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

Editorials

Adele Statzell-Tallman (1939-2025)

I sadly announce the recent loss of our colleague Adele Statzell-Tallman, of the University of Miami, Florida, USA. I had the priviledge of participating in two research cruises in the Bahamian archipelago in Adele's company. Her love of the sea and its creatures was exceeded only by her kindness and sense of humour. All those who knew Adele will miss her dearly. Jack Fell, her close colleague for many years, has kindly provided an obituary.

Michael Breitenbach (1943–2024)

A long-time reader of the Yeast Newsletter, Michael Breitenbach, of the University of Salzburg, has left us last year. His colleagues have written a short biography:
Ian W Dawes, Terrance G Cooper, Mark Rinnerthaler. 2025. Aging research has lost a brilliant investigator — Michael Breitenbach, 1943–2024. FEMS Yeast Research 25:foaf008
https://doi.org/10.1093/femsyr/foaf008

Species descriptions in the Yeast Newsletter

At the last meeting of authors of the online version of *The Yeasts*, it was noted that Article 29 of the Madrid Code of Nomenclature stipulates that since 2012, "effective publication" includes PDF documents available online and possessing a valid ISSN number, therefore qualifying the Yeast Newsletter as a venue for the publication of novel yeast species. The Yeast Newsletter has hitherto published any material of reasonable length submitted by its readership, with minor editorial polishing, but without formal peer review. The eventual acceptance of peer-reviewed taxonomic papers would represent a major shift in the role of the Yeast Newsletter, and I plan on approaching this endeavour with prudence. At this time, I am happy to welcome Dr. Heide-Marie Daniel to the YNL editorial board, specifically to assist with the eventual peer-review process. A draft set of guidelines is presented this issue. Interested readers are invited to submit comments.

I wish all our readers a happy and scientifically rewarding New Year!

M.A. Lachance

I 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>.

Recent publications.

1 Horianopoulos LC, Chavez CM, Rokas A, Hittinger CT. 2025. A trait syndrome ties cell morphology to glycolysis across the yeast subphylum. bioRxiv - https://doi.org/10.1101/2025.10.27.684252

Traits that co-vary across species can provide fundamental insights into the trade-offs and constraints that govern their evolution. In a recent article in Current Biology, Li et al.1 reported that glucose uptake rates (GUR) are inversely correlated with the cell surface area-to-volume (SA:V) ratio across 11 yeast species. Here we substantially expand this analysis to 282 species to test whether the GUR-SA:V correlation generalizes across the ancient Saccharomycotina yeast subphylum and to determine the contribution of shared evolutionary history to the co-variation of these two traits. Using regression models that account for co-variation due to phylogeny, we found that extracellular acidification rates (ECAR, which we used as a proxy for GUR) had a significant correlation with SA:V across Saccharomycotina. In contrast to Li et al.1, our increased sample sizes provided statistical power to reveal additional significant correlations of ECAR with genome sizes and growth rates. Our findings dramatically extend and expand those of Li et al.1 and suggest that a trait syndrome governs several metabolic, genomic, and morphological traits across yeasts.

2 Horianopoulos LC, Rokas A, Hittinger CT. 2025. Convergent evolution of aerobic fermentation through divergent mechanisms acting on key shared glycolytic genes. bioRxiv https://doi.org/10.1101/2025.10.02.679963

As the tree of life becomes increasingly accessible to molecular investigations, describing mechanisms underlying evolutionary convergence and constraint will be crucial to understanding diversification. The lineage including the model yeast *Saccharomyces cerevisiae* evolved aerobic fermentation in part through an ancient whole genome duplication and retention of glycolytic genes. To evaluate the glycolytic rates across diverse yeasts, we developed and deployed an extracellular acidification rates (ECAR) assay on 299 species that span more than 400 million years of evolution and identified a clade in the genus *Saturnispora* that convergently evolved aerobic fermentation. Through comparative genomics and transcriptomics, we found that several glycolytic genes had higher expression and novel cis-regulatory elements in aerobically fermenting *Saturnispora* species. When the transcription factor required for their activation was deleted in *Saturnispora dispora*, the mutants had reduced glycolytic rates and increased respiration. Intriguingly, many of the upregulated genes are orthologous to duplicated glycolytic genes in *S. cerevisiae*. These divergent genetic mechanisms suggest that there are strong evolutionary constraints on how some traits like aerobic fermentation can arise convergently.

3 Barros KO, Fisher KJ, Crandall JG, Magni G, Serate J, Xie D, Zhang Y,Silva SS, Sato TK, Hittinger CT, Rosa CA. 2025. An evolved strain of *Spathaspora passalidarum* produces ethanol from sugarcane bagasse and switchgrass lignocellulosic hydrolysates. bioRxiv - https://doi.org/10.1101/2025.09.26.678828

Lignocellulosic hydrolysates, derived from plant biomass, contain various inhibitors that can hinder microbial growth. This study aimed to enable the growth and ethanol production by the xylose-fermenting yeast *Spathaspora passalidarum* in the presence of lignocellulosic hydrolysate inhibitors, particularly acetic acid. Ultraviolet (UV)-induced mutagenesis and adaptive laboratory evolution (ALE) were used to select for mutants with higher tolerance to these inhibitors. The initial mutant strain, MT01, was selected for increased growth in medium containing xylose and acetic acid. This strain underwent further evolution, resulting in the strain ME3.5.5, which showed significant improvements in both growth and ethanol production compared to the parental strain when tested in sugarcane bagasse hemicellulosic hydrolysate (SBHH). Genomic analysis identified non-synonymous and frameshift mutations in four genes, including CYR1 (encoding adenylate cyclase). These findings suggest that genetically optimized *S. passalidarum* strains could play a crucial role in advancing industrial bioethanol production from lignocellulosic biomass by overcoming the inhibitory effects of compounds found in lignocellulosic hydrolysates.

4 Quintrel P, Muñoz-Guzmán F, Villarreal P, Peña TA, Garate NI, Muñoz-Tapia C, Oporto CI, Crandall JG, Larrondo LF, Hittinger CT, Fischer G, Cubillos FA. 2025. Allelic variation in *MAL33* drives ecological adaptation of maltose metabolism in *Saccharomyces eubayanus*. bioRxiv https://doi.org/10.1101/2025.09.15.676268

Maltose is one of the most abundant sugars in brewer's wort, and its efficient utilization is critical for successful fermentation. However, maltose consumption varies naturally among *Saccharomyces eubayanus* strains isolated from different host trees, such as *Quercus* and *Nothofagus*. To identify the genetic determinants underlying these phenotypic differences, we performed bulk segregant analysis (BSA) and quantitative trait loci (QTL) mapping using an F2 offspring derived from QC18 (*Quercus*-associated) and CL467.1 (*Nothofagus*-associated) strains. QTL mapping identified two significant genomic regions on subtelomeric loci of chromosomes V-R and XVI-L, each containing complete *MAL* loci composed of *MAL32* (encoding maltase), *MAL31* (transporter), and *MAL33* (transcriptional activator) genes. Comparative polymorphism analyses identified mutations in *MAL32* and *MAL33* of QC18, including frameshift mutations resulting in premature stop codons. Functional validation demonstrated that the heterologous expression of $MAL33_{ChrV}$ from CL467.1 fully restored maltose utilization in QC18, indicating the functional presence of *MAL33* cis-regulatory sequences and *MAL32* and *MAL31* genes in QC18. While structural protein predictions identified truncation and impaired functionality in the maltose-responsive activation domain of Mal33p from QC18, overexpression of QC18's own $MAL33_{ChrV}$ allele also improved maltose metabolism, suggesting dosage-dependent transcriptional limitations rather than complete functional loss. These results indicate that allelic variations in the maltose-responsive activation domain of Mal33p lead to differences in maltose consumption between strains. We hypothesized that reduced maltose metabolism in QC18 is an adaptive response to the distinct sugar composition in *Quercus robur* bark, contrasting with the starch-rich environment of *Nothofagus pumilio*. These findings highlight subtelomeric *MAL* gene diversity as a reservoir of evolutionary plasticity, representing a key evolutionary mechanism that influences maltose adaptation among natural *Saccharomyces* isolates.

5 David KT, Horianopoulos L, Gonçalves C, Steenwyk JL, Pontes A, Gonçalves P, Hittinger CT, Pennell M, Rokas A. 2025. Discovery of additional ancient genome duplications in yeasts. bioRxiv https://doi.org/10.1101/2025.08.31.673279

Whole genome duplication (WGD) has had profound macroevolutionary impacts on diverse lineages, preceding adaptive radiations in vertebrates, teleost fish, and angiosperms. In contrast to the many known ancient WGDs in animals and especially plants, we are aware of evidence for only four in fungi. The oldest of these occurred ~100 million years ago (mya) and is shared by ~60 extant *Saccharomycetales* species, including the baker's yeast *Saccharomyces cerevisiae* (Fig. 1). Notably, this is the only known ancient WGD in the yeast subphylum *Saccharomycotina*. The dearth of ancient WGD events in fungi remains a mystery. Some studies have suggested that fungal lineages that experience chromosome and genome duplication quickly go extinct, leaving no trace in the genomic record, while others contend that the lack of known WGD is due to an absence of data. Under the second hypothesis, additional sampling and deeper sequencing of fungal genomes should lead to the discovery of more WGD events. Coupling hundreds of recently published genomes from nearly every described *Saccharomycotina* species with three additional long-read assemblies, we discovered three novel WGD events. While the functions of retained duplicate genes originating from these events are broad, they bear many similarities to the well-known WGD that occurred in the *Saccharomycetales*. Our results suggest that WGD may be a more common evolutionary force in fungi than previously believed.

