Yeast

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http://www.uwo.ca/biology/YeastNewsletter/Index.html

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Recent publications.

1 Jetha P, Mojzita D, Maiorova N, de Ruijter JC, Maaheimo H, Hilditch S, Peddinti G, Castillo S, Toivari M, Penttilä M, Molnár I. 2025. Discovery of *Cortinarius* O-methyltransferases for the heterologous production of dermolutein and physcion. Biotechnol Biofuels Bioprod 18:25 - DOI: 10.1186/s13068-025-02625-6

2 Huang Y, Zhong W, Varga KE, Benkő Zs, Pócsi I, Yang C, Molnár I. 2025. Promoting the glycosylation of drug-like natural products in a *Saccharomyces cerevisiae* chassis by deleting endogenous glycosidases. Bioresource Technol 422: 132258 - DOI: 10.1016/j.biortech.2025.132258

3 Krogerus K, Rettberg N. 2025. Creating better brewing yeast with the 1011 yeast genomes data sets. Yeast 42:5-15 - DOI: 10.1002/yea.3990

4 Flores J, König S, Hutzler M, Kunz O, Krogerus K, Lehnhardt F, Magalhães F, Svedlund N, Grijalva-Vallejos N, Gibson B. 2025. Genetic pre-adaptations in *Saccharomyces cerevisiae* Andean chicha isolates facilitate industrial brewery application. Food Microbiol - DOI: 10.1016/j.fm.2025.104815.

II Laboratory of Genetics, Wisconsin Energy Institute, DOE Great Lakes Bioenergy Research Center, Center for Genomic Science Innovation, J. F. Crow Institute for the Study of Evolution, University of Wisconsin, Madison, WI 53726, USA. Communicated by Chris Todd Hittinger <cthittinger@wisc.edu>.

I am pleased to announce that Madison, WI, USA, was chosen by the International Commission on Yeasts to host the International Congress on Yeasts in 2028! We hope to see you there. Details will follow.

Recent publications.

1 Harrison MC, Rinker DC, LaBella AL, Opulente DA, Wolters JF, Zhou X, Shen XX, Groenewald M, Hittinger CT, Rokas A. 2025. Machine learning identifies novel signatures of antifungal drug resistance in *Saccharomycotina* yeasts. bioRxiv - https://doi.org/10.1101/2025.05.09.653161.

Antifungal drug resistance is a major challenge in fungal infection management. Numerous genomic changes are known to contribute to acquired drug resistance in clinical isolates of specific pathogens, but whether they broadly explain natural resistance across entire lineages is unknown. We leveraged genomic, ecological, and phenotypic trait data from naturally sampled strains from nearly all known species in subphylum Saccharomycotina to examine the evolution of resistance to eight antifungal drugs. The phylogenetic distribution of drug resistance varied by drug; fluconazole resistance was widespread, while 5-fluorocytosine resistance was rare, except in Lipomycetales. A random forest algorithm trained on genomic data predicted drug-resistant yeasts with 54-75% accuracy. In general, frequency of drug resistance correlated with prediction accuracy, with fluconazole resistance being consistently predicted with the highest accuracy (74.9%). Fluconazole resistance accuracy was similar between models trained on genome-wide variation in the presence and number of InterPro protein annotations across Saccharomycotina (74.9% accuracy) and those trained on amino acid sequence alignment data of Erg11, a protein known to be involved in fluconazole resistance (74.3-74.9% accuracy). Interestingly, the top Erg11 residues for predicting fluconazole resistance across Saccharomycotina do not overlap with, are not spatially close to, and are less conserved than those previously linked to resistance in clinical isolates of *Candida albicans*. In silico deep mutational scanning of the *C. albicans* Erg11 protein revealed that amino acid variants implicated in clinical cases of resistance are almost universally destabilizing while variants in our most informative residues are energetically more neutral, explaining why the latter are much more common than the former in natural populations. Importantly, previous experimental analyses of *C. albicans* Erg11 have shown that amino acid variation in our most informative residues, despite having never been directly implicated in clinical cases, can directly contribute to resistance. Our results suggest that studies of natural resistance in yeast species never encountered in the clinic will yield a fuller understanding of antifungal drug resistance.

2 Haase MAB, Lazar-Stefanita L, Baudry L, Wudzinska A, Zhou X, Rokas A, Hittinger CT, Musacchio A, Boeke JD. 2025. Ancient co-option of LTR retrotransposons as yeast centromeres. bioRxiv - https://doi.org/10.1101/2025.04.25.647736.

The evolutionary origins of the genetic point centromere in the brewer's yeast *Saccharomyces cerevisiae*, a member of the order Saccharomycetales, are still unknown. Competing hypotheses suggest that the point centromere tripartite genetic centromere DNA elements (CDEs) either evolved from ancestral epigenetic centromeres by descent with modification or were gained through horizontal transfer from selfish DNA plasmids. Here, we identified centromeres in the sister order Saccharomycodales and termed them "proto-point centromeres" due to sequence features that bridge the evolutionary gap between point centromeres and ancestral centromeres types. Comparative genomic analyses across multiple yeast orders showed an unexpected evolutionary link between point and proto-point centromeres to the long terminal repeats (LTRs) of Ty5 retrotransposons. Strikingly, one Saccharomycodales species, *Saccharomycodes ludwigii*, harbors compact Ty5-based centromeres, where its CDEII elements are divergent AT-rich Ty5 LTRs. These living fossil centromeres show how retrotransposon cis-regulation was likely co-opted for genetic centromere specification. These insights show that point centromeres are direct descendants of retrotransposons and have evolved by descent with modification. Ultimately, the many diverse centromere types across the yeast subphylum may share a common ancestry rooted in retrotransposon activity.

3 Gonçalves C, Steenwyk JL, Rinker DC, Opulente DA, LaBella AL, Harrison MC, Wolters JF, Zhou X, Shen XX, Covo S, Groenewald M, Hittinger CT, Rokas A. 2025. Stable hypermutators revealed by the genomic landscape of DNA repair genes among yeast species. bioRxiv - https://doi.org/10.1101/2025.03.15.643480.

Mutator phenotypes are short-lived due to the rapid accumulation of deleterious mutations. Yet, recent observations reveal that certain fungi can undergo prolonged accelerated evolution after losing DNA repair genes. Here, we surveyed 1,154 yeast genomes representing nearly all known yeast species of the subphylum Saccharomycotina to examine the relationship between reduced DNA repair repertoires and elevated evolutionary rates. We identified three distantly related lineages—encompassing 12% of species—with substantially reduced sets of DNA repair genes and the highest evolutionary rates in the entire subphylum. Two of these "faster-evolving lineages" (FELs) — a subclade within the order Pichiales and the *Wickerhamiella/Starmerella* (W/S) clade (order Dipodascales) — are described here for the first time, while the third corresponds to a previously documented *Hanseniaspora* FEL. Examination of DNA repair gene repertoires revealed a set of genes predominantly absent in these three FELs, suggesting a potential role in the observed acceleration of evolutionary rates. Genomic signatures in the W/S clade are consistent with a substantial mutational burden, including pronounced A|T bias and signatures of endogenous DNA damage. The W/S clade appears to mitigate UV-induced damage through horizontal acquisition of a bacterial photolyase gene, underscoring how gene loss may be offset by nonvertical evolution. These findings highlight how the loss of DNA repair genes gave rise to hypermutators that persist across macroevolutionary timescales, with horizontal gene transfer as an avenue for partial functional compensation.

4 Lee S, West C, Opulente DA, Harrison MC, Wolters JF, Shen XX, Zhou X, Groenewald M, Hittinger CT, Rokas A, LaBella AL. 2025. Genomic factors limiting the diversity of Saccharomycotina plant pathogens. bioRxiv - https://doi.org/10.1101/2025.02.27.640420.

The Saccharomycotina fungi have evolved to inhabit a vast diversity of habitats over their 400-million-year evolution. There are, however, only a few known fungal pathogens of plants in this subphylum, primarily belonging to the genera *Eremothecium* and *Geotrichum*. We compared the genomes of 12 plant-pathogenic Saccharomycotina strains to 360 plant-associated strains to identify features unique to the phytopathogens. Characterization of the oxylipin synthesis genes, a compound believed to be involved in *Eremothecium* pathogenicity, did not reveal any differences in gene presence within or between the plant-pathogenic and plant-associated strains. A reverse-ecological approach, however, revealed that plant pathogens lack several metabolic enzymes known to assist other phytopathogens in overcoming plant defenses. This includes L-rhamnose metabolism, formamidase and nitrilase genes. This result suggests that the Saccharomycotina plant pathogens are limited to infecting ripening fruits as they are without the necessary enzymes to degrade common phytohormones and secondary metabolites produced by plants.

5 Aranguiz K, Horianopoulos LC, Elkin L, Abá KS, Jordahl D, Overmyer KA, Wrobel RL, Coon JJ, Shiu SH, Rokas A, Hittinger CT. 2025. Machine learning reveals genes impacting oxidative stress resistance across yeasts. Nat Commun in press - https://doi.org/10.1101/2024.08.14.607963.

Reactive oxygen species (ROS) are highly reactive molecules encountered by yeasts during routine metabolism and during interactions with other organisms, including host infection. Here, we characterized the variation in resistance to ROS across the ancient yeast subphylum Saccharomycotina and used machine learning (ML) to identify gene families whose sizes were predictive of ROS resistance. The most predictive features were enriched in gene families related to cell wall organization and included two reductase gene families. We estimated the quantitative contributions of features to each species' classification to guide experimental validation and showed that overexpression of the old yellow enzyme (OYE) reductase increased ROS resistance in *Kluyveromyces lactis*, while Saccharomyces cerevisiae mutants lacking multiple mannosyltransferase-encoding genes were hypersensitive to ROS. Altogether, this work provides a framework for how ML can uncover genetic mechanisms underlying trait variation across diverse species and inform trait manipulation for clinical and biotechnological applications.

6 David KT, Schraiber JG, Crandall JG, Labella AL, Opulente DA, Harrison MC, Wolters JF, Zhou X, Shen XX, Groenewald M, Hittinger CT, Pennell M, Rokas A. 2025. Convergent expansions of keystone gene families drive metabolic innovation in a major eukaryotic clade. Proc Natl Acad Sci USA in press - https://doi.org/10.1101/2024.07.22.604484.

Many remarkable innovations have repeatedly occurred across vast evolutionary distances. When convergent traits emerge on the tree of life, they are sometimes driven by the same underlying gene families, while other times many different gene families are involved. Conversely, a gene family may be repeatedly recruited for a single trait or many different traits. To understand the general rules governing convergence at both genomic and phenotypic levels, we systematically tested associations between 56 binary metabolic traits and gene count in 14,710 gene families from 993 species of Saccharomycotina yeasts. Using a recently developed phylogenetic approach that reduces spurious correlations, we discovered that gene family expansion and contraction was significantly linked to trait gain and loss in 45/56 (80%) of traits. While 601/746 (81%) of significant gene families were associated with only one trait, we also identified several 'keystone' gene families that were significantly associated with up to 13/56 (23%) of all traits. These results indicate that metabolic innovations in yeasts are governed by a narrow set of major genetic elements and mechanisms.

7 Feng B, Li Y, Liu H, Steenwyk JL, David KT, Tian X, Xu B, Gonçalves C, Opulente DA, LaBella AL, Harrison MC, Wolters JF, Shao S, Chen Z, Fisher KJ, Groenewald M, Hittinger CT, Shen XX, Rokas A, Zhou X, Li Y. 2025. Unique trajectory of gene family evolution from genomic analysis of nearly all known species in an ancient yeast lineage. Mol Syst Biol in press - https://doi.org/10.1101/2024.06.05.597512.

Gene gains and losses are a major driver of genome evolution; their precise characterization can provide insights into the origin and diversification of major lineages. Here, we examined gene family evolution of 1,154 genomes from nearly all known species in the medically and technologically important yeast subphylum Saccharomycotina. We found that yeast gene family and genome evolution are distinct from plants, animals, and filamentous ascomycetes and are characterized by small genome sizes and smaller gene numbers but larger gene family sizes. Faster-evolving lineages (FELs) in yeasts experienced significantly higher rates of gene losses — commensurate with a narrowing of metabolic niche breadth — but higher speciation rates than their slower-evolving sister lineages (SELs). Gene families most often lost are those involved in mRNA splicing, carbohydrate metabolism, and cell division and are likely associated with intron loss, metabolic breadth, and non-canonical cell cycle processes. Our results highlight the significant role of gene family contractions in the evolution of yeast metabolism, genome function, and speciation, and suggest that gene family evolutionary trajectories have differed markedly across major eukaryotic lineages.

8 Barten LM, Crandall JG, Xie D, Serate J, Handowski E, Jen A, Overmyer KA, Coon JJ, Hittinger CT, Landick R, Zhang Y, Sato TK. 2025. pH adjustment increases biofuel production from inhibitory switchgrass hydrolysates. Bioresour Technol epub - https://doi.org/10.1016/j.biortech.2025.132651.

Biofuels derived from renewable and sustainable lignocellulosic biomass, such as switchgrass, offer a promising means to limit greenhouse gas emissions. However, switchgrass grown under drought conditions contains high levels of chemical compounds that inhibit microbial conversion to biofuels. Fermentation of drought switchgrass hydrolysates by engineered *Saccharomyces cerevisiae* and *Zymomonas mobilis* results in lower ethanol production than does fermentation of hydrolyzed switchgrass from a typical rainfall year. Here, it is demonstrated that this inhibitory effect can be alleviated by altering the pH of drought switchgrass hydrolysates produced by two different pretreatment methods: Ammonia Fiber Expansion (AFEX) and Soaking in Aqueous Ammonia (SAA). Fermentation rates and biofuel production by *Saccharomyces cerevisiae* and *Zymomonas mobilis* were higher at pH 5.8 than at pH 5.0 from all feedstock years and following both pretreatment methods. SAA pretreatment of drought switchgrass furthermore enabled increased fermentation rates and biofuel titers compared to AFEX pretreatment. A synthetic mimic of switchgrass hydrolysate was developed and identified relief from pH-dependent inhibition by lignocellulose-derived inhibitors as the cause of increased biofuel production above a pH of 5.0. These results demonstrate that SAA pretreatment and pH adjustment can significantly improve fermentation and biofuel production from inhibitory feedstocks by industrial microorganisms.

9 Alvarenga FBM, Barros KO, Batista TM, Souza GFL, Santos ARO, Abegg MA, Sato TK, Hittinger CT, Lachance MA, Rosa CA. 2025. *Vanderwaltozyma urihicola* sp. nov., a yeast species isolated from rotting wood and beetles in a Brazilian Amazonian rainforest biome. Int J Syst Evol Microbiol **75**:006718 - https://doi.org/10.1099/ijsem.0.006718

Five yeast isolates belonging to a candidate for novel species were obtained from rotting wood and the gut of a passalid beetle larva in a site of Amazonian rainforest biome in Brazil. Sequence analysis of the Internal Transcribed Spacer (ITS)-5.8S region and the D1/D2 domains of the large subunit rRNA gene showed that the isolates represent a novel species of the genus *Vanderwaltozyma*. The closest relative of the novel species is *Vanderwaltozyma huisunica*. These species differs due to 44 nt substitutions and 21 indels in the sequences of the ITS region, as well as by 15 substitutions and four indels in the sequences of the D1/D2 domains. A phylogenomic analysis of the *Vanderwaltozyma* species with genomes sequenced showed that this novel species is an outgroup to the other species of this genus. We propose the name *Vanderwaltozyma urihicola* sp. nov. (CBS 18107^{T}, MycoBank MB 856975) to accommodate these isolates. The species is homothallic, producing one to two ascospores per ascus. The habitat of *V. urihicola* is rotting wood in the Brazilian Amazonian rainforest biome.

10 Crandall JG, Zhou X, Rokas A, Hittinger CT. Specialization restricts the evolutionary paths available to yeast sugar transporters. Mol Biol Evol 41:msae228 - https://doi.org/10.1093/molbev/msae228

Functional innovation at the protein level is a key source of evolutionary novelties. The constraints on functional innovations are likely to be highly specific in different proteins, which are shaped by their unique histories and the extent of global epistasis that arises from their structures and biochemistries. These contextual nuances in the sequence-function relationship have implications both for a basic understanding of the evolutionary process and for engineering proteins with desirable properties. Here, we have investigated the molecular basis of novel function in a model member of an ancient, conserved, and biotechnologically relevant protein family. These Major Facilitator Superfamily sugar porters are a functionally diverse group of proteins that are thought to be highly plastic and evolvable. By dissecting a recent evolutionary innovation in an α-glucoside transporter from the yeast *Saccharomyces eubayanus*, we show that the ability to transport a novel substrate requires high-order interactions between many protein regions and numerous specific residues proximal to the transport channel. To reconcile the functional diversity of this family with the constrained evolution of this model protein, we generated new, state-of-the-art genome annotations for 332 Saccharomycotina yeast species spanning approximately 400 million years of evolution. By integrating phylogenetic and phenotypic analyses across these species, we show that the model yeast α-glucoside transporters likely evolved from a multifunctional ancestor and became subfunctionalized. The accumulation of additive and epistatic substitutions likely entrenched this subfunction, which made the simultaneous acquisition of multiple interacting substitutions the only reasonably accessible path to novelty.

11 Alder-Rangel A, Rangel AEA, Casadevall A, Gusa A, Xue C, Boone CM, Hittinger CT, Masuda CA, Olivares- Yañez C, Bell-Pedersen D, Washington EJ, Braus G, Janbon G, Pócsi I, Stajich JE, Dunlap JC, Bennett JW, Heitman J, Lu L, Landi L, Shinohara ML, Del Poeta M, Acheampong MA, Maltz MR, Lorenz MC, Nowrousian M, Glass NL, Broderick NA, Pedrini N, Osherov N, Billmyre RB, Sarrocco S, LeibundGut-Landmann S, Vicente VA, Lin X, Zhao XQ, Bahn YS, Lewis ZA, Rangel DEN. 2025. Celebrating the fifth edition of the International Symposium on Fungal Stress – ISFUS, a decade after its 2014 debut. Fungal Biol epub - https://doi.org/10.1016/j.funbio.2025.101590.

The Fifth International Symposium on Fungal Stress 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.

12 Clark NL, Hittinger CT, Li-Brarlay H, Rokas A, Sackton TB, Unckless RL. 2025. Integrating intermediate traits in phylogenetic genotype-to-phenotype studies. Integr Comp Biol epub - https://doi.org/10.1093/icb/icaf037.

A major goal of research in evolution and genetics is linking genotype to phenotype. This work could be direct, such as determining the genetic basis of a phenotype by leveraging genetic variation or divergence in a developmental, physiological, or behavioral trait. The work could also involve studying the evolutionary phenomena (e.g., reproductive isolation, adaptation, sexual dimorphism, behavior) that reveal an indirect link between genotype and a trait of interest. When the phenotype diverges across evolutionarily distinct lineages, this genotype-to-phenotype problem can be addressed using phylogenetic genotype-to-phenotype (PhyloG2P) mapping, which uses genetic signatures and convergent phenotypes on a phylogeny to infer the genetic bases of traits. The PhyloG2P approach has proven powerful in revealing key genetic changes associated with diverse traits, including the mammalian transition to marine environments and transitions between major mechanisms of photosynthesis. However, there are several intermediate traits layered in between genotype and the phenotype of interest, including but not limited to transcriptional profiles, chromatin states, protein abundances, structures, modifications, metabolites, and physiological parameters. Each intermediate trait is interesting and informative in its own right, but synthesis across data types has great promise for providing a deep, integrated, and predictive understanding of how genotypes drive phenotypic differences and convergence. We argue that an expanded PhyloG2P framework (the PhyloG2P matrix) that explicitly considers intermediate traits, and imputes those that are prohibitive to obtain, will allow a better mechanistic understanding of any trait of interest. This approach provides a proxy for functional validation and mechanistic understanding in organisms where laboratory manipulation is impractical.

III State Scientific-Research Institute for Genetics and Selection of Industrial Microorganisms (GosNIIgenetika), NRC "Kurchatov Institute", I-Dorozhnyi 1, Moscow 117545, Russia. Communicated by E.S. Naumova <lena_naumova@yahoo.com>.

The following are papers for 2024 and 2025 or in press.

1 Borovkova AN, Shalamitskiy MYu, Naumova ES. 2024. Comparative genetic analysis of pectinase genes *PGU* of the yeast *Saccharomyces cerevisiae*: selection of strains with high pectinolytic activity. Biotechnologiya 40 (5): 35–44 (in Russian).

2 Tuaeva AYu, Ponomareva AM, Melkina OE, Naumova ES. 2025. Dairy yeast *Kluyveromyces marxianus*: molecular polymorphism and dynamics of lactose fermentation. Biotechnologiya 41(3) (in press) (in Russian).

Using RAPD-PCR we studied a genetic relatedness of 57 *Kluyveromyces marxianus* strains isolated from various industrial and artisanal dairy products. The strains studied was found to differ significantly in the

dynamics of hydrolysis of 5% lactose. Based on the results of HPLC analysis. seven strains were selected that most intensively ferment lactose and are of interest for further molecular genetic studies and selection of dairy yeasts for their practical application.

3 Borokova AN, Tuaeva AYu, Naumova ES. 2025. Intraspecific polymorphism of *Saccharomyces paradoxus* yeasts: geographical populations. Microbiology (Moscow) 94 (5): (in press).

In the Siberian Botanical Garden of Tomsk State University, 28 strains of *Saccharomyces* yeasts were isolated from the bark of *Quercus robur* and the soil beneath them. Based on the sequencing of the D1/D2 domain and the ITS1 region of rDNA, three strains were assigned to the species *S. cerevisiae*, and the rest to the species *S. paradoxus*. Using multigene phylogenetic analysis of nuclear genes (*NEJ*1, *EST*2, *HDF*1, *HDF*2), the genetic relationship of West Siberian strains of *S. paradoxus* with European, Far Eastern, North American and Hawaiian populations was studied. According to the results obtained, the West Siberian strains belong to the European population. Apparently, the border between the European and Far Eastern populations of *S. paradoxus* lies east of Tomsk Oblast.

IV Abertay University Yeast Research Group, Dundee, Scotland. Communicated by Graeme Walker <gwalkerconsultancy@gmail.com>.

I have recently retired from Abertay University after 37 years and am now Emeritus Professor of Zymology. Please note my new email above.

The following is the abstract of a presentation given at the Chartered Institute of Brewers & Distillers Convention (Hobart, Tasmania, March 2025).

1 Walker G. 2025. Non-*Saccharomyces* yeasts for distilled spirit fermentations

Yeast species of the *Saccharomyces* genus represent the predominant microorganisms exploited for industrial fermentations worldwide. However, *Saccharomyces cerevisiae* is only one of around 2500 yeast species that have to date been isolated and characterised, and there is a vast untapped gene pool within biodiverse yeasts. This presentation firstly provides a brief overview of so-called non-conventional yeasts (eg. *Schizosaccharomyces* pombe, *Kluyveromyces marxianus*, *Torulaspora delbrueckii*, *Dekkera bruxellensis*, and selected other species) for brewing and distilling applications. Some of these yeast species are often unwanted contaminants in industrial fermentations, but some can provide some interesting and desired flavour attributes in beverages. In Scotland the regulations for Scotch whisky only state the use of "yeast" (*Saccharomyces cerevisiae* is not specified), so this opens up the potential for wide yeast biodiversity to be exploited in traditional malt whisky fermentations. We have researched several non-*Saccharomyces* species for malt whisky fermentations and results presented highlight the potential of selected yeast strains for flavour elaboration in malt-based spirits.

Collaborative work with the Scotch Whisky Research Institute and Lallemand Biofuels & Distilled Spirits is gratefully acknowledged.

V Department of Biological, Chemical, and Environmental Sciences, Wheaton College, Norton, Massachusetts, USA. Communicated by Primrose Boynton <boynton_primrose@wheatoncollege.edu>.

Recent publication.

1 Unni R, Kavlak OE, Stukenbrock EH, Boynton PJ. 2025. Fitness effects of killer virus infection on wild *Saccharomyces paradoxus*. Fungal Ecology 75:101418.

Endosymbioses have profound impacts on eukaryotic organisms. However, symbiont effects on host fitness in natural conditions are difficult to study, especially for microbial hosts. We used killer viruses (intracellular satellite viruses that cause host cells to produce antifungal toxins) and the wild yeast *Saccharomyces paradoxus* to study a symbiont's effect on its host's fitness in oak litter. We cured hosts of naturally-occurring killer viruses and compared killer and cured individuals' fitnesses in laboratory medium

and oak litter using a unique field chamber design. In the laboratory, the impact of virus loss on host fitness could be positive, negative, or neutral, depending on host identity. Trends in the forest were similar to those in the lab, although only overall strain fitness differences were significant and curing impacts differed between the forest and laboratory. These results demonstrate the importance of incorporating environmental context into studies of host-symbiont interactions.

Summaries of Undergraduate research projects.

2 Mima Germain: Exploring sporulation inhibition of *Saccharomyces paradoxus*

Mima Germain (class of 2027) is exploring *Saccharomyces* mitochondria function, salt stress, and sporulation. She started with a classroom project in which she and classmates observed that salt stress inhibits sporulation in several *S. paradoxus* isolates. She followed this up with an independent research project exploring how salt's impact on mitochondrial function might influence sporulation. Surprisingly, Ms. Germain observed some (albeit low) sporulation in petite *S. paradoxus* individuals. Salt completely inhibited petite sporulation and incompletely inhibited grande sporulation in her assays. She intends to continue with this project in the Spring 2026 semester and is interested in ideas from experts on why she might have made her surprising observations. Please contact Primrose Boynton (boynton_primrose@wheatoncollege.edu) if you have insights about Ms. Germain's data. She has summarized her work online in an outreach website: https://sites.google.com/wheatoncollege.edu/sporulationinhibition-gg/home-introduction

3 Kelsea Palm: The murder she inhibited: Understanding curing with cycloheximide in killer yeast

Kelsea Palm (class of 2025) completed a two-semester project on how the drug cycloheximide cures *Saccharomyces* of killer viruses. She spent the Fall 2024 semester demonstrating that cycloheximide can cure hosts of killer viruses in both solid and liquid culture and determining optimal cycloheximide concentrations for virus curing. In the Spring 2025 semester, she observed that curing is more frequent during exponential growth phase than other growth phases in liquids. Ms. Palm has produced a final report on her research, available upon request (contact Primrose Boynton, boynton_primrose@wheatoncollege.edu).

Ongoing research will further characterize cycloheximide curing of killer viruses with a goal of understanding the mechanism of virus curing.

4 Natalie Moore: Yummy nitrogen: Possible local adaptation to nitrogen in Harvard Forest

Natalie Moore (class of 2025) characterized the phenotypes of *Saccharomyces paradoxus* isolated from long-term experimental forest plots treated with heat and nitrogen fertilization. In the summer and fall of 2024, Ms. Moore isolated several *S. paradoxus* isolates from experimental soil warming and nitrogen fertilization plots at Harvard Forest, and determined that *S. paradoxus* is frequent in control, heated, fertilized, and heated plus fertilized plots that had been treated since 1991 or 2006. Following her interest in adaptation to nitrogen exposure, she measured isolates' growth rates in nitrogen-limited and carbon-limited growth media. She discovered that *S. paradoxus* from nitrogen fertilized plots had lower growth rates than those from control plots across environments, suggesting some side-effects to growth in or adaptation to the experimental conditions. She is currently preparing her results for submission to a peer-reviewed scientific journal.

VI Department of Genetics and Applied Microbiology, University of Debrecen, 4031 Debrecen, Hungary. Communicated by Matthias Sipiczki <gecela@post.sk>.

Recent publications.

1 Brysch Herzberg M, Jia GS, Sipiczki M, Seidel M, Zhang WC, Du LL. 2024.0 Reinstatement of the fission yeast species *Schizosaccharomyces versatilis* Wickerham et Duprat, a sibling species of *Schizosaccharomyces japonicus*. Yeast 41:108–127.

2 Sipiczki M, Czentye K, Kállai Z. 2024. High intragenomic, intergenomic, and phenotypic diversity in pulcherrimin-producing *Metschnikowia* yeasts indicates a special mode of genome evolution. Sci Rep 14:10521.

3 Sipiczki M, Czentye K. 2024. Reversible stochastic epigenetic-like silencing of the production of pulcherriminic acid in the antimicrobial antagonist *Metschnikowia pulcherrima*. Sci Rep 14:29677.

4 Sipiczki M, Baghela A. 2025. Identification of *Starmerella aleppica* f.a, sp. nov. and large indels in the rRNA cistron that split the *Starmerella* genus. Int J Syst Evol Microbiol Jan;75(1).

VII Laboratory of Yeast Systematics, Tokyo NODAI Research Institute Tokyo University of Agriculture, 1-1-1 Sakuragaoka, Setagaya, Tokyo 156-8502, Japan. Communicated by Masako Takashima <mt207623@nodai.ac.jp>.

Recent publications.

1 Keita Aoki, Moriya Ohkuma, Takashi Sugita, Yuuki Kobayashi, Naoto Tanaka, Masako Takashima. 2025. Analyses of hyphal diversity in Trichosporonales yeasts based on fluorescent microscopic observations. Microbiology Spectrum - doi: 10.1128/spectrum.03210-24.

2 Yuuki Kobayashi, Naoto Tanaka, Minenosuke Matsutani, Moriya Ohkuma, Ri-ichiroh Manabe, Masako Takashima. 2025. Whole-genome based phylogeny and comparative genomics of Sporidiobolales and related taxa of Basidiomycetes. IMA Fungus 16:e141626 - DOI: 10.3897/imafungus.16.141626. This paper has been accepted and will appear in print shortly.

VIII Center for Applied & Environmental Microbiology, Georgia State University, Atlanta, Georgia, USA. Communicated by Donald G. Ahearn <dgahearn@att.net>.

Letter to the Editor

Are rare drug-resistant yeast clusters health threats or cohorts of man?

Considerations: clonal instabilities and niche effects among the emerging yeast infections involving the *Candida/Clavispora* Complex; are strain clusters among clades of *C. auris* intermingled with *C. duobus haemulonii*?

Clonal instabilities and environmental stresses may underlie variances in taxonomic species-strain distinctions, geographical distributions, commercial applications and treatment modes for the emerging yeast infections involving the *Candida/Clavispora/ Candidozyma* Complex(es). Obscure stresses ranging from exposures to blood sepsis of confined elderly, adaptive histories in culture collections, marine coastal sites and laboratory processes may interact with a rare strain or progeny of *C. haemulonii* Complex, *C. auris* (supposed killer yeast co-infecting with SARS-2-COVID-19), *C. lusitaniae* and similar emerging new species considered health threats (1, 2, 5, 8-11,15). Cryptic unstable PCR target sites with potentials for rapid adaption to environmental stresses appear to be strain related. Niche multi-stresses, sequences and intensities, and epigenetic, rapidly adaptive or possibly dimensional involvement of sRNA-DNA may alter functions among given strains. Misidentifications, insufficient genomic barcodes, strain-related virulence, drug resistance, transient commensal functions may remain flexible or bound to a given culture by the status of technologies of the laboratory and ecological investigations (1, 3, 5, 7, 13, 15). Currently SARS-free candidemia by multiple drug resistant species is reportedly increasing among the compromised and confined. The SARS-free or COVID-19 terminology essentially applies in the USA to a general geographical recognition of coronavirus activities in wastewaters and extent of varied flu-like symptoms among an immediate population. A specific disease-virulence association for species-strains across the *C. haemulonii* Complex and *C. auris* remains problematic. The compiled literature of recent omics sciences indicates questionable premature applications of a Gold Standard categorization to clusters of yeast in diverse taxa. e.g., *Candida parapsilosis complex, Metschnikowia pulcherrima* (3, 4, 7, 11- 15). Such possibilities of genetically unique strain clusters are propagated for the *Candida haemulonii* Complex, for new species considered health threats, for medical staff in routine clinical laboratories, for visiting nurse practitioners servicing confined elderly, and for remote patient monitoring. Treatment of *C. auris* for non-critical patients by various worldwide clinicians now accepts assessment of patient history and treatment of the syndrome prior to selection of an antifungal. This regimen and the omnisciences involving industry, taxonomy, medicine and ecology need further investigation for rapid intrinsic adaptions among opaque clusters of *Candida/Clavispora*, perhaps *Metschnikowia*, excluding *M. pulcherrima*.

Whether current identification practices (i.e. status of the arts) applies to all strains of the Complex, their

potential virulence associations, or a binding or locking of unstable PCR target sites by niche stresses remain questionable.

(1) Could old Type and recent cultures of *C. duobushaemulonii*, *C. auris* and *C. lusitaniae* from blood sepsis of patients or marine environments, upon sustainment under multi-stresses, *e.g.* in neutrophiles and macrophages for several generations, provide progeny that gain or lose heat tolerances, or amphotericin B, and/or azole resistance?

(2) Could an evolutionary gene, a dehydration intolerance, rapid sRNA or mDNA epigenic systems coexist in different combinations and degrees among strains of the Complex?

(3) Could recent individual isolates, clonal cells of the *C. haemulonii Complex (*particularly *C. duobus-haemolunii, C. vulturna)* and their progeny be adapted to grow at 40-42 or higher?

(4) Could the *C. haemulonii* Complex and *Candida lusitaniae* share common marine ancestors involving possible diverse branching and hybrid relationships?

(5) Could an old and a recent strain be interlocked into a micro-niche with an antifungal microbe such as *Streptomyces nodosus*, a marine coral, fish ectoparasites, an apple or a vineyard and subsequently have less fitness to survive in a new niche?

(6) Could multi-stresses involving temperatures and niche exposures alter dimensional arrangements and functions of sRNA or mitRNA-DNA among clusters with genetically diverse domains?

(7) Could asci-ascospores evolve or reoccur among haploid clades or subgroups as a secondary feature in a haploid or aneuploid existence?

(8) Could simple repeated testing of a single clonal strain and its progeny (an evolutionary short-term study) provide evidence of cryptic unstable PCR target sites such as ITS, D1/D2 or 26sRNA?

(9) Could single domains ("drug resistant", or "mating type") in a clonal culture (strain) under niche stress become functional or nonsense in diverse metabolic or genomic pathways?

(10) Could a hidden strain of *C. auris* have the potential for a grave co-infection with another yeast strain or virus among various elderly? Does long COVID remain an issue?

The majority of disease-virulence associations in the literature for the above taxa have been inferred with pre-identified cultures sourced from hospitals and culture collections. Some early-concatenated barcodes appear insufficient for defining specific strain clusters. Unrecognized Niche effects could block or reorient genomic sites, affecting in varied degrees, functions distinct from those in *C. albicans*. Also, species-strains of the Complex and similar species may be depicted with unstable functions (genotypic and phenotypic) and surmised as additional health threats. Future investigations with focus on possible virulence diversities of unstable domains among such clonal strains under multi-stresses seems essential. Presently, of immediate importance, treatment of the syndrome of confined elderly prior to application of currently recognized antifungals such as amphotericin B, azoles, and echinocandins appears advisable for the rapidly adaptive *Candida/Clavispora* Complex.

Candidiasis and candidemia by non-epigenetic *C. albicans* or *C. parapsilosis* of potential drug resistance, more commonly identified among elderly, should have continued updated medical direction (MD) with emphasis on the host syndrome. Annual antiviral therapy for protection against possible co-infections should be maintained. Past high mortality rates estimated for patients linked to SARS and blood stream infections with *C. auris* appear in stark contrast to current low mortalities estimated for the entire Complex among the elderly. Compiled literature suggests involvement of loss of fitness of rare, opaque epigenetic functions rather than chromosomal dominance that could more often involve yeast and patient interaction. Virulence factors implied for *C. auris* from healthy and colonized-diseased hosts (particularly redundant AI Reviews and research with insufficient data on mortalities and treatments) may need to be readdressed for today's AI projections of strain diversities. The status in time for diversities in any niche appears foremost for persistence among this unique Complex. These considerations and conjectures based on current clonal progeny may apply for other rare genetic fungal clusters (1-15). Some assumed health threats might be misleading; certain strains can continue as a beneficial cohort for humans rather than a rare disease threat.

To address the above, please consider the State of the Art of Science/Technology with details of any variations in prior methods, including the source and identification numbers of clonal types from varied culture collections.

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Recent publications.

1 Alvarenga FBM, Barros, KO, Batista TM, Souza GFL, Santos ARO, Abegg MA, Sato TK, Hittinger CT, Lachance MA, Rosa CA. 2025. *Vanderwaltozyma urihicola* sp. nov., a yeast species isolated from rotting wood and beetles in a Brazilian Amazonian rainforest biome. IJSEM 75(3) - doi.org/10.1099/ijsem.0.006718.

See abstract under Dr. Hittinger's entry.

2 Silva MR, Paraíso F, Al-Oboudi J, Abegg M, Aires A, Barros KO, Brito PH, Jarzyna M, Sylvester K, Langdon QK, Opulente DA, Carriconde F, Fell JW, Hofmann TA, Lachance MA, Legras JL, Libkind D, Pontes A, Gonçalves P, Rosa CA, Groenewald M, Hittinger CT, Sampaio JP. 2025. A taxogenomic view of the genus *Torulaspora* – expanding from ten to twenty-two species. Persoonia Mol phylog evol fungi. Accepted for publication May 2025.

The yeast genus *Torulaspora* (subphylum Saccharomycotina, family Saccharomycetaceae) is mostly known from its type species, *T. delbrueckii*, a frequent colonizer of wine and sourdough bread fermentations. The genus currently contains ten species that are typically found in various natural terrestrial environments in temperate and tropical climates. Here we employ taxogenomic analyses to investigate a large collection of *Torulaspora* strains obtained in multiple surveys we carried out in Asia, Australasia, North America, South America, and Europe, and to which we added several strains maintained in culture collections. Our analyses detected twelve novel species that are formally described here, thereby more than doubling the species diversity of *Torulaspora*. We also sketch a genotype-phenotype map for the genus and show how the complex relationship between key genes and the physiological traits they control both between and within species. This remarkable increase in the number of species in the genus *Torulaspora* highlights how limited the current inventory of fungal taxa is. It also shows how integrated taxogenomic approaches can foster the assessment of species circumscriptions in fungi.

Obituary

Vladimir Mrša

Professor Emeritus

1 June 1957 – 15 June 2024

Official photo PBF Zagreb, Croatia

Vlado was born in Zagreb and completed there his primary and secondary education. He pursued his university education and obtained a doctorate at the Biotechnology Department, Faculty of Technology, University of Zagreb. For his PhD thesis, he worked on the project of Professor Pavao Mildner, Head of the Laboratory for Biochemistry, also under the supervision of Professor Ries. Vlado investigated the physiological role of the carbohydrate part of yeast mannoproteins, specifically enzymes secreted into the periplasmic space. At that time, the field of glycoprotein research was still in its infancy, making it a challenging field of research. Vlado was an efficient, hardworking researcher who was fully dedicated to his thesis. With the support of his mentor and other senior colleagues who worked on the same project, he successfully carried out the research and defended his PhD thesis at the Faculty of Science, University of Zagreb in 1984.

Eager to expand his knowledge further, he searched for postdoctoral opportunities abroad and after securing a DAAD fellowship, he joined Professor Widmar Tanner's laboratory at the University of Regensburg in 1988. Professor Tanner was a leading, world-renowned researcher in the field of yeast glycoproteins. Over the course of two years, Vlado's research led to impressive results that were published in high-ranking journals. These two years of joint work with Professor Tanner and their mutual appreciation were the basis for a long-lasting collaboration and friendship and Vlado's return to Regensburg for further research in 1996 and 1998. The result of their 18-year collaboration were nine joint papers that significantly advanced our understanding of yeast cell wall glycoprotein functions and contributed to the growing knowledge in the field of glycoprotein research. Vlado's scientific career was greatly enriched by his collaboration with Prof Tanner and earned him an international reputation among researchers in the field of yeast molecular biology. In a later phase of his research career, Vlado focused on studies to develop techniques for the construction of a yeast cell wall display system to immobilise various homologous or recombinant proteins on the surface of the yeast cell wall. Such yeast cell constructs could have great potential for use in various modern biotechnological processes.

On his journey through the academic ranks, from assistant professor to full professor, from competent researcher to Dean of the faculty, and from congress organiser to secretary general of Croatian Academy of Technical Sciences, Vlado had a significant impact on the development of education at the Faculty of Food Technology and Biotechnology and on education and research in Croatia. From the time we met during studies at University of Zagreb, in the early days of my scientific life, we worked together on many occasions. Worthy of mention is the organisation of the ISSY in Bled, Slovenia, in 1997. At the commissioners meeting during the 13th International Congress on Yeasts (ICY), held at Madison, Wisconsin, USA, in August 2012, Vlado and I, on behalf of Croatia and Slovenia, prepared a joint candidacy for another ISSY to be held on the border between the two countries. Sadly, the Commissioners did not accept their proposal.

Prof. Dr. Vladimir Mrša, Croatia, joining as yeast commissioner at the 2011 ISSY in Mexico. Photo P. Raspor

The progress of research in any scientific field is determined mostly by the work of dedicated and enthusiastic scientists whose high motivation drives the important findings in that field. Professor Vladimir Mrša was one such yeast scientist - a highly dedicated researcher and highly competent professor, who made a remarkable impact in the field of yeast biochemistry and molecular biology. Through decades, his work contributed significantly to our understanding of the physiological role of yeast-secreted mannoproteins and the molecular mechanisms of cell wall biogenesis. Some of the methods he coined continue to be in use today in yeast cell wall research.

Peter Raspor

International Commission on Yeasts (ICY)
Mycology and Eukaryote Microbiology (MEM) Division
International Union of Microbiological Societies (IUMS)
ICY Commissioners Meeting, 02/10/2024, Cape Town, South Africa
Minutes

Present

35 Commissioners in attendance, including 5 newly nominates

Apologies

Apologies were received from 33 Commissioners

A scheduled meeting of the ICY commissioners was held in Cape Town on 02/10/2024 on the occasion of ICY16/ICY2024 organised by the South African Commissioners Florian Bauer, Evodia Setati and colleagues. The meeting was chaired by ICY President, Diethard Mattanovich.

1 Chair's Business

The Chair opened the meeting, welcomed participants and outlined the agenda. This has been circulated in advance and as no amendments were proposed, this was adopted.

- A brief tour de table was performed to allow all the commissioners introduce themselves.
- The previous Chair, Hiroshi Takagi, supplied all Commissioners with a glass of Japanese Awamori and proposed a toast "Kampei" to Florian and the South African team in recognition of the success of ICY16.

2 The minutes of the last ICY Commissioner's meeting (held on the occasion of ISSY37 in Adelaide, Australia, 2023 had previously been circulated and no substantive amendments were proposed before or at this meeting. Accordingly, the minutes were accepted.

3 Election of New Commissioners

There were five nominations for new Commissioners representing China, the Netherlands, Austria and Germany. Details of nominated new Commissioners had been previously circulated by the Chair and he reported that in all cases, there was an overwhelming majority of Commissioners supportive of the nomination. No serious concern was expressed by any Commissioner about any of the nominees. The Chair proposed the full slate of nominated Commissioners and this was unanimously accepted by those present. Accordingly, the following are now Commissioners of the ICY:

Mark Rinnerthaler (Austria), Xiangwei He (China), Xin-Qing Zhao (China), Elke Nevoigt (Germany), Marizeth Groenewald (Netherlands)

For their affiliations, see the Commissioners' list (https://www.icy-yeast.org/commissioners/). The new commissioners in attendance were invited back into the chamber, congratulated and introduced to the Commission.

4 Retired Commissioners

The Chair reported the retirement of the following six Commissioners: Michael Breitenbach (AT), Huiqiang Lou (China), Li-Lin Du (China), Eckhart Boles (DE), Ida van der Klei (NL), Peter Biely (Slovakia) and they were thanked for their service. It was noted that retired Commissioners are always welcome to ICY Commissioners meetings, and indeed the presence of Teun Boekhout (Emeritus Commissioner for NL) was acknowledged. The Chair undertook to pass on the thanks and best wishes of the Commission.

5 Bereavements

The Chair acknowledged the sad passing this year of Vladimir Mrša, ICY Commissioner for Croatia. His contributions to the yeast community were acknowledged. Neža Čadež (Commissioner for Slovenia) read a letter from Peter Raspor (Commissioner for Slovenia) that recognised Vladimir's contributions especially to publishing, including as Editor in Chief of Food Technology and Biotechnology. He invited those interested in contributing to a memorial issue to contact him. A moment silence in memory of Vladimir was held.

6 Status of the current ICY16

Florian Bauer gave an update on ICY2024. The congress has 295 paying delegates and has been a great success. The meeting is on course to balance its budget and most likely return a small surplus. The Chair and commission complimented Florian, his team, and the event organising company on the meeting organisation.

John Morrissey, Editor in Chief of FEMS Yeast Research reminded Commissioners of that FEMSYR has a call for papers linked to the conference open and this is of mutual benefit as the launch of the collection in 2025 will be an opportunity also to promote the ICY and future meetings.

7 Updates for Future ISSY Meetings

The Chair also reiterated the principle that the ICY organises two main types of meeting – general and specialized. It is important that organisers of ISSY meetings keep this point in mind and do not attempt to be too broad.

Updates on scheduled future meetings were provided by the respective organisers.

- ISSY38 will take place in Warsaw, 1st – 5th September 2025

Poland Commissioner Ewelina Celinska provided an update on planning for this meeting. The title will be "Yeast as the Omnitool". The website is live https://issy38.com.pl/ and it is possible to register already for the conference. The Commission endorsed the planning.

- ISSY39 will take place in South Korea, Nov 8th – 12th 2026

The chair delivered an update on behalf of the South Korean Commissioners Hyun-Ah Kang and Ji-Sook Hahn. Planning is progressing well and the meeting title will be "Fermenting the future: from bread to breakthroughs". The website is live https://www.issy39.org/confs/info/welcome/. There was broad support from the commission and the prospect of ISSY39 in South East Asia was very attractive to the commission.

- ISSY40 – a proposal for 2027

A proposal has been made to hold ISSY40 in Brazil. Brazilian Commissioner, Andreas Gombert presented an overview of planning on behalf of himself and Rosane Schwan (also in attendance) who will be the meeting organisers. The theme would be Yeast Biodiversity and Ecology and possible dates were in Sept/Oct 2027. There was some discussion around possible locations for the meeting and the timing was also discussed. The Commission formally approved this meeting and asked Andreas and Rosane to continue planning and to report back at the next Commissioners' meeting.

- ICY17 2028

USA Commissioner Chris Hittinger presented a proposal to organise ICY17 in Madison, Wisconsin, in 2028. Likely dates would be mid to late August (before USA Labor Day). There was discussion and a vote. The proposal was accepted unanimously. Chris will provide an update at the next Commissioners' meeting.

- ISSY41 – would take place in 2029

The Uruguay Commissioner, Francisco Carrau made a formal proposal to host the ISSY41 meeting in Uruguay. The theme could be "Food, Beverages and Health" or similar. The point was made and generally accepted that ordinarily ISSY meetings would not be committed so far in advance (2029) but this was an exception as the proposal for Uruguay has been on the table for some time and Uruguay stepped aside to support Brazil for 2027. The Commission formally approved this meeting by unanimous vote.

8 Chair's business (2)

The outgoing Chair, Diethard Mattanovich, provided a summary of activity during the 3 years of his tenure. The disruption caused by the COVID19 pandemic was noted. It was a period of major successes, however:

- A very successful on-line ICY15
- A new website (https://www.icy-yeast.org/)
- New logos
- Rejuvenation and reinvigoration of the Commission – 24 new Commissioners

There was also some discussion of issues that are ongoing including the relationship with the Finance and Policy Committee who organise ICYGMB, with the IUMS and others. Andrey Yurkov (Commissioner for Germany) is Vice Chair of the IUMS Division Mycology and Eukaryotic Microbiology and will participate in these discussions.

9 Election of a new Chair

Florian Bauer (Stellenbosch University, South Africa) was proposed as the next Chair of the ICY and a vote taken. The proposal was accepted by unanimity and Florian Bauer elected. Florian made some brief remarks, thanking the outgoing Chair, and mentioning some important priorities including relationships with other organisations (IUMS, ICYGMB), financial sustainability, and representation and diversity.

10 AOB

Teun Boekhout mentioned that work on the on-line "The Yeasts" database continues and he invited anybody willing to contribute to this to please contact him.

11 Closing Remarks from Chair

The Chair thanked commissioners for their contributions and our South African colleagues for organising and hosting the meeting and commissioners' dinner. He wished everybody the best for the rest of the meeting.

Forthcoming Meeting

The International Commission on Yeasts, the Local Conference Organizing Committee, and the International Scientific Committee, have the great pleasure to invite you to the 38th International Specialized Symposium on Yeasts (ISSY38). The symposium will be held as an in-person event from 1 to 5 September 2025 in Warsaw, Poland.

It is the first time in the symposium's 60-year history that it will be held in Poland. The symposium is jointly organized by the International Commission on Yeasts (ICY), the Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, the Wroclaw University of Environmental and Life Sciences, and the Biology Department of the University of Warsaw. The venue of ISSY38 will be at the beautiful historical campus of University of Warsaw.

The theme of the ISSY38 conference is Yeast – the Omni-Tool. This theme will bring together a broad cross section of investigators working on various yeast species, researchers in basic science and industry scientists, and students, allowing them to share their latest discoveries. It will facilitate and encourage communication between the international yeast society and Polish yeast researcher communities, as many Polish universities and institutes have strong and rapidly growing research teams studying fundamental and applied aspects of yeast biology and biotechnology.

The main topics of ISSY38 will be:

- Deciphering of molecular mechanisms of eukaryotic cells with yeast
- Yeast screens
- Metabolism and metabolomics
- Yeasts as molecular factories
- Fermentation, food and beverages
- Yeast in population and evolution models
- Humanized yeast in health research

The deadline for Standard registration is August 24th, 2025, at 23:59

Go to https://issy38.com.pl/rejestracja to register.

If you have not done it yet, please distribute the information about the conference among your colleagues and encourage them to participate in this event.

Please visit our website https://issy38.com.pl, to get acquainted with all the details regarding the conference, including:

Special deals for travel: https://issy38.com.pl/travel,

Accommodation: https://issy38.com.pl/accommodation,

Congress tours: https://issy38.com.pl/congress_tours.

We look forward to seeing you in Warsaw!

Adrianna Skoneczna & Zbigniew Lazar

Fifty Years Ago

Y E A S T

A News Letter for Persons Interested in Yeast

Official Publication of the
International Commission on Yeasts and Yeast-like Microorganisms
of the International Association of Microbiological Societies (IAMS)

June 1975 Volume XXIV Number 1

Note from Kyria Boundy-Mills: Today we work with yeast strains isolated and characterized by past generations of researchers, use species that they defined, and we build on their discoveries. We continue to make basic and applied discoveries using Saccharomyces cerevisiae, Schizosaccharomyces pombe and other yeast species. Fifty years ago, methods included spontaneous and chemically induced mutations, genetic mapping, spheroplasts, and "petite" mutants (which are different from "wee" mutants).

Douglas S. King recently joined the staff at ATCC and initiated a study of the genus *Trichosporon* that would involve computer evaluation of the data. He listed 88 newly accessions yeast strains, including many from D. Yarrow of CBS, researchers at several universities in the USA, Belgium, India, UK, Japan, Poland and the Netherlands.

Sally A. Mayer of ATCC published work on the physiological, morphological, immunological and DNA relatedness of strains classified as *Candida sake*, and reassigned some to *C. maltose, C. tropicalis,* or *C. cloacae.*

Myung Sam Park of Chonnam National University, Korea isolated wild yeasts from various regions and seasons in Korea, from tree exudates, *Drosophila*, and fruits. Many species were isolated from natural environments for the first time.

Errol Reiss, newly appointed Research Microbiologist at the Center for Disease Control, Atlanta, Georgia USA, began studies of the immunochemistry of yeasts of medical importance to develop better reagents for immunodiagnosis of mycoses.

Marie Kopecká of Purkyne University, Brno, Czechoslovakia announced lectures held in April 1975 for Professor O. Necas' 50th birthday, and listed lectures to be held at the Czechoslovak Microbiological Society meeting in September 1975 on antibiotic lomofungin, cell wall regeneration, protoplasts. **A. Svoboda, J. Havelkova** and **M. Kopecká** completed Ph.D. theses under the guidance of Professor **O. Necas.**

N. Elinov of the Chemical Pharmaceutical Institute, Leningrad, USSR described a method to prepare mannan of *Rhodotorula rubra* labelled with tritium.

Byron F. Johnson of the National Research Council of Canada published work on a new method of obtaining zygotes in *Saccharomyces cerevisiae*, kinetic analysis of spontaneous mutations to the petite state, and morphometric analysis of Schizosaccharomyces pombe.

F. K. Zimmermann of the Technische Hochschule Darmstadt, German Federal Republic described work in collaboration with P. Schreiber, R. Kern and B. K. Vig on genetics of maltose and alpha-methylglucoside fermentation, carbon metabolite repression, induction of genic petite mutants using nitrous acid, the effects of the antifungal drug econazole nitrate on yeast cells, and mitotic crossing over.

Robert K. Mortimer, University of California Berkeley, USA studied the genetics of hydrocarbon utilization by *Saccharomycopsis lipolytica*. A mutant excretes large quantities of a blood-red pigment, identified as protoporphyrin IX. The Yeast Genetic Stock Center, funded by the National Science Foundation, will furnish strains free of charge to qualified investigators. An address was posted to be added to the YGSC mailing list to receive the next printed strain catalog.

P. Tauro of Haryana Agricultural University, Hissar, India summarized work on sporulation in *S,. cerevisiae* and a method to detect respiratory deficient yeast mutants.

Reed B. Wickner of the National Institutes of Health, USA gave a talk at the 1975 Squaw Valley Plasmid Meeting on genetics of double-stranded RNA plasmid in killer strains of *S. cerevisiae.*

S. C. Purohit, Institut fur Biologie, Frankfurt, West Germany summarized two recent papers on repair of X-ray damage in living cells using yeast.

Frank T. Bayliss, Edinboro State College, Pennsylvania USA moved to San Francisco State University, and worked on ribosomal mutants of *S. cerevisiae* including spontaneous mutants resistant to blastocidin S, trichodermin, cryptopleurine, and neomycin. Linkages between loci were identified using 50 markers.

Michio Kozaki of Tokyo University of Agriculture, Japan described recent studies on yeast immunology using sake yeast.

Terrance Cooper , University of Pittsburgh, Pennsylvania USA studied the biochemical and genetic characteristics of urea uptake and the induction of allophanate hydrolase in *S. cerevisiae*.

A. Goffeau of the Laboratoire d'Enzymologie de Louvain, Belgium listed recent publications on RNA synthesis, a method to prepare sphaeroplasts of *Schizosaccharomyces pombe* using snailgut enzyme treatment, mitochondrial "petite-negative" yeasts, membrane biogenesis, and mitochondrial response to herbicides.

Takashi Suzuki, Takeda Chemical Industries Ltd., Japan shared the abstracts of two publications on aconitase.

Eric Zeuthen of the Carlsberg Foundation, Copenhagen, Denmark published work on the exchanges of CO_2 and O_2 gases in synchronized and normal cell cycles of *Schizosaccharomyces pombe*.

Saburo Fukui and Atsuo Tanaka of Kyoto University, Japan summarized their work on catalase activities of hydrocarbon-utilizing *Candida* yeasts.

James Barnett of University of Plain, Norwich, England listed recently published work on diagnostic keys, effects of carbon source on cell shape, predictive classification of yeasts, and use of D-ribose and other sugars by yeasts.

E. Schweizer, Universität Würzburg, West Germany published work on yeast fatty acid synthesis using independently isolated and temperature sensitive mutants of the fatty acid synthetase complex in S. cerevisiae.

J. Jayaraman of Madurai University, India described work on mitochodriogenesis in spheroplasts of *Saccharomyces cerevisiae* using cycloheximide and chloramphenicol, which inhibit protein synthesis in the cytoplasm and mitochondria, respectively.

Arnold L. Demain of Massachusetts Institute of Technology, USA mutagenized *Hansenula polymorpha* using ethyl methanesulfonate and selected for resistance to 5-fluorotryptophan to select mutants able to produce 240 mg/L tryptophan, compared to 3.5 mg/L produced by the wild yeast.

Michael C. Barney of Miller Brewing Company presented work on lyophilization for long-term storage of brewer's yeast at the American Society of Brewing Chemists meeting in New York, May 1975.

E. Minárik of the Research Institute for Viticulture and Enology, Bratislava, Czechoslovakia studied the effect of fungicides on the yeast flora of grapes, and sulphite and sulphide formation by yeasts during wine fermentation.

C. P. Kurtzman and L. J. Wickerham of the USDA Northern Regional Research Lab, Peoria IL USA published their studies of color variants of *Aureobasidium pullulans*, a new specimen holder for scanning electron microscopy of microorganisms, and taxonomy of round-spored species of *Pichia.*

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