, F., Höfer, A.M., Zangl, I., Schüller, C., Köhler, A.M., Gerke, J., Krappmann, S., Finkernagel, F., Harting, R., Strauss, J., Heimel, K., Braus, G.H., 2023. Induction of *Aspergillus fumigatus* zinc cluster transcription factor OdrA/Mdu2 provides combined cellular responses for oxidative stress protection and

multiple antifungal drug resistance. mBio 14, e0262802623. https://doi.org/10.1128/mbio.02628-23.
Scheffold, A., Bacher, P., LeibundGut-Landmann, S., 2020. T cell immunity to commensal fungi. Curr. Opin. Microbiol. 58, 116–123. https://doi.org/10.1016/j.mib.2020.09.008.
Schumacher, D.I., Lutkenhaus, R., Altegoer, F., Teichert, I., Kuck, U., Nowrousian, M., 2018. The transcription factor PRO44 and the histone chaperone ASF1 regulate distinct aspects of multicellular development in the filamentous fungus *Sordaria macrospora*. BMC Genet. 19, 112. https://doi.org/10.1186/s12863-018-0702-z.
Shade, A., 2023. Microbiome rescue: directing resilience of environmental microbial communities. Curr. Opin. Microbiol. 72, 102263. https://doi.org/10.1016/j.mib.2022.102263.
Siebe, P., Mark, F., Alexander, L., Michael, S.A., Susanne, Z., 2025. Revealing robust antioxidant defences of a mycoparasitic *Trichoderma* species. Fungal Biol. 129, 101549. https://doi.org/10.1016/j.funbio.2025.101549.
Silva, N.M.D., Reis, G.F., Costa, F.F., Grisolia, M.E., Geraldo, M.R., Lustosa, B.P.R., Lima, B., Weiss, V.A., de Souza, E.M., Li, R., Song, Y., Nascimento, M.M.F., Robl, D., Gomes, R.R., de Hoog, G.S., Vicente, V.A., 2023. Genome sequencing of *Cladophialophora exuberans*, a novel candidate for bioremediation of hydrocarbon and heavy metal polluted habitats. Fungal Biol. 127, 1032–1042. https://doi.org/10.1016/j.funbio.2023.03.003.
Stempinski, P.R., Ramos Irizarry, P., McConnell, S.A., Liporagi Lopes, L.C., Rodrigues Dos Santos Júnior, S., Wear, M.P., Casadevall, A., 2025. A *Cryptococcus neoformans* polysaccharide conjugate vaccine made with filtered polysaccharide elicits protective immunity in mice. Fungal Biol. 129, 101544. https://doi.org/10.1016/j.funbio.2025.101544.
Tariq, D., Maurici, N., Bartholomai, B.M., Chandrasekaran, S., Dunlap, J.C., Bah, A., Crane, B.R., 2024. Phosphorylation, disorder, and phase separation govern the behavior of Frequency in the fungal circadian clock. Elife 12. https://doi.org/10.7554/eLife.90259.
Thammahong, A., Puttikamonkul, S., Perfect, J.R., Brennan, R.G., Cramer, R.A., 2017. Central role of the trehalose biosynthesis pathway in the pathogenesis of human fungal infections: Opportunities and challenges for therapeutic development. Microbiol. Mol. Biol. Rev. 81. https://doi.org/10.1128/MMBR.00053-16.
Varland S, Duarte Silva R, Kjosås I, Faustino A, Bogaert A, Billmann M, Boukhatmi H, Kellen B, Costanzo M, Drazic A, Osberg C, Chan K, Zhang X, Tong AHY, Andreazza S, Lee JJ, Nedyalkova L, Ušaj M, Whitworth, AJ, Andrews BJ, Moffat J, Myers CL, Gevaert K, Boone C, Gonçalo Martinho R, Arnesen T (2023). N-terminal acetylation shields proteins from degradation and promotes age-dependent motility and longevity. *Nature Commun*.Oct 27;14(1):6774.doi: 10.1038/s41467-023-42342-y.
Vega, F.E., Goettel, M.S., Blackwell, M., Chandler, D., Jackson, M.A., Keller, S., Koike, M., Maniania, N.K., Monzon, A., Ownley, B.H., Pell, J.K., Rangel, D.E.N., 2009. Fungal entomopathogens: new insights on their ecology. Fungal Ecol. 2, 149–159.
