Yeast

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Marc-André Lachance, Editor
University of Western Ontario, London, Ontario, Canada N6A 5B7
<lachance@uwo.ca>

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Editorials

Graham Stewart (1942-2026)

I regret to announce the loss of our colleague, Graham Stewart. For 25 years, Graham served in various capacities at the Labatt Brewing Company, in London, Ontario, Canada, ten of which as Technical Director. He then became Professor of Brewing and Distilling and Director of the International Centre for Brewing and Distilling, at Heriot-Watt University, in Edinburgh, Scotland, and continued his scientific activities as Professor Emeritus. He was President of the International Commission on Yeasts, having organized the 1980 International Yeast Symposium at the University of Western Ontario, as well as President of the the Institute of Brewing and Distilling in 1999 and 2000. Graham was an excellent colleague and a strong supporter of the Yeast Newsletter. Graeme Walker has kindly provided his memories of Graham.

Anniversaries

We are celebrating Volume 75 of the Yeast Newsletter and the 60th anniversary of the foundation of the International Commission on Yeasts. A brief history of the Commission has been provided by Peter Biely. The newsletter was adopted as the society's official publication at the time of its foundation in 1966 at the Second International Symposium on Yeasts, held in Bratislava. The Yeast Newsletter is in fact 76 years old. It was initiated by Leslie Hedrick of the Illinois Institute of Technology. Editorship was soon passed on to Emil Mrak, at the University of California, Davis, and in 1953 to his fellow Davisite, Herman Phaff, who kept it going till 1988, at which time I assumed responsibility.

Yeast Hunter Club

Maciej Wnuk, Justyna Ruchała, and colleagues at the University of Rzeszów in Poland initiated a new group, the Yeast Hunter Club, aimed at channelling the efforts of scientists, worldwide, whose activities include the isolation of yeasts from nature. Details are given in this issue. Interested colleagues are encouraged to contact the organizers.

M.A. Lachance

I National Centre for Genetic Resources of Microorganisms, NRC "Kurchatov Institute", I-Dorozhnyi 1, Moscow 117545, Russia. Communicated by E.S. Naumova <lena_naumova@yahoo.com>.

The following are papers for 2026.

1 Lyutova LV, Naumova ES. 2026. Genetic relatedness of marine *Kluyveromyces* species. Microbiology (Moscow) 95 (4) (in press).

The genetic relatedness of 22 strains of *Kluyveromyces aestuarii*, *K. nonfermentans*, and *K. siamensis* isolated from marine habitats in North and South America (United States, Brazil), East Asia (China, Taiwan, Japan, Thailand), and Australia was studied using molecular karyotyping, RAPD-PCR, phylogenetic analysis, and genetic hybridization analysis. The deep-sea species *K. nonfermentans* formed sterile hybrids with *K. aestuarii* and *K. siamensis*, had a unique karyotypic profile, and differed significantly in the nucleotide sequences of the 5.8S-ITS rDNA region and two nuclear genes (*ACT1* and *EF-1α*). The phylogenetically more closely related species *K. siamensis* and *K. aestuarii* possessed similar molecular karyotypes, were partially genetically isolated (ascospore viability of 9–19%), and are apparently still in the process of divergence. *K. aestuarii* was shown to consist of two geographic populations that exhibited genome divergence at the level of taxonomic varieties.

2 Tuaeva A.Yu., Lyutova L.V., Kachmazov G.S., Naumova E.S. 2026. Determination of β-galactosidase activity of *Kluyveromyces* dairy yeasts. Biotechnologiya, 41(3) (in press).

A comparative analysis of lactose hydrolysis rate and β-galactosidase specific activity was conducted in *Kluyveromyces lactis* and *K. marxianus* strains isolated from artisanal and industrial dairy products. Using Southern hybridization, the chromosomal localization of *LAC* loci in 81 *K. lactis* strains was determined: the majority of isolates possessed the *LAC2* locus or a combination of the *LAC1/LAC2* loci. It has been shown that to assess the biotechnological potential of *Kluyveromyces* yeast, it is necessary to take into account both the enzymatic activity and the fermentation capacity of the strain. *K. lactis* and *K. marxianus* strains combining high β-galactosidase specific activity with the ability to completely hydrolyze lactose were selected; they are of interest for further molecular genetic research and breeding programs.