6 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.

7 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.

8 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. Mol Biol Evol https://doi.org/10.1093/molbev/msaf285

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 genes involved in DNA repair. Here, we surveyed 1,154 yeast genomes representing nearly all known yeast species of the subphylum Saccharomycotina (phylum Ascomycota) to examine the relationship between reduced gene repertoires broadly associated with genome stability functions (e.g., DNA repair, cell cycle) and elevated evolutionary rates. We identified three distantly related lineages—encompassing 12% of species—that had both the most streamlined sets of genes involved in genome stability (specifically DNA repair) 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 genome stability gene repertoires revealed a set of genes predominantly absent in these three FELs, suggesting a potential role in the observed acceleration of evolutionary rates. In the W/S clade, genomic signatures are consistent with a substantial mutational burden, including pronounced A|T bias and endogenous DNA damage. Interestingly, we found that the W/S clade also contains DNA repair genes possibly acquired through horizontal gene transfer, including a photolyase of bacterial origin. These findings highlight how hypermutators can persist across macroevolutionary timescales, potentially linked to the loss of genes related with genome stability, with horizontal gene transfer as a possible avenue for partial functional compensation.

9 Bajgain Y, Langdon QK, Krien CM, Jarzyna M, Buh KV, Haase MAB, Pasles A, Wolters JF, Groenewald M, Hittinger CT, Opulente DA. 2025. Taxogenomic analysis of a novel yeast species, *Lachancea rosae* sp. nov. f.a., isolated from the wild rose *Rosa californica*. Yeast 42:213-21 https://doi.org/10.1002/yea.70000

A novel *Saccharomycotina* yeast strain, yHQL494, was isolated from the rose hip of the wild rose *Rosa californica* from Castle Crags State Park, California, USA. Phylogenetic analyses of both whole genome data and the sequences from the D1/D2 region of the large ribosomal subunit (LSU) rRNA gene placed strain yHQL494 within the genus *Lachancea* and grouped it into a clade with *Lachancea lanzarotensis* and *Lachancea meyersii*. Taxogenomic analyses were conducted on publicly available genome sequences to gain a deeper insight into the carbon and nitrogen gene-trait associations across the *Lachancea* clade. The results of these analyses were found to be consistent across *Lachancea* species. Growth assays and microscopic analyses were conducted to determine the physiological characteristics of strain yHQL494, including the presence of hyphae or pseudohyphae, ascospore formation, fermentation abilities, and assimilation of carbon and nitrogen compounds. Based on the phenotypic and genomic characteristics of the strain yHQL494^T (=NRRL Y-64858^T, =CBS 18,574^T), we propose a new species, *Lachancea rosae* sp. nov. f.a.

10 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. G3 15:jkaf184 - https://doi.org/10.1093/g3journal/jkaf184

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 with 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.

11 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 432:132651 - 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.

12 Barros KO, Al-Oboudi J, Freitas LFD, Sousa FMP, Batista TM, Santos ARO, Morais PB, Sampaio JP, Lachance MA, Hittinger CT, Rosa CA. 2025. Taxogenomic analysis of *Pichia senei* sp. nov. and new insights into hybridization events in the *Pichia cactophila* species complex. FEMS Yeast Res 25:foaf037 https://doi.org/10.1093/femsyr/foaf037

Three strains of a novel yeast species were isolated from necrotic cactus tissues of *Cereus saddianus* and *Micranthocereus dolichospermaticus* and from phytotelmata of *Bromelia karatas*. DNA sequence analysis of the Internal Transcribed Spacer (ITS) region and D1/D2 domains of the large subunit ribosomal RNA, along with whole genome phylogenomic analysis, showed that this yeast is most closely related to *Pichia insulana, Pichia cactophila*, and *Pichia inconspicua*. The new species differs by 10–13 nucleotide substitutions from these species in D1/D2 sequences and exhibits <90% genome-wide average nucleotide identity to them. The name *Pichia senei* sp. nov. is proposed for the novel species, which is homothallic and produces asci with one to four hat-shaped ascospores. The holotype is CBS 16311 (MycoBank MB 858723). Taxogenomic analyses of the *P. cactophila* species complex, including *P. senei*, provide new insights about the hybridizations events that shaped this group. *Pichia insulana* and *P. inconspicua* are identified as the parental lineages that originated *P. cactophila*, and *P. senei* also appears closely related to one of the progenitors of *P. inconspicua*. We assess phylogeny, heterozygosity, and ploidy to explore the processes shaping diversity, showing how genomic data support yeast species delimitation and reveal complex hybridization.

13 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 16:5866 - https://doi.org/10.1038/s41467-025-60189-3

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 characterize the variation in resistance to the ROS-inducing compound *tert*-butyl hydroperoxide across the ancient yeast subphylum Saccharomycotina and use machine learning (ML) to identify gene families whose sizes are predictive of ROS resistance. The most predictive features are enriched in gene families related to cell wall organization and include two reductase gene families. We estimate the quantitative contributions of features to each species' classification to guide experimental validation and show that overexpression of the old yellow enzyme (OYE) reductase increases ROS resistance in *Kluyveromyces lactis*, while *Saccharomyces cerevisiae* mutants lacking multiple mannosyltransferase-encoding genes are 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.

14 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 122:e2500165122 https://doi.org/10.1073/pnas.2500165122

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.

15 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 21:1066-89 - https://doi.org/10.1038/s44320-025-00118-0

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 1154 genomes from nearly all known species in the medically and technologically important yeast subphylum Saccharomycotina. We found that yeast gene family evolution differs from that of plants, animals, and filamentous ascomycetes, and is characterized by smaller overall gene numbers yet larger gene family sizes for a given gene number. 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.

16 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 129:101590 - https://doi.org/10.1016/j.funbio.2025.101590

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.

17 Clark NL, Hittinger CT, Li-Byarlay H, Rokas A, Sackton TB, Unckless RL. 2025. Integrating intermediate traits in phylogenetic genotype-to-phenotype studies. Integr Comp Biol 65:63-73
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.

II 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 2025.

1 Tuaeva AYu, Ponomareva AM, Melkina OE, Naumova ES. 2025. Dairy yeast *Kluyveromyces marxianus*: molecular polymorphism and dynamics of lactose fermentation. Biotechnologiya 41(3):30–38.

2 Borokova AN, Tuaeva AYu, Naumova ES. 2025. Intraspecific polymorphism of *Saccharomyces paradoxus* yeasts: geographical populations. Microbiology (Moscow) 94(5):733–747.

3 Naumova ES, Lee CF, Boundy-Mills KL, Naumov GI. 2025. *Komagataella petrovskyi* sp. nov, a new species of the yeast genus *Komagataella*. Microbiology (Moscow) 94 (6):940–947.

A novel ascosporogenous methylotrophic yeast species *Komagataella petrovskyi* sp. nov. is described using the type strain UCDFST 67-562T (=CBS 15016 = VKPM Y-4329 = NRRL Y-63971) isolated by H. Phaff from exudate of an elm tree *Ulmus davidiana* var. *japonica* in 1967 (Tomakomai, Japan). The new species was differentiated from *K. kurtzmanii*, *K. mondaviorum*, *K. pastoris*, *K. phaffii*, *K. populi*, *K. pseudopastoris*, and *K. ulmi* by divergence in gene sequences for D1/D2 LSU rRNA, ITS1-5.8S-ITS2, RNA polymerase subunit I, and translation elongation factor-1α. The GenBank accession numbers for the D1/D2, ITS region, *EF-1α* and *RPB1* genes are MF276797, MF276793, MF278889 and MF278894, respectively. *Komagataella petrovskyi* sp. nov. is registered in MycoBank under MB 821790.

III 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 Aoki K, Ohkuma M, Sugita T, Kobayashi Y, Tanaka N, Takashima M. 2025. Nuclear division phenotypes in Sporidiobolales and Trichosporonales. Microbiol Spectr 13(11):e0132725 https://doi.org/10.1128/spectrum.01327-25

2 Kobayashi Y, Sugiyama J, Sk R, Shiwa Y, Aoki K, Tanaka N, Takashima M. 2025. Phylogenomic insights into Taphrinomycotina and genomic features of *Saitoella coloradoensis* based on whole-genome sequencing at the chromosome level, with a proposal of the new class Saitoellomycetes. Mycologia (accepted).

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

A letter to the Editor that appeared in the June issue of the Yeast Newsletter has now been published as a commentary.

1 Ahearn DG. 2025. Commentary. Emerging yeast infections in confined elderly: niche effects and rapid, opaque diversities affecting multisciences for strains of *Candida/Clavispora/Candidozyma* complex. Microorganisms (MDPI) 13:2007 - https://doi.org/10.3390/microorganisms13092007

Undetected, rare diversities scattered among medically important emerging yeast, both in historical literature and recent AI research, are questioned and proffered for rapid and variable niche adaptations. These variable stresses may appear most notable among the medical sciences concerned with emerging yeast infections. Misidentified species, questionable therapies, and possible disease functions and retractions or rejections of manuscripts are identified in part, with the *C. haemulonii* Complex, *C. auris*, and *C. lusitaniae*. Analysis of the Commentary below, including a thorough definition of the disputed details among the references, implies that further researches on EVs and sRNA are needed by multi-sciences.

V Lodz University of Technology. Faculty of Biotechnology and Food Sciences, Department of Environmental Biotechnology, Wolczanska 171/173, 90-530 Lodz, Poland. Communicated by Prof. Dorota Kregiel <dorota.kregiel@p.lodz.pl>.

The following papers have been published.

1 Perek, Z, Krupa, S, Nizioł, J, Kręgiel, D, Ruman, T, Gutarowska, B. 2025. Metabolomic insights into the antimicrobial effects of *Metschnikowia* yeast on phytopathogens. Molecules (MDPI) 30:3268 https://doi.org/10.3390/molecules30153268

One of the most important features of *Metschnikowia pulcherrima* is its strong antimicrobial activity against phytopathogens, which makes it a suitable candidate for use in biocontrol during crop cultivation. However, the mechanisms of its antimicrobial activity are not currently well understood. In this study, we used metabolomic methods to investigate the possible mechanisms of antimicrobial activity by *M. pulcherrima* against phytopathogenic fungi. First, we tested the antimicrobial activity of five selected isolates against eleven phytopathogenic molds. Based on the results, selected yeast–pathogen co-cultures were cultivated on liquid and solid media. The supernatants from the liquid co-cultures were analyzed using the UHPLC-QToF-UHRMS and MS/MS methods. Co-culture growth on solid agar media was examined using the LARAPPI/CI MSI method. The yeast exhibited strong antagonism toward the mold phytopathogens. The LARAPPI/CI MSI method revealed the presence of various compounds with potential antifungal activity. The complex UHPLC-QToF-UHRMS analysis confirmed that the metabolic response of *M. pulcherrima* depends on specific yeast–pathogen interactions.

2 Kregiel, D, Dziekonska-Kubczak, U, Czarnecka-Chrebelska, K, Pielech-Przybylska, K. 2025. Chemical fingerprints of honey fermented by conventional and non-conventional yeasts. Molecules (MDPI) 30:2319 https://doi.org/10.3390/molecules30112319

Previous studies have shown the positive effects of non-conventional *Metschnikowia* spp. yeasts in mixed cultures with *Saccharomyces cerevisiae* on the properties of fruit wines. In this study, we investigated the effects of using conventional *S. cerevisiae* and non-conventional *Metschnikowia pulcherrima* yeasts as starter cultures in controlled mixed fermentations of honey wort. Other non-conventional yeasts were also tested for comparison, including *Wickerhamomyces anomalus*, *Dekkera/Bretannomyces bruxellensis*, and *Wickerhamomyces anomalus*. We evaluated the tolerance of the tested yeasts to high sugar content and analyzed the metabolic profiles of both monocultures and mixed systems. The *M. pulcherrima* strain showed the highest tolerance to 30% w/v glucose. The chemical complexity of fermented honey was improved using *M. pulcherrima* in co-starters with *S. cerevisiae*. The fermented honey samples were characterized by lower ethanol content, higher glycerol level, and rich volatilomes containing higher levels of both esters (ethyl acetate, 3-methylbutyl acetate, 2-methylpropyl acetate) and aliphatic alcohols (2-methylpropan-1-ol, 3-methylbutan-1-ol, and 2-methylbutan-1-ol). Similar characteristics were obtained using mixed populations of four strains: *S. cerevisiae*, *M. pulcherrima*, *D. bruxellensis*, and *W. anomalus*.

3 Liu, J, Rygała, A, Zhang, B, Kręgiel, D. 2025. Potential of *Metschnikowia* yeasts in green applications: a review. Front Microbiol 16:1652494 - https://doi.org/10.3389/fmicb.2025.1652494

The unconventional yeasts *Metschnikowia* spp. represent a valuable microorganisms with enormous yet untapped potential. *Metschnikowia* species are briefly reviewed, demonstrating that taxonomic and genomic analysis can open numerous opportunities to exploit their unique character and potential in the development of modern winemaking and brewing, probiotics and biocontrol, and the synthesis of single-cell proteins. These yeasts can be used in both bioprocesses and biorefineries, contributing to the production of biofuels and unique products recovered from agro-industrial wastes. This review, through a comprehensive bibliographic analysis, examines various green strategies for the production of alcohols, lipids, unsaturated fatty acids, and other valuable metabolites. Furthermore, the article discusses the challenges and barriers hindering the full implementation of *Metschnikowia* spp. in new approaches and technologies.

VI Department of Food Science, University of Guelph, Guelph, ON, Canada. Communicated by Linda Horianopoulos <lhoriano@uoguelph.ca>.

The Horianopoulos lab opened in the Department of Food Science at the University of Guelph in September 2025. We are interested in studying the natural diversity of yeast metabolism and stress resistance and harnessing these traits for applications through traditional and precision fermentations. We are recruiting graduate students and open to collaborations across the yeast community.

Recent publications.

1 Horianopoulos LC, Rokas A, Hittinger CT. 2025. Convergent evolution of aerobic fermentation through divergent mechanisms acting on key shared glycolytic genes. bioRxiv https://doi.org/10.1101/2025.10.02.679963

As the tree of life becomes increasingly accessible to molecular investigations, describing mechanisms underlying evolutionary convergence and constraint will be crucial to understanding diversification. The lineage including the model yeast *Saccharomyces cerevisiae* evolved aerobic fermentation in part through an ancient whole genome duplication and retention of glycolytic genes. To evaluate the glycolytic rates across diverse yeasts, we developed and deployed an extracellular acidification rates (ECAR) assay on 299 species that span more than 400 million years of evolution and identified a clade in the genus *Saturnispora* that convergently evolved aerobic fermentation. Through comparative genomics and transcriptomics, we found that several glycolytic genes had higher expression and novel cis-regulatory elements in aerobically fermenting *Saturnispora* species. When the transcription factor required for their activation was deleted in *Saturnispora dispora,* the mutants had reduced glycolytic rates and increased respiration. Intriguingly, many of the upregulated genes are orthologous to duplicated glycolytic genes in *S. cerevisiae.* These divergent genetic mechanisms suggest that there are strong evolutionary constraints on how some traits like aerobic fermentation can arise convergently.

2 David KT, Horianopoulos LC, Goncalves C, Steenwyk JL, Pontes A, Goncalves P, Hittinger CT, Pennell M, Rokas A. Discovery of additional ancient genome duplications in yeasts. bioRxiv https://doi.org/10.1101/2025.08.31.673279

Whole genome duplication (WGD) has had profound macroevolutionary impacts on diverse lineages, preceding adaptive radiations in vertebrates, teleost fish, and angiosperms. In contrast to the many known ancient WGDs in animals and especially plants, we are aware of evidence for only four in fungi. The oldest of these occurred ~100 million years ago (mya) and is shared by ~60 extant Saccharomycetales species, including the baker's yeast *Saccharomyces cerevisiae*. Notably, this is the only known ancient WGD in the yeast subphylum Saccharomycotina. The dearth of ancient WGD events in fungi remains a mystery. Some studies have suggested that fungal lineages that experience chromosome and genome duplication quickly go extinct, leaving no trace in the genomic record, while others contend that the lack of known WGD is due to an absence of data. Under the second hypothesis, additional sampling and deeper sequencing of fungal genomes should lead to the discovery of more WGD events. Coupling hundreds of recently published genomes from nearly every described Saccharomycotina species with three additional long-read assemblies, we discovered three novel WGD events. While the functions of retained duplicate genes originating from these events are broad, they bear many similarities to the well-known WGD that occurred in the Saccharomycetales. Our results suggest that WGD may be a more common evolutionary force in fungi than previously believed.

3 Aranguiz K, Horianopoulos LC, Elkin L, Segura Abá K, Jordahl D, Overmyer KA, Wrobel RL, Coon JJ, Shiu S-H, Rokas A, Hittinger CT. (2025) Machine learning uncovers gene families impacting oxidative stress resistance across yeasts. Nature Communications 16(1):5866.

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 characterize the variation in resistance to the ROS-inducing compound *tert*-butyl hydroperoxide across the ancient yeast subphylum Saccharomycotina and use machine learning (ML) to identify gene families whose sizes are predictive of ROS resistance. The most predictive features are enriched in gene families related to cell wall organization and include two reductase gene families. We estimate the quantitative contributions of features to each species' classification to guide experimental validation and show that overexpression of the old yellow enzyme (OYE) reductase increases ROS resistance in *Kluyveromyces lactis*, while *Saccharomyces cerevisiae* mutants lacking multiple mannosyltransferase-encoding genes are 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.

VII Department of Agricultural, Food and Environmental Sciences and Industrial Yeasts Collection DBVPG, University of Perugia, Borgo XX Giugno 74, I-06121 Perugia, Italy. Communicated by Pietro Buzzini <pietro.buzzini@unipg.it>.

Recent publications.

1 Oskolkov N, Sandionigi A, Götherström A, Canini A, Turchetti B, Zucconi L, Mimmo T, Buzzini P, Borruso L. 2024. Unraveling the ancient fungal DNA from the Iceman gut. BMC Genomics 25:1225 - https://doi.org/10.1186/s12864-024-11123-2

Background: Fungal DNA is rarely reported in metagenomic studies of ancient samples. Although fungi are essential for their interactions with all kingdoms of life, limited information is available about ancient fungi. Here, we explore the possibility of the presence of ancient fungal species in the gut of Ötzi, the Iceman, a naturally mummified human found in the Tyrolean Alps (border between Italy and Austria). **Methods**: A robust bioinformatic pipeline has been developed to detect and authenticate fungal ancient DNA (aDNA) from muscle, stomach, small intestine, and large intestine samples. Results: We revealed the presence of ancient DNA associated with *Pseudogymnoascus* genus, with *P. destructans* and *P. verrucosus* as possible species, which were abundant in the stomach and small intestine and absent in the large intestine and muscle samples. **Conclusion**: We suggest that Ötzi may have consumed these fungi accidentally, likely in association with other elements of his diet, and they persisted in his gut after his death due to their adaptability to harsh and cold environments. This suggests the potential co-occurrence of ancient humans with opportunistic fungal species and proposes and validates a conservative bioinformatic approach for detecting and authenticating fungal aDNA in historical metagenomic samples.

2 Bernetti A, Barili S, Sannino C, Mugnai G, Borruso L, Pinchuk I, Pezzolla P, Turchetti B, Gigliotti G, Buzzini P. 2025. Selective response of soil bacterial and fungal taxa to biodegradable polymers. Environ. Res. 264:120344 - https://doi.org/10.1016/j.envres.2024.120344

Biodegradable mulching films offer an eco-friendly alternative to petroleum-based plastics in agriculture, but their effects on soil parameters are not well understood. A microcosm experiment (20 °C, 75% field capacity) investigated the impact of two doses (0.021% and 1% w/w) of a biodegradable polymer on soil chemical and microbiological properties over a year. The 1% dose significantly ($p < 0.05$) increased CO_2 emissions, water-extractable organic C, and hydrolytic activity. A significant ($p < 0.05$) effect on microbial alpha- and beta-diversity was noted only during short- and medium-term incubations. In contrast, a taxon-related response was found for both bacterial and fungal taxa affecting the abundance of the genera *Aquicella*, *Cellvibrio*, *Bacillus*, *Ramlibacter*, and Saccharibacteria *genera incertae sedis* among bacteria, and *Malassezia*, *Orbilia* and *Rhodotorula* among fungi (including both yeast and filamentous lifestyles). Microbial functions revealed a greater impact on fungal communities compared to bacterial ones. However, after one year of exposition, only a marginal effect on the abundance of both bacterial and fungal functional groups was found in the microcosms. A significantly higher concentration of tightly bound exopolysaccharides in the presence of 1% biodegradable polymer at the start of the experiment suggested their key role in microbial degradation of bioplastics via biofilm formation.

3 Turchetti B, Mugnai G, Andreani D, Sannino C, Buzzini P. 2025. *Mrakia* spp. yeasts: extremophilic organisms with underexplored biotechnological potential. In: Sibirny AA (ed) Biotechnology of Yeasts and Filamentous Fungi. Grand Challenges in Biology and Biotechnology. Springer, Cham https://doi.org/10.1007/978-3-031-74726-7_11

Studies on the yeast genus *Mrakia* can be considered crucial to understanding the physiological and molecular bases of its adaptation to cold and also to selecting novel strains useful for food, chemical, cosmetic, and pharmaceutical applications. The present chapter summarizes the current state of the art on the taxonomy, ecology, physiology, and biotechnology of *Mrakia* spp. yeasts, with special emphasis on their role as starter cultures for fermentation processes and as producers of many valuable molecules of biotechnological interest. The future implications of its exploitation, also considering the most recent genomic studies, are discussed. Based on these, the genus *Mrakia* undoubtedly deserves special attention in view of its great, although still understudied, biotechnological potential.

4 Yurkov A, Turchetti B, Buzzini P. 2025. Microbial life in extreme habitats. In: Buzzini P, Turchetti B, Yurkov A (eds) Extremophilic Yeasts. Springer, Cham. - https://doi.org/10.1007/978-3-031-97453-3_1

Microorganisms are found across diverse ecosystems, including environments that are inhospitable to most life forms. Although yeasts are generally not regarded as resilient as prokaryotic extremophiles, many exhibit remarkable adaptability to harsh conditions such as high salinity, extreme temperatures, desiccation, and highly acidic or alkaline pH levels. Their survival is enabled by a range of physiological and molecular mechanisms, including specialized membrane compositions, efficient DNA repair systems, and unique metabolic pathways. The classification of yeasts as extremophilic or extremotolerant is somewhat subjective and context-dependent, but experimental evidence can support the attribution of certain species to extreme environments. Some yeasts are broad-spectrum survivors, capable of enduring multiple stressors, rather than being narrowly adapted to a single condition. Extreme conditions are present in a wide variety of habitats, often involving multiple stressors simultaneously. Poly-extremophilic environments are more common than previously assumed. In addition to natural extreme habitats, human activity has created numerous artificial extreme environments. Some, like certain foods, are shaped by microbial activity, while others, such as urban habitats, mimic desert-like conditions and are frequently colonized by extremophiles. This chapter provides an overview of extremophilic habitats, the yeasts that thrive in them, and the adaptations that support their survival. Understanding these adaptations not only enhances our knowledge of yeast biology and evolution but also offers promising avenues for biotechnological applications requiring robust microbial systems.

5 Turchetti B, Sannino C, Mugnai G, Buzzini P. 2025. Psychrophilic and Psychrotolerant Yeasts. In: Buzzini P, Turchetti B, Yurkov A (eds) Extremophilic Yeasts. Springer, Cham. https://doi.org/10.1007/978-3-031-97453-3_3

Cold habitats, defined by temperatures below 5 °C, cover much of the Earth and are vital for microbial diversity, particularly psychrophilic (cold-loving) and psychrotolerant (cold-tolerant) yeasts. These habitats, once thought lifeless, play key roles in biogeochemical cycles. Global warming has led to a steady reduction of these cold environments, spurring increased research into their microbial inhabitants. Studies have shifted from traditional culturing to more advanced methods like metagenomics, revealing a wider diversity of yeasts, both culturable and unculturable. Basidiomycota, especially genera like *Cystobasidium*, *Mrakia*, *Vishniacozyma*, *Dioszegia*, *Glaciozyma*, *Naganishia*, *Saitozyma*, *Solicoccozyma*, and *Vanrija*, dominate these ecosystems due to their efficient cold adaptations, such as polysaccharide capsule formation. Recent studies also suggest a greater diversity within Ascomycota such as *Aureobasidium* and *Candida*. Yeasts in these regions can be endemic or cosmopolitan, with some species showing psychrophilic behavior, while others exhibit psychrotolerant traits. Psychrophilic and psychrotolerant yeasts thrive in cold environments, adapting to harsh conditions like low temperatures, limited water availability, high ion concentrations, and UV radiation. These yeasts have developed several mechanisms to survive, including the synthesis of cold-active enzymes, antifreeze proteins, cryoprotectants, and extracellular polymers to prevent ice formation. Their membranes remain fluid at subzero temperatures due to increased unsaturated fatty acids. Genomic studies of Antarctic yeasts reveal genes that help them adapt to oxidative and cold stress. Cold-adapted yeasts have significant biotechnological potential, including the production of cold-active enzymes for industrial use, such as in food and detergent industries. They also produce antifreeze proteins with applications in cryopreservation and food preservation. These yeasts play crucial roles in bioremediation, biological pest control, and the production of biosurfactants. Despite the importance of cold habitats, they remain underexplored and vulnerable to climate change, highlighting the need for conservation and further research into these microorganisms.

6 Sannino C, Mugnai G, Turchetti B, Buzzini P. 2025. Yeasts at extreme pH conditions. In: Buzzini P, Turchetti B, Yurkov A (eds) Extremophilic Yeasts. Springer, Cham. https://doi.org/10.1007/978-3-031-97453-3_6

Some yeast species exhibit remarkable adaptability to extreme pH conditions, thriving in both highly acidic and highly alkaline environments. Acidophilic yeasts are commonly found in ecosystems such as acid mine drainage sites, acidic water environments, volcanic lakes, solfatara fields, and peat bogs, where pH values can drop below 3. These yeasts have evolved specialized mechanisms to maintain intracellular pH homeostasis, including active proton pumps, membrane remodeling, and stress response proteins. In contrast, alkaliphilic yeasts inhabit environments such as soda lakes, saline–alkaline soils, and industrial waste sites, where pH levels exceed 9. Their survival strategies involve ion transport systems, cytoplasmic buffering mechanisms, and metabolic reprogramming to counteract alkaline stress. These extremophilic yeasts play fundamental ecological roles in nutrient cycling, organic matter decomposition, and metal detoxification. Moreover, they offer promising applications in biotechnology, particularly in the production of enzymes, organic acids, and a few bioactive compounds. Acidophilic yeasts have been explored for their potential in bioremediation, bioleaching, and fermentation under low-pH conditions, while alkaliphilic yeasts are valuable for industrial processes requiring stability at high pH, such as detergent production and waste treatment.

7 Mugnai G, Sannino C, Borruso L, Andreani D, Battistel D, Turchetti B, Buzzini P, Guglielmin M. 2025. Cold-based glaciers and underlying permafrost: A possible new habitat for fungi. Appl. Soil Ecol. 216:106529 - https://doi.org/10.1016/j.apsoil.2025.106529

Recent studies have increasingly focused on cold-adapted microbial communities in polar and sub-polar habitats, including the effects of global warming. Among them, much research has concentrated on bacterial communities, while fungi, which are essential for carbon and nitrogen cycling, remain sometimes little considered. This study investigates how the structure of fungal communities (including yeast and filamentous life forms) in an Antarctic coastal cold-based glacier and in the underlying permafrost (which is an understudied habitat exhibiting challenging conditions for fungal life) is driven by both the key abiotic drivers and by the putative presence of ecological cooperation among dominant taxa. Results revealed a total of 337 fungal OTUs across the different layers (ice, brine, and permafrost): overall, yeasts dominated over filamentous life forms. *Meyerozyma* and *Taphrina* were found as the dominant genera in the deepest layers, suggesting the existence of a potential ecological cooperation finalized in a mutual support for survival in such extreme conditions. Beta-diversity analysis showed significant ($P < 0.05$) differences between fungal communities in glacier ice and permafrost, with brine as a transitional layer. Some abiotic parameters (i.e., Ca^{2+}, Cl^{-}, EC, K^{+}, Mg^{2+}, Na^{+}, NO_{3-}, SO_{42-}, and total nitrogen) were the key factors affecting the structure of fungal communities in the permafrost samples. This research offers new insights into fungal biodiversity between Antarctic cold-based glaciers and underlying permafrost, suggesting ecological equilibria affected by abiotic parameters. The dominance of *Meyerozyma* and *Taphrina* OTUs provides evidence of relict fungal taxa capable of long-term survival under extreme conditions over time.

8 Yurkov A, Visagie CM, Crous PW, Hashimoto A, Baschien C, Begerow D, Kemler M, Schoutteten N, Stadler M, Wijayawardene NN, Hyde KD, Zhang N, Boekhout T, ICTF Yeast Working Group, May TW, Thines M, Hawksworth DL. 2024. Cultures as types and the utility of viable specimens for fungal nomenclature IMA Fungus 15:20 - https://doi.org/10.1186/s43008-024-00155-8

The debates over the requirement of the International Code of Nomenclature for algae, fungi, and plants (ICNafp) for a viable specimen to represent the name-bearing type material for a species or infraspecific taxon have a long history. Taxonomy of fungi commonly studied as living cultures exemplified by yeasts and moulds, strongly depend on viable reference material. The availability of viable cultures is also particularly useful for several groups of filamentous and dimorphic fungi. While the preservation of metabolically inactive cultures is permitted and recommended by the ICNafp, there is room for improvement. Below, we review the history and current status of cultures as the name-bearing type material under the Code. We also present a roadmap with tasks to be achieved in order to establish a stable nomenclatural system that properly manages taxa typified by viable specimens. Furthermore, we propose setting up rules and defining the nomenclatural status of ex-type cultures under Chapter F, the section of the ICNafp that includes provisions specific to names of fungi.

9 Danise T, De Castro O, Zaccone C, Guggenberger G, Menta C, Innangi M, De Luca D, Di Iorio E, Turchetti B, Fioretto A. 2025. Implications of nurse species in mixed forest plantations management on soil fungal community diversity Appl. Soil Ecol. 206:105892 - https://doi.org/10.1016/j.apsoil.2025.105892

Mixed plantations provide numerous benefits in terms of ecosystem and socioeconomic services, as well as on soil chemical and biological parameters; thus, a forest management allowing to recover overexploited soils is highly recommended. Although nurse species may deeply affect soil properties, few studies are present in literature assessing their role. A study site characterized by a mixed plantation established on a former agricultural area was selected in order to evaluate the impact of a specific forest management on marginal soils, with a special emphasis on the role of nurse species. The intercropping systems investigated feature two economically important species, *Populus alba* and Juglans regia, along with one of following nurse trees, *Alnus cordata*, *Elaeagnus umbellata* (both N-fixing species), and *Corylus avellana*. Each stand was replicated three times, and an adjacent agricultural field was included for comparison. Methodologically, topsoils (0–10 cm of depth) were sampled and several chemical and biological parameters determined. Fungal taxa, as well as fungal ecological guilds and their functional roles, were identified by means of metabarcoding analysis. Ectomycorrhizal fungi dominated tree consociations (53.5 %), while non-mycorrhizal saprophytes dominated the arable, control soil (5.3 %). Two-Block Partial Least Squares showed differences both among tree consociations, where the presence of *the Alnus cordata* resulted in the highest concentration of organic carbon (19.10 ± 1.8 mg g^{-1}), total nitrogen (1.78 ± 0.1 mg g^{-1}), lignin (11.25 ± 1.1 mg g^{-1}), cellulose (1.54 ± 0.2 mg g^{-1}), and bioavailable phosphorus (8.99 ± 1.2 mg kg^{-1}), as well as fluorescein diacetate hydrolase enzyme activity, and between tree consociation and the arable land. Thus, the utilization of *Alnus cordata* as a nurse species seems to be the best solution for a forest management capable of improving soil chemical and biological quality, providing a viable strategy for the restoration of marginal soils, particularly in a climate change scenario.

10 Ansaldi N, duo Saito R, Turchetti B, de García V, Uttaro AD, Trochine A. 2025. Exploring the use of brewery spent liquids for lipid production in basidiomycetous yeasts. Waste Biomass Valor. 16:4399–4413 - https://doi.org/10.1007/s12649-025-02928-7

Purpose: This study investigates lipid production in nine basidiomycetous yeast strains from seven species, isolated from natural cold environments, using brewery spent liquids (BSLs) as well as glucose and maltose as carbon sources. **Methods:** Yeast strains were evaluated for biomass, lipid production, and sugar consumption across the three carbon sources. Chemical oxygen demand (COD), nitrogen (N), phosphorus (P), and sugar removal from brewery wastewaters were also assessed. Principal Component Analysis (PCA) was used to analyze the effect of each carbon source on the lipid profiles. **Results:** *Holtermanniella wattica* CRUB 2130, CRUB 2131, *Solicoccozyma aeria* CRUB 2153, and *Sporobolomyces ruberrimus* CRUB 1640 exhibited high lipid production on BSL, reaching yields up to 7.6 g L ^{1}. In contrast, *Rhodotorula taiwanensis* CRUB 1425 showed moderate to low lipid production, poor COD removal, and low biomass production. *Tausonia pullulans*, *Vanrija albida* CRUB 2161, and *Solicoccozyma* sp. CRUB 2155 also had moderate to low lipid production but were effective in N and P removal. Although COD removal did not meet discharge guidelines, some yeasts met local requirements for N and P removal. The main fatty acids (FAs) in all strains were palmitic, stearic, oleic, and linoleic acids, with some also producing α-linolenic acid, influenced more by strain than carbon source. **Conclusions:** *S. aeria* CRUB 2153, *S. ruberrimus* CRUB 1640, and *H. wattica* strains demonstrated superior oleagenicity on BSL and the ability to consume higher sugars, making them promising candidates for lipid production using BSL, maltose, or starch-rich wastes.

Recently published book.

11 Buzzini P, Turchetti B & Yurkov A. 2025. Extremophilic Yeasts, Springer Cham, Germany - https://link.springer.com/book/10.1007/978-3-031-97453-3

This book presents the latest findings on the biodiversity, adaptation strategies, and biotechnological significance of extremophilic and extremotolerant yeasts. It is a valuable resource for researchers interested in the microbiology of these intriguing microorganisms. The book is divided into three parts: **Part I** gives an overview of prokaryotic and eukaryotic microbial life in extreme habitats; **Part II** focuses on the biodiversity, adaptation strategies and biotechnological applications of extremophilic yeasts, categorized according to the specific limiting abiotic parameters, such as thermotolerant (high temperature), psychrophiles and psychrotolerant (low temperature), acidophiles and acidotolerant (low pH), alkaliphiles and alkalitolerant (low pH), alkaliphiles and alkalitolerant (high pH), halophiles and halotolerant (high salinity), osmophiles and osmotolerant (low water activity), piezophilic and piezotolerant (high hydrostatic pressure), metallotolerant (high metal concentration), and oxidative stress-tolerant yeasts; **Part III** discusses the use of extremophilic yeasts in extreme foods and their biotechnological applications under extreme conditions.

The book includes contributions from leading eminent scientists to present the latest insights into the biodiversity, adaptation strategies, and biotechnological significance of extremophilic and extremotolerant yeasts. It aims to provide a valuable resource for research interested in the microbiology of these intriguing microorganisms. It is written for biologists, mycologists, chemists and all researchers whose field of study focuses on yeast biotechnology.

Table of Contents

VIII School of Life Sciences, Institute of Life Sciences and Green Development, Hebei University, Baoding, 071002, Hebei, China. Communicated by Qi-Ming Wang. <wangqm@hbu.edu.cn>.

Recent publications.

1 Liu MM, Tian ZY, Wang YM, Wang QM. 2025. Enhancement of skin defense against UVB damage by fermentation of *Leonurus japonicus* with *Saccharomyces cerevisiae.* Phytomedicine 147:157206 https://doi.org/10.1016/j.phymed.2025.157206

2 Zhao YJ, Liu MM, Qin-Ma, Boekhout T, Wang QM. 2025. *Malassezia cafarchiae* sp. nov., a novel species isolated from the ear canal of cats infested with *Otodectes Cynotis*. Mycopathologia 190(6):113 https://doi.org/10.1007/s11046-025-01018-5

3 Liu M M, Bai J, Tian ZY, Zheng TT, Boekhout T, Wang QM. 2025. Oxymatrine ameliorates *Malassezia* overgrowth-induced psoriasis in vivo and in vitro by inhibiting the biofilm formation and inflammation. Mycology - https://doi.org/10.1080/21501203.2025.2511903

4 Zhu H-H, Liu M-M, Boekhout T, Wang Q-M. 2025. Improvement of a MALDI-TOF database for the reliable identification of *Candidozyma auris* (formerly *Candida auris*) and related species. Microbiol Spectr 13(1):e0144424 - https://doi.org/10.1128/spectrum.01444-24

IX Department of Microbiology and Biochemistry, Faculty of Natural and Agricultural Sciences University of the Free State, PO Box 339, Bloemfontein 9300, Republic of South Africa. Communicated by Olihile M. Sebolai <SebolaiOM@ufs.ac.za>.

Recent publication.

1 Maliehe M, Albertyn J, Sebolai OM. 2025. Assessing the anti-*Cryptococcus* antifungal potential of artemisinin. Int J Molec Sci (MDPI) – https://doi.org/10.3390/ijms26209953

Recent work by Maliehe et al. has uncovered compelling evidence that artemisinin, best known for its antimalarial properties, may hold antifungal potential against *Cryptococcus neoformans*. In vitro assays revealed that artemisinin disrupts fungal growth and morphology, likely through the induction of oxidative stress and mitochondrial dysfunction. The compound also enhanced the phagocytosis of yeast cells by macrophages and haemocytes and improved survival rates in larvae infected with artemisinin-treated cells, suggesting both direct and host-mediated antifungal effects. This study adds momentum to the search for novel treatments amid rising fluconazole resistance and highlights the value of drug repurposing in medical mycology.

X International Centre of Brewing and Distilling, Heriot-Watt University, Riccarton, Edinburgh, EH14 4AS, UK and Canadian Institute of Fermentation Technology, Dalhousie University, P.O. Box 15000, Halifax, NS B3H 4R2, Canada. Communicated by R. A. Speers <alex.speers@gmail.com>.

The following are recent conference presentations.

1 Speers RA, MacIntosh A. 2025. Craft beer pasteurisation - All-OK or apocalypse soon? Submitted to. the MBAA Ontario Section Meeting. Jan 27.

2 Speers RA. 2025. Beer-It's complicated. Acadia University. Allways Learning Series. Wolfville, NS. Oct 3.

3 Kaur M, Evans DE, Speers A, Stewart D, Bowman J. 2025. A quantitative polymerase chain reaction (qPCR) based diagnostic test for premature yeast flocculation (PYF) in malts. Institute of Brewing and Distilling (IBD) 2025 Convention. Hobart, Aus. March 3-7.

4 Li Y-S, Evans DE, Kilfoil G, Speers RA. 2025. Improving the ASBC Yeast-14 method for PYF detection with additional industrial lager yeast varieties. Institute of Brewing and Distilling (IBD) 2025 Convention. Hobart, Aus. March 3-7.

XI Culture Collection of Yeasts, Institute of Chemistry, Slovak Academy of Sciences, Dúbravská cesta 9, 845 38 Bratislava, Slovakia. Communicated by Renáta Vadkertiová <renata.vadkertiova@savba.sk>.

Recent publications.

1 Caboňová M, Vadkertiová R, Adamčík S, Bacigálová K, Slovák M, Zaib S, Caboň M. 2024. Taxonomic reintroduction of *Taphrina viridis* (Taphrinales, Ascomycota) associated with *Alnus alnobetula* as one of five well defined European species colonizing alders. Mycokeys 108:249-267 - https://doi.org/10.3897/mycokeys.108.127292

Phylogenetic analysis of four DNA regions (ITS, LSU, mtSSU and *tef1α*) supported the existence of five European *Taphrina* species which colonise *Alnus* in Europe. In addition to previously well-defined species, *T. viridis* is, for the first time recognised, by molecular study as a species related to *T. sadebeckii*. Analysis of publicly available sequences of barcoding regions suggested that *T. viridis* is only associated with *A. alnobetula* and no other *Taphrina* species colonize this host tree. Symptomatic, morphological, and physiological characterisation of *T. viridis* are provided together with the key for identification of *Alnus* associated *Taphrina* species in Europe and North America.

2 Vadkertiová R, Horváthová Á. 2025. Metallotolerant yeasts. In: Buzzini P, Turchetti B, Yurkov A. (eds) Extremophilic Yeasts. Springer, Cham - https://doi.org/10.1007/978-3-031-97453-3_8

Heavy metals (HMs) include elements essential for all living organisms in small amounts, such as iron (Fe), zinc (Zn), and copper (Cu), as well as metals and metalloids which may be toxic even in low concentrations, for example, lead (Pb), cadmium (Cd), mercury (Hg), arsenic (As), and antimony (Sb). Heavy metal pollution is a serious environmental problem worldwide. Industrialization, domestic activities, and agriculture can release excess amounts of heavy metals into the soil, water, and air, leading to health risks to people and the endangerment of all biota present in the environment. Individual yeast species possess mechanisms which eliminate the adverse effects of HMs on their cells. They can prevent HMs from entering the cells, sequester them into storage cellular structures, change their more toxic forms into less toxic forms, and bind them to extracellular structures such as exopolysaccharides or melanins. Different metallotolerant ascomycetous and basidiomycetous yeast species are present in sites slightly contaminated with heavy metals to sites heavily contaminated with heavy metals, where they inhabit various types of soil and water bodies, above and below ground parts of plants, and are also found in wastewater, sewage treatment plants, and extreme environments. Yeasts exhibit variability in their tolerance to HMs even within a community of yeasts isolated from the same site. Species highly tolerant to heavy metals are found especially in heavily polluted areas, and many of them also show multi-tolerance to heavy metals. The cultivation of metallotolerant yeasts in the presence of different HMs at different concentrations affects the profiles and amounts of exopolymeric substances, carotenoids, and melanins produced.

3 Bajus M, Vivodová Z, Bačovčinová M, Labancová E, Kučerová D, Horváthová Á, Holeková K, Hačkuličová D, Vadkertiová R, Kollárová K. 2025. The yeast *Papiliotrema laurentii* alleviates drought-induced stress in maize and affects oxidative status, LEA genes, hormone concentrations, and fatty acid allocation, Current Plant Biology, 44, 100542. https://doi.org/10.1016/j.cpb.2025.100542.

Drought stress can significantly affect maize growth; hence, new substances with a potential to alleviate drought-induced damage in plants are being investigated. Here, we studied the biostimulant potential and mechanisms of the yeast *Papiliotrema laurentii* CCY 17–3–24. The maize grains were treated with *P. laurentii* suspensions of different yeast concentrations (10^6, 10^7, 10^8, and 10^9 cells ml^{-1}) during the imbibition and germination. The yeast did not have plant-growth promoting effects in well-watered plants; however, it stimulated the growth of the drought-stressed maize in the concentration 10 cells ml^{-1} (e.g, shoot dry weight by 21.6 %). Furthermore, the relative water content and oxidative stress were improved in plants treated with the yeast compared to drought-stressed plants (e.g, decreased H_2O_2 concentration by 46.1 % in roots). The expression of *LEA* genes, which can be triggered by hormones, was significantly downregulated in yeast-treated plants compared to untreated plants. Although the yeast-treated plants showed slightly improved hormone concentrations (IAA, ABA) in drought compared to untreated plants (IAA concentration increased approximately by 19 %), the action of *P. laurentii* was not likely connected to its ability to produce hormones, neither its ability to change the accumulation of proline. However, based on the oleaginous nature of *P. laurentii*, its positive influence on plants suffering from drought can be possibly explained by the production of fatty acids and their uptake by plants. This was supported by the increased concentration of fatty acids, especially in the roots of the yeast-treated plants (by 205.3 %).

XII Department of Biology, University of Western Ontario, London, Ontario, Canada N6A 5B7. Communicated by M.A. Lachance <lachance@uwo.ca>.

Recent publications.

1 Avchar RP, Pontes A, Lachance MA, Sharma A, Sampaio JP. 2025. *Metschnikowia ratanii* f.a. sp. nov. an novel ascomycetous yeast species isolated from flowers of *Lantana camara* in India. Int J Syst Evol Microbiol 75(7):006851 - https://doi.org/10.1099/ijsem.0.006851

Four yeast strains isolated from the nectar of *Lantana camara* flowers in Pune, India, represent a novel asexual ascomycetous species in the genus *Metschnikowia*. Phylogenetic analyses of the internal transcribed spacer and D1/D2 regions of the LSU rRNA gene place this species within a subclade of large-spored *Metschnikowia* species that includes *Metschnikowia aberdeeniae*, *Metschnikowia shivogae* and *Metschnikowia hibisci*. The new species differs by its ability to grow at 35 °C. Whole-genome sequencing and comparative analyses revealed average nucleotide identity values of 76–77% and digital DNA–DNA hybridization values of 14–16% relative to related species, confirming its novelty. The species is described as *Metschnikowia ratanii* sp. nov., with strain MCC 10123 as the ex-type strain and MCC 9961, MCC 9962 and MCC 9928 as additional cultures. The MycoBank number is MB 858027.

2 Barros KO, Al-Oboudi J, Freitas LFD, Sousa FMP, Batista T, Santos ARO, Morais PB, Sampaio JP, Lachance MA, Hittinger CT Rosa CA. 2025. Taxogenomic analysis of *Pichia senei* sp. nov. and new insights into hybridization events in the *Pichia cactophila* species complex. FEMS Yeast Res 25:foaf037 - https://doi.org/10.1093/femsyr/foaf037

3 Costa C, Lopes MR, Barros KO, Souza GFL, Santos ARO, Souza LMD, Rosa LH, Abegg MA, Morais PB, Lachance MA, Rosa CA. 2025. *Spathaspora cesarfonsecae* sp. nov., a xylose-fermenting yeast isolated from gut of passalid beetles and rotting wood in the Amazonian rainforest biome. Int J Syst Evol Microbiol (accepted July 2025) - https://doi.org/10.1099/ijsem.0.006871

4 Lachance MA, Caceres C, Fredericks M, Duffy M, Stewart Merrill T. 2025. Reviving Élie Metschnikoff's Monospora: the obligately parasitic yeast *Australozyma monospora* sp. nov. FEMS Yeast Research 25:foaf041 - https://doi.org/10.1093/femsyr/foaf041

A vast literature explores a model system that consists of a prey crustacean, the water flea *Daphnia* spp., and an obligately pathogenic yeast that has been referred to as *Metschnikowia bicuspidata* and thought to represent the material used by Metschnikoff in his study of innate immunity. Typification of species bearing that name and indeed the whole genus has been problematic as regards yeasts that only grow or form aciculate ascospores *in hospite*. The neotype of *M. bicuspidata*, unlike the *Daphnia* parasite, is easily cultured on a variety of laboratory media, although it too can cause serious infections in a variety of mostly aquatic animals. It has become evident that the Daphnia parasite studied by Metschnikoff or current workers is not closely related to *M. bicuspidata* as currently understood. Analysis of whole genome DNA extracted from the yeast repeatedly found in infected *Daphnia* specimens shows that it belongs to the recently circumscribed genus *Australozyma*. The yeast is described here as *Australozyma monospora* sp. nov. The species, although haplontic and heterothallic, forms single-spored asci without mating. It also appears that all species in the genus are restricted to asexual reproduction, which may explain their rare status. The holotype is MICH 346683. The name is registered in Mycobank under the number MB 859667.

5 Santos ARO, Ávila GR, Torre OHP, Pompéia SL, Andrietta MGS, Rosa CA, Lachance MA. *Metschnikowia maris* comb. nov., a large-spored yeast species endemic to Serra do Mar Atlantic Rainforest biome, Sao Paulo State, Brazil. Int J Syst Evol Microbiol (accepted August 2025) - https://doi.org/10.1099/ijsem.0.006891

Two yeast isolates from passion flowers were sampled in the southern part of the Serra do Mar Atlantic Rainforest in Sao Paulo State, Brazil. Barcode sequencing and mating experiments showed them to be representatives of *Metschnikowia matae* var. *maris*, thus originally named due to the availability of only a single isolate and uncertainties regarding reproductive isolation. The two new isolates being of the complementary mating type to the previously known strain, intravarietal crosses were performed. They yielded a preponderance of two-spored asci, unlike crosses with *M. matae* var. *matae*, which led to largely sterile asci. We therefore elevate the variety maris to the rank of species, with the name *Metschnikowia maris* comb. nov. The holotype is UFMG-CM-Y397T (MATα). Strain UFMG-CM-Y7613A (MATa) is designated as allotype. The new combination is registered as MB 859665.

Presentations at conferences.

6 Lachance MA. 2025. A lifetime of research on yeasts. Entretiens Scientifiques Lallemand Oenology. Porto, Portugal.

7 Lachance MA. 2025. Evolution of parasitism in *Metschnikowia*. Encontro Nacional sobre Leveduras, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

8 Lachance MA. 2025. Metschnikoff's Yeast. CanFunNet Virtual Conference

In 1884, Metschnikoff published groundbreaking observations of yeast ascospores stabbing the guts of water fleas and being attacked by phagocytes, earning him the 1908 Nobel prize. He named the yeast *Monospora bicuspidata*, which taxonomists later reassigned to *Metschnikowia*, *Monosporella*, and *Metschnikowiella*, only to be declared a *nomen dubium* in 1961. While its taxonomy has remained obscure, the yeast has been adopted by several laboratories as part of a model system for host-pathogen interactions, under the name *Metschnikowia bicuspidata*. Sequence-based studies have now shown that although *Metschnikowia bicuspidata* is indeed a pathogen, it is not Metschnikoff's yeast. I have examined fresh specimens of the *Daphnia* pathogen and explored its genome to clarify its systematics. I shall present a new genus and species assignment as well as evidence that the organism has lost the ability to reproduce sexually while retaining ascospore formation as an infection mechanism.

Obituary

Adele Statzell-Tallman (1939-2025)

With deep sadness, I report the death of Adele Statzell-Tallman on June 11, 2025. Adele worked in my lab for many decades and was well known to the yeast community. A brief description of her many accomplishments and advances in yeast science complements the attached obituary written by her family.

Adele obtained a BS degree from Ursinus College, Pennsylvania and a MS degree in mycology from University of Pennsylvania in 1967. Shortly thereafter she started her research career in my lab at the Marine Laboratory, University of Miami, Florida. Our first joint publication was in 1969.

Adele was skilled in laboratory techniques and was a relentless field scientist. She explored many shore lines and offshore waters and tramped through miles of mangroves in the Florida Everglades, Bahamas and Caribbean to explore the vast diversity of yeast species. Her collections produced hundreds of strains, that had to be grown, maintained and identified by the standard morphological and biochemical techniques. A horrendous task.

In addition to routine methods, Adele used her artistic talents to provide drawings and photography of yeast morphology for species descriptions. An expert with the microscope micro-manipulator, Adele was able to separate and grow individual basidiospores, leading to our knowledge of multiple-allelic basidiomycetous mating systems. Her study of yeast life cycles led to the description of unknown yeasts, most notably the genus *Kwoniella*. Adele rapidly incorporated emerging molecular techniques into her studies, contributing extensively to our understanding of phylogenetic relationships.

Adele was a lead or contributing author on multiple publications, including chapters in two editions of The Yeasts, A taxonomic study. According to ResearchGate, Adele has 2270 citations. Members of the yeast community with whom Adele published include Herman Phaff, Clete Kurtzman, Teun Boekhout, Alvaro Fonseca, David Yarrow and Kyria Boundy-Mills.

As our laboratory manager, Adele was fondly known in the scientific community for her careful teaching and mentoring of students, undergraduate and graduate, post docs and visiting scientists. Teun Boekhout, who was a young post-doc in our lab, recently wrote “I have very good memories from my time at your lab. Adele acted like a mom for me. She also lent her bike to me. Her house at the Grove with the Audubon books still is in my mind as kind of a secret place.”

R.I.P. Adele Statzell-Tallman: scientist, artist, mentor and dear friend to the yeast community.

Jack Fell

***

Adele Tallman, beloved sister, scientist, and steward of the sea, passed away peacefully June 11, 2025, at the age of 86 in her longtime hometown of Miami, Florida.

Born on June 2, 1939, Adele dedicated her life to the pursuit of knowledge, beauty, and harmony with the natural world. A longtime Floridian, she was a pillar in the marine biology community, having served over 50 years at the University of Miami's School of Marine Science. Her contributions to ocean science and environmental stewardship left an indelible mark on both her colleagues and the ecosystems she worked tirelessly to protect.

Adele's passions were as vast and deep as the oceans she studied. She was an avid sailor, often seen navigating the waters of Biscayne Bay with grace and determination. Her love for plants, animals, and the arts infused every corner of her life-her home was a living gallery of tropical flora, marine memorabilia, and original artwork that celebrated the natural world she so deeply cherished.

She is survived by her devoted sister, Elsa Diamond, as well as a wide circle of friends, students, and fellow nature lovers who were touched by her wisdom, warmth, and unwavering sense of wonder. She was married to Sid Tallman for more than 20 years and she is also survived by her nieces and nephews, Kimberly Jackson, William Statzell, Jeanne Osborne, Susan Burgos, Andrew Diamond, Robert Statzell and Richard Diamond.

A future private memorial will be held for close family and friends. In lieu of flowers, donations may be made in Adele’s name to the University of Miami's Rosenstiel School of Marine, Atmospheric, and Earth Science or the Fairchild Botanical Gardens.

Adele's spirit will live on in the tides she studied. the winds she sailed, and the hearts of all who loved her.

Forthcoming Meeting

50th Annual Conference on Yeasts - 48th ACY
Smolenice, Slovakia 19 May – 22 May, 2026

It is our great pleasure to invite you to the 50th Annual Conference on Yeasts (ACY). The 50th ACY is organized by the Commission on Yeasts of the Czechoslovak Society of Microbiology and the Institute of Chemistry SAS, and will take place on May 19 - 22, 2026 in Smolenice Castle, Slovakia. The main topics of the 50th ACY will be:

- Molecular and Cell Biology of Yeasts
- Biotechnology of Yeasts
- Yeast Diversity and Interactions

The conference has been regularly held in the Congress Centre of the Slovak Academy of Sciences in the beautiful Smolenice Castle, located in the Small Carpathians (about 50 km from the capital city Bratislava). The splendid interiors of the castle and the beautiful natural surroundings contribute to a relaxing atmosphere at the meetings and provide a lot of space for informal and stimulating discussions of scientists. Thanks to the speakers, friendly atmosphere and unique location, the yeast conference is also exciting for students and young scientists.

For more information: https://yeastconference.sk
Milan Čertík
Renáta Vadkertiová

Draft Guidelines for the Publication of Yeast Species Descriptions in the Yeast Newsletter

(Modified from https://doi.org/10.1002/yea.3465)

The Yeast Newsletter will publish concise, but high-quality descriptions of new yeast species. Submissions will be subjected to rigorous peer review. The following elements will be considered:

- Evidence of high-quality work.
- Focused, up-too-date review of the relevant taxonomic literature.
- A brief but clear statement of the sampling design, isolation method, substrate, and geographic origin of all isolates.
- A statement of the appropriate methods used to detect the sexual life cycle.
- A clear indication of the authorities accountable for the new name.
- Compliance with the Madrid Code's (https://www.iaptglobal.org/_functions/code/madrid) requirements, including proper typification:
  - Deposition of the holotype in conformity with Articles 8 and F11
  - Deposition of isotypes (plus a separate allotype as appropriate) in two institutional culture collections, in accordance with Recommendation 8B1, preferably including the Westerdijk Fungal Biodiversity Institute (formerly CBS) collection. The spirit of this provisions, which is to make cultures genuinely available for study, will be honoured.
  - Registration of the name in a recognized registry (*e.g.*, MycoBank).
- Correct statement of the etymology of epithet.
- A clear statement of the relevant concepts used in delineating the proposed species.
- A list of salient growth properties. A longer list of tests performed should be deposited as supplementary data.
- A clear description of the sexual life cycle, or in the absence of such, the mention f.a. (*forma asexualis*) in the title if the genus contains species with a known sexual cycle.
- High-quality, high-resolution, well-composed micrographs of asexual and sexual states, as applicable.
- Accession numbers of barcode and genome sequences deposited in a world database.
- A neighbor-joining analysis of appropriate barcode sequences for close relatives of the proposed species, including representatives of unique phylotypes that have a high percent identity with that of the proposed taxon. A genome-based phylogeny as required. The tree may be placed in the main document or the supplemental data depending on size and relevance. Trees should be compact, with large fonts, and submitted in vector (editable) format in a PPT file.
- Average nucleotide identity (ANI – 10.1007/s10482-017-0844-4) values for immediate relatives.
- Multiple isolates, as evidenced by a statement on the variation observed among isolates, as determined in the same laboratory. In the absence of multiple isolates, a justification for the description of a species from a single isolate.

Format

Articles will be limited to two pages in length and will consist of a title that contains the name of the new species, a list of authors and their affiliations, followed by the main text. Authors should be limited to individuals that have contributed directly. Individual contributions should be specified in the supplemental data.

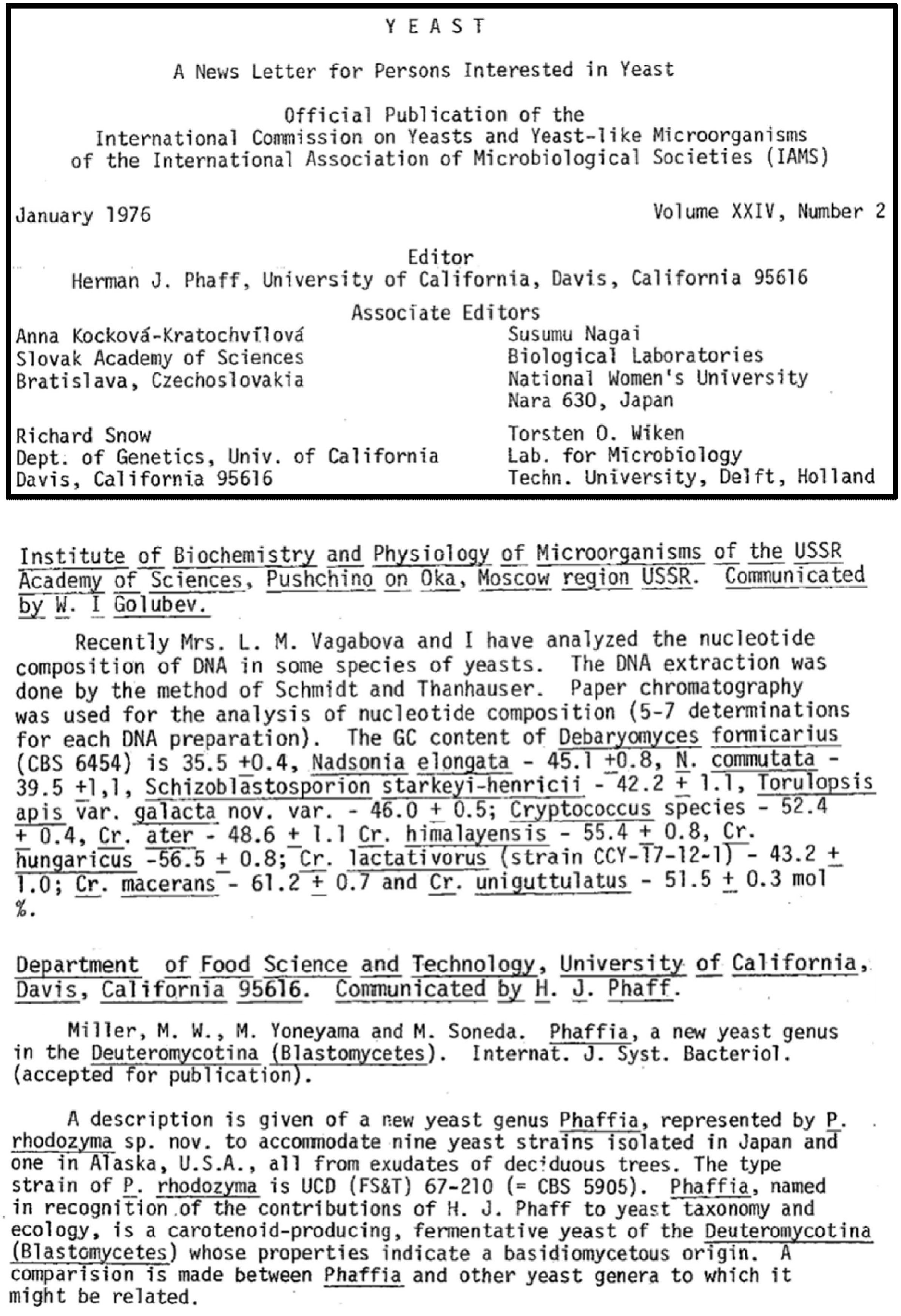
Additional data in the form of relevant figures or tables may be submitted as supplemental data.

Figures should be submitted in vector (editable) format in a PPT file. They may include additional micrographs, trees, diagrams, karyotype analyses, or charts that contribute to the systematics of the proposed taxon. Tables should be prepared in Excel, with the minimum possible formatting.

Other taxonomic papers

Descriptions of multiple species, species descriptions accompanied by explorations of the ecology, evolution, genetics, biochemistry, or applications, proposals for name changes or the creation or modification of higher taxa should be submitted as conventional articles in other established journals.

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)

January 1976 Volume XXIV, Number 2

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Institute of Biochemistry and Physiology of Microorganisms of the USSR Academy of Sciences, Pushchino on Oka, Moscow region USSR. Communicated by W. I Golubev.

Recently Mrs. L. M. Vagabova and I have analyzed the nucleotide composition of DNA in some species of yeasts. The DNA extraction was done by the method of Schmidt and Thanhauser. Paper chromatography was used for the analysis of nucleotide composition (5-7 determinations for each DNA preparation). The GC content of *Debaryomyces formicarius* (CBS 6454) is 35.5 ±0.4, *Nadsonia elongata* - 45.1 ±0.8, *N. commutata* - 39.5 ±1,1, *Schizoblastosporion starkeyi-henricii* - 42.2 ± 1.1, *Torulopsis apis* var. *galacta* nov. var. - 46.0 ± 0.5; *Cryptococcus* species - 52.4 ± 0.4, *Cr. ater* - 48.6 ± 1.1 *Cr. himalayensis* - 55.4 ± 0.8, *Cr. hungaricus* -56.5 ± 0.8; *Cr. lactativorus* (strain CCY-17-12-1) - 43.2 ± 1.0; *Cr. macerans* - 61.2 ± 0.7 and *Cr. uniguttulatus* - 51.5 ± 0.3 mol %.

Department of Food Science and Technology, University of California, Davis, California 95616. Communicated by H. J. Phaff.

Miller, M. W., M. Yoneyama and M. Soneda. *Phaffia*, a new yeast genus in the *Deuteromycotina (Blastomycetes)*. Internat. J. Syst. Bacteriol. (accepted for publication).

A description is given of a new yeast genus *Phaffia*, represented by *P. rhodozyma* sp. nov. to accommodate nine yeast strains isolated in Japan and one in Alaska, U.S.A., all from exudates of deciduous trees. The type strain of *P. rhodozyma* is UCD (FS&T) 67-210 (= CBS 5905). *Phaffia*, named in recognition of the contributions of H. J. Phaff to yeast taxonomy and ecology, is a carotenoid-producing, fermentative yeast of the *Deuteromycotina (Blastomycetes)* whose properties indicate a basidiomycetous origin. A comparision is made between *Phaffia* and other yeast genera to which it might be related.

Clinical Mycology Section, National Institute of Allergy and Infectious Diseases, NIH, Bethesda, Md. 20014. Communicated by K. J. Kwon-Chung.

Sexual Life Cycle of Cryptococcus neoformans

A basidiomycetous life cycle was found in Cryptococcus neoformans. When compatible pairs of isolates were inoculated on malt extract agar and incubated at temperatures between 15 to 37°C for 2 to 3 weeks, the sexual reproduction initiates with conjugation of two yeast cells which is followed by hyphal formation with clamp connections. Dikaryotic hyphae produce long basidia, singly or in a group, each having a subglobose to flask-shaped apex. Chains of sessile basidiospores are produced on the apex of each basidium by repetitious budding from four spots on the apex. Basidiospores are hyaline, ovate to globose and finely rough, measuring 1.8 to 2.5 μm. The perfect state of C. neoformans is described as Filobasidiella neoformans Kwon-Chung in the Filobasidiaceae of the Ustilaginales. Published in Mycologia, November - December issue of 1975.

VII. Ruhr-Universität Bochum, Institut für Physiologische Chemie, 4630 Bochum, Germany. Communicated by Wolfgang Duntz.

The following studies on the structure of α factor, the mating type specific sexual hormone of α cells of S. cerevisiae which specifically inhibits DNA synthesis and cell division in a cells, have been completed and will be published presently.

1. Heterogeneity of α factor.

Several compounds exhibiting α factor activity are found in culture filtrates of α cells. These compounds represent a group of related linear peptides of 13 or 12 amino acids, designated as α_1, α_2, α_3, and α_4. The main compounds, α_1, and α_2, differ by an amino-terminal tryptophan residue which is present in α_1 and lacking in α_2. Otherwise the primary structures are identical. α_3 and α_4 are oxidation products of α_1 and α_2, respectively.

2. Primary structure of factor(s).

The following amino acid sequence has been found for α_1 and α_2:

H_2N-(Trp)-His-Trp-Leu-Gln-Leu-Lys-Pro-Gly-Gln-Pro-Met-Tyr-COOH· α_3 and α_4 are the methionine sulfoxides of α_1 and α_2.