Vicente, I., Quaratiello, G., Baroncelli, R., Vannacci, G., Sarrocco, S., 2022. Insights on KP4 killer toxin-like proteins of *Fusarium* species in interspecific interactions. J. Fungi. 8. https://doi.org/10.3390/jof8090968.
Wang, Y., Wear, M., Kohli, G., Vij, R., Giamberardino, C., Shah, A., Toffaletti, D.L., Yu, C. A., Perfect, J.R., Casadevall, A., Xue, C., 2021. Inositol metabolism regulates capsule structure and virulence in the human pathogen *Cryptococcus neoformans*. mBio 12, e0279021. https://doi.org/10.1128/mBio.02790-21.
Washington, E.J., Zhou, Y., Hsu, A.L., Petrovich, M., Tenor, J.L., Toffaletti, D.L., Guan, Z., Perfect, J.R., Borgnia, M.J., Bartesaghi, A., Brennan, R.G., 2024. Structures of trehalose-6-phosphate synthase, Tps1, from the fungal pathogen *Cryptococcus neoformans*: A target for antifungals. Proc Natl Acad Sci U S A 121. https://doi.org/10.1073/pnas.2314087121 e2314087121. 202314087 [pii].
Xue, C., Tada, Y., Dong, X., Heitman, J., 2007. The human fungal pathogen *Cryptococcus* can complete its sexual cycle during a pathogenic association with plants. Cell Host Microbe 1, 263–273. https://doi.org/10.1016/j.chom.2007.05.005.
Yuan, B., Wang, W.-B., Wang, X.-Q., Liu, C.-G., Hasunuma, T., Kondo, A., Zhao, X.-Q., 2024. The chromatin remodeler Ino80 regulates yeast stress tolerance and cell metabolism through modulating nitrogen catabolite repression. Int. J. Biol. Macromol. 258, 129041. https://doi.org/10.1016/j.ijbiomac.2023.129041.
Zapparata, A., Baroncelli, R., Brandström Durling, M., Kubicek, C.P., Karlsson, M., Vannacci, G., Sarrocco, S., 2021. Fungal cross-talk: an integrated approach to study distance communication. Fungal Genet. Biol. 148, 103518. https://doi.org/10.1016/j.fgb.2021.103518.
Zeng, D.W., Yang, Y.Q., Wang, Q., Zhang, F.L., Zhang, M.D., Liao, S., Liu, Z.Q., Fan, Y.C., Liu, C.G., Zhang, L., Zhao, X.Q., 2024. Transcriptome analysis of *Kluyveromyces marxianus* under succinic acid stress and development of robust strains. Appl. Microbiol. Biotechnol. 108, 293. https://doi.org/10.1007/s00253-024-13097-3.
Zhang, M.-M., Yuan, B., Li, Y.-Z., Wang, X.-L., Champreda, V., Rangel, D.E.N., Zhao, X.-Q., 2025. Differential global gene transcription of Saccharomyces cerevisiae by zinc sulfate addition under acetic acid stress and identification of novel zinc and stress-responsive genes related to cell wall function. Fungal Biol., 101573 https://doi.org/10.1016/j.funbio.2025.101573.
Zhang, M.M., Yuan, B., Wang, Y.T., Zhang, F.L., Liu, C.G., Zhao, X.Q., 2024. Differential protein expression in Set5p-mediated acetic acid stress response and novel targets for engineering yeast stress tolerance. J. Proteome Res. 23, 2986–2998. https://doi.org/10.1021/acs.jproteome.3c00617.
Zhu, G., Chen, S., Zhang, Y., Lu, L., 2023. Mitochondrial membrane-associated protein Mba1 confers antifungal resistance by affecting the production of reactive oxygen species in *Aspergillus fumigatus*. Antimicrob. Agents Chemother. 67, e0022523, 00225-23 [pii]aac.00225-23 [pii].
Zhu, G., Fu, M., Zhang, Y., Lu, L., 2024. A ubiquitin-mediated post-translational degradation of Cyp51A contributes to a novel azole resistance mode in *Aspergillus fumigatus*. Microbiol. Res. 289, 127891. https://doi.org/10.1016/j.micres.2024.127891.