II 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 Kręgiel D, Oracz J, Czarnecka-Chrebelska K, Nowak A. 2026. New insights into cranberry bioactivity: polyphenol composition, adhesive effects against food spoilage yeasts, and influence on intestinal cells. Molecules (MDPI) 31:418 - https://doi.org/10.3390/molecules31030418

The purpose of this study was to characterise the effect of cranberry (*Vaccinium macrocarpon*) juice on unicellular and multicellular systems, specifically food spoilage yeasts (*Wickerhamomyces anomalus*, *Dekkera bruxellensis* and *Rhodotorula mucilaginosa*) and intestinal cells (IEC-6 and Caco-2 cells). The effects of both raw cranberry juice and juice digested in vitro were investigated. The juices were analysed for polyphenol content using high-performance liquid chromatography coupled with mass spectrometry. The cranberry juice was evaluated for its impact on yeast surface hydrophobicity and anti-adhesive action using the MATH test and luminometry/microscopy, respectively. We also assessed the effects of raw and digested cranberry juices on IEC-6 and Caco-2 cells by measuring cell viability, metabolic modulation, genotoxicity, and antioxidant activity. Chromatographic analysis of the raw cranberry juice revealed the presence of diverse bioactive compounds, identified as hydroxybenzoic and hydroxycinnamic acids, flavonols, and anthocyanins. After digestion, the cranberry juice remained a rich source of phenolic acids. The yeast strain *R. mucilaginosa* was characterised by the highest hydrophobicity and adhesive abilities, but cell adhesion in the presence of raw cranberry juice was several times lower for all the tested strains. Both tested cranberry juices reduced ROS levels and were well tolerated by intestinal epithelial cells, without significant cytotoxic or genotoxic effects. Our findings provide new insights into the safety of using cranberry juice across unicellular and multicellular systems. However, further validation in real-world settings is necessary before practical applications.

2 Perek Z, Boruta T, Ścigaczewska A, Bizukojć M, Gutarowska B. 2025. Biotechnological potential of *Metschnikowia pulcherrima* yeasts for biomass production in agricultural biocontrol. Appl Sci (MDPI) 2025, 15, 13236 - https://doi.org/10.3390/app152413236

This study aimed to select *Metschnikowia pulcherrima* strains with antimicrobial potential and high biomass content, optimize their cultivation conditions, evaluate growth characteristics at different scales, and assess antimicrobial activity on apple plants (*Malus domestica* cv. Golden Delicious) infected with phytopathogens. Of the nine tested strains, *M. pulcherrima* D2 was selected for its strong inhibitory activity against all tested phytopathogenic molds: *Venturia inaequalis, Botrytis cinerea, Phoma exigua, Colletotrichum coccodes, Monilia laxa, Alternaria alternata, Alternaria tenuissima, Fusarium sambucinum*, and *Fusarium oxysporum*, both in vitro on laboratory media (inhibition zones from 13.5 to 35.0 mm) and in vivo on stems, leaves, flowers, and fruits of apple. Morphological observations of treated plants showed the complete absence or significant delays of disease symptoms for up to 10 days. Disease symptoms for several pathogens (*V. inaequalis, A. alternata, A. tenuissima, B. cinerea, F. sambucinum*) remained reduced by ≥50% for up to 31 days post-treatment compared to the untreated control. Optimal cultivation conditions for *M. pulcherrima* D2 were established: a complex medium containing yeast extract (5.0 g/L), soy peptone (5.0 g/L), and glucose (2.6 g/L), at pH 5 and 25 °C, with shaking at 180 rpm, resulted in high biomass contents (107–108 CFU/mL). Scale-up in 5 L bioreactors confirmed efficient biomass production (108 CFU/mL and from 3.1 to 3.9 g/L of dry biomass). These findings highlight the strong biotechnological potential of *M. pulcherrima* D2 for the development of a biocontrol agent to protect apple fruits and trees against fungal phytopathogens.

3 Liszkowska Walisiak W, Motyl I, Cieciura Włoch W, Miśkiewicz K, Kowalska G, Berłowska J. 2026. Effect of Low Temperature Fermentation by Yeast and Lactic Acid Bacteria on the Quality of Wheat Bread. Food and Bioprocess Technology 19: 236 https://doi.org/10.1007/s11947-026-04318-w

Low-temperature fermentation is gaining recognition for its ability to enhance the flavour and texture of bread, in line with consumer preferences for natural, high-quality products. The aim of this study was to evaluate the effects of low-temperature (15 °C) fermentation using fresh and lyophilised monoculture of yeast and yeast-LAB cocultures on wheat bread quality. A modified two-phase baking technique was used. Three types of breads were compared: those made from lyophilised sourdough/sponge, from fresh sourdough/sponge fermented with a lyophilised starter, and from fresh sourdough/sponge. Sucrose (1%, 5%, 10%), calcium carbonate (0.5%, 1%, 2%), and peptone (1%, 5%, 10%) were tested as cryoprotectants. Bread quality was assessed based on physicochemical analyses (specific volume, colour, texture profile), electronic nose (volatile compounds), electronic tongue (taste), and sensory evaluation. A combination of 5% sucrose and 0.5% calcium carbonate was found to be the most effective starter for preserving yeast and lactic acid bacteria (LAB) viability in the lyophilised starters (98% for LAB, 86% for yeast). Breads made from fresh sourdough/sponge exhibited higher loaf volumes compared to samples prepared from lyophilised starters. Rehydrated lyophilised starters led to breads with increased hardness, gumminess, and chewiness. Bread prepared from fresh sourdough fermented by a lyophilised mixed culture (*S. cerevisiae* D3 and *L. brevis* B46) demonstrated the highest ester content and received the highest scores in the sensory analysis for taste, aroma, and overall acceptability. The results of this study confirm that low-temperature fermentation with selected cold-adapted and appropriately cryopreserved microbial strains can produce high-quality wheat bread with enhanced sensory profiles. This method may therefore be considered for potential applications in the baking industry.

III 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, Nova Scotia, Canada B3H 4R2. Communicated by R. A. Speers <alex.speers@gmail.com>.

Recent publications or presentations.

1 Reid SJ, Josey M, MacIntosh AJ, Maskell D and Speers RA. 2021. Predicting fermentation rates in ale, lager and whisky. Fermentation, Special Issue Brewing & Distilling 2.0 7:13 https://doi.org/10.3390/fermentation 7010013. *Selected by Fermentation Editor as Editor's Choice.*

2 Speers RA. 2022. A review of pasteurization literature for alcohol and non-alcohol beers. MBAA Technical Quarterly 59:129-135.

3 Reid SJ, Speers RA, Lumsden WB, Willoughby NA, Maskell DL. 2023. The influence of yeast format and pitching rate on Scotch malt whisky fermentation kinetics and congeners and effect on new-make spirit. J. Inst. Brew. 129:1-17.

4 Speers RA. 2024. Foundations of pasteurization for regular and non-alcohol beers. Presentation and Demonstration. CBC Conference Las Vegas, NV. April. 21-25.

5 Speers RA, MacIntosh A. 2025. Craft beer pasteurisation - All-OK or Apocalypse Soon? Presented at the MBAA Ontario Section Meeting. Jan 27. Hamilton, Ontario.

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

7 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.

8 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.

IV Department of Agriculture, Division of Grape and Wine Sciences, University of Naples Federico II, Viale Italia 60, 83100 Avellino, Italy. Communicated by G. Blaiotta <blaiotta@unina.it> <giuseppe.blaiotta@personalepec.unina.it>.

Recent publication.

1 Tramice A, Liti G, Iodice A, Abbamondi GR, Carlea F, Petruzziello E, Cutignano A, Paris D, Iodice C, De Chiara M, Aponte M, De Filippis F, Vischioni C, Motta A, Blaiotta G, Giuseppina Tommonaro G. 2025. First evidence of metabolically active intracellular bacteria in *Saccharomyces cerevisiae*. J. Agric. Food Chem 73:26220−26231.

Quorum sensing (QS) is a cell-to-cell signaling system that takes place at a key concentration (quorum) of signal molecules and via a peculiar signaling pathway. Both bacteria and yeasts possess QS mechanisms, mediated by specific molecules (farnesol, tyrosol, 2-phenylethanol, tryptophol) in yeasts, and N-acylhomoserine lactones (AHLs) and modified oligopeptides in bacteria. Here, we report the first chemical evidence of bacterial QS activity in yeast *Saccharomyces cerevisiae* (OS3 and V5 strains) by UPLC-MS/MS identification of N-octanoyl- and N-decanoyl-L-homoserine lactones in cell-free culture media extracts. The AHLs' presence was unexpected, as they are produced exclusively by bacteria. Tyrosol, a yeast signal molecule, was identified and quantified by NMR analysis. Metataxonomic analysis suggested the existence inside *S. cerevisiae* cells of bacteria, including Firmicutes, Bacteroidota, and Proteobacteria. Our study paves the way for investigations into bacterial detection within *S. cerevisiae* cells and their role in biotechnological performance in the food fermentation fields.

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

Starting in August 2026, I will be transferring my work on the ecology and evolution of environmental and model yeasts to a new position as Associate Professor of Biology at California State University Polytechnic in San Luis Obispo.

Recent publication.

1 Germain G, Lamphere S, Molinari E, Boynton P. 2026. Sodium chloride stress inhibits *Saccharomyces paradoxus* meiosis. microPublication Biology - 10.17912/micropub.biology.002115.

Meiosis is a common response to nutrient deprivation in yeasts. Our goal was to determine whether the yeast *Saccharomyces paradoxus* performed meiosis under other abiotic stress factors, specifically salt stress. We predicted that *S. paradoxus* meiosis would increase in the presence of salt because osmotic stress activates the IME1 transcription factor in its model yeast relative *S. cerevisiae*. Contrary to our prediction, the sporulation rate of *S. paradoxus* decreased as salinity increased. We hypothesize that this is due to salt inhibiting mitochondrial function, but more studies are needed to determine the cause. This work was done during a sophomore-level Course-Based Undergraduate Research Experience (CURE).

Undergraduate student Rebecca Bryson did an Honors Bachelor's thesis at Wheaton College. Her thesis was deposited in Wheaton College's thesis archive and can be accessed there.

2 Rebecca Bryson: Human disturbance modestly influences killer phenotypes in *Saccharomyces paradoxus*

Human disturbance is known to shape biodiversity, but its effects on microbial populations and traits are not well understood. This study examines how environmental variation associated with human activity influences population structure and competitive phenotypes in the wild yeast *Saccharomyces paradoxus*. Soil samples were collected from six forested sites across Massachusetts, and isolates were assigned to genetic populations using microsatellite markers. Killer phenotypes, which allow yeast to inhibit competitors through toxin production, were also assessed. Population distribution differed significantly among sites, indicating spatial structuring at a local scale. I observed two out of the three documented North American populations in this study, with one population only being found in a single sampling location. Killer phenotypes were present but varied across locations. Analysis of human disturbance showed a positive relationship between town population size and killer frequency, suggesting that more disturbed environments may favor toxin-producing strains. However, distance from roads was not a strong predictor. Overall, these results suggest that while population structure is shaped primarily by local environmental factors, human disturbance may influence competitive traits in microbial populations.

VI Department of Soil Biology, Faculty of Soil Science, Lomonosov Moscow State University, 119234, Leninskie gory, 1/12, Moscow, Russia; All-Russian Collection of Microorganisms (VKM), G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, pr. Nauki 5, Pushchino, Russia. Communicated by A.V. Kachalkin <kachalkin_a@mail.ru>.

Recent publications.

1 Yakovleva EY, Maximova IA, Merzlikin DS, Kachalkin AV, Markov AV. 2025. Different species of yeast alter the lifespan and fecundity of *Drosophila melanogaster*. Biology Bulletin Reviews. 15(1):109-128 - DOI: 10.1134/S207908642470021X

In this work, we assessed the influence of the natural yeast microbiota, as well as individual yeast species, on lifespan, age-related dynamics of fecundity, and mortality in a control fly line and a fly line with a depleted yeast microbiota. We used *Starmerella bacillaris*, *Zygosaccharomyces bailii*, and *Saccharomyces cerevisiae* as yeast species for testing. We have shown that a decrease in the amount of symbiotic yeasts on the medium, on the surface of the body, or in the intestine leads to an increase in lifespan and a decrease in fecundity for flies reared on standard medium. Inoculation of *S. cerevisiae* on the medium shifts the reproduction of the control flies to an earlier age, while two other yeast species increase fecundity significantly. Inoculation of *S. bacillaris* and *S. cerevisiae* (which are not typical for the microbiota of the tested fly lines) on the medium reduced the lifespan more than inoculation with *Z. bailii*, which is typical for the microbiota of the control line.

2 Dlauchy D, Kachalkin A, Glushakova A, Buda K, Fehйr C, Péter G. 2025. Description of *Wickerhamia europaea* sp. nov. and revisitation of the ascospore number of *W. fluorescens*. International Microbiology. 28:1321–1330. - DOI: 10.1007/s10123-024-00622-7

During the course of two independent studies, six conspecific yeast strains were recovered from flowers, soil, bird faeces and wood of different geographical origins. According to sequence comparisons and phylogenetic analysis, they represent an undescribed *Wickerhamia* species. We propose *Wickerhamia europaea* sp. nov. to accommodate the above noted strains.

3 Glushakova A, Kachalkin A. 2025. Extracellular phospholipase, protease and hemolysin production by strains of opportunistic yeasts from the excreta of Mew Gulls breeding in natural and urban habitats. Veterinary Research Communications 49(63):1–8. DOI: 10.1007/s11259-024-10627-2

Extracellular hydrolytic activity (phospholipase, protease and hemolysin production) was evaluated in 178 strains of potentially pathogenic ascomycetous (*Candida parapsilosis, Candida tropicalis*) and basidiomycetous (*Rhodotorula mucilaginosa*) yeasts isolated from the excreta of Mew Gulls. Two bird colonies, one nesting in a natural habitat and the other in an urban habitat at the landfill, were studied simultaneously during their 7-month breeding season. Significant differences in phospholipase and protease production were found between natural and anthropophized strains. Both virulent activities were higher in strains of potentially pathogenic yeast species isolated from the excreta of Mew Gulls nesting in the anthropogenic habitat near the landfill.

4 Glushakova A, Kachalkin A. 2025. Shared core and host specificities of culturable pathogenic yeast microbiome in fresh and dry feces of five synanthropic wild birds (Rock Pigeon, European Starling, White Wagtail, Great Tit and House Sparrow). Birds MDPI) 6(3):41-1-17 - DOI: 10.3390/birds6030041

The study focused on comparing the diversity of ascomycetous, potentially pathogenic yeast species (*Candida* spp.) in the fresh and dry feces of five synanthropic birds (Rock Pigeon, European Starling, White Wagtail, Great Tit and House Sparrow). A total of 638 strains were isolated belonging to 9 yeast species (*Arxiozyma bovina*, *Candida albicans*, *Nakaseomyces glabratus*, *Clavispora lusitaniae*, *C. tropicalis*, *C. parapsilosis*, *Pichia kudriavzevii*, *Debaryomyces hansenii* and *D. fabryi*). Significant differences in the microbiome of the pathogens were found in the fresh feces of the different hosts. The most diverse pathogen–yeast complexes were found in the fresh feces of pigeons. In contrast to the fresh feces, the dry samples did not differ significantly in terms of pathogen diversity between the different birds. And, they were generally characterized by a lower number of culturable, potentially pathogenic yeasts. Fresh and dry feces from synanthropic birds in the city (especially pigeons) are thus a source of a large number of potentially pathogenic yeasts.

5 Glushakova A, Berezhnov A, Kachalkin A. 2025. Pathogenicity study of ascomycetous opportunistic yeasts from fresh feces of pigeons using *Tenebrio molitor* larvae as a host model. Scientific reports 15:42133-1-7 - DOI: 10.1038/s41598-025-26115-9

In this study, we investigated in vivo the virulence of potentially pathogenic ascomycetous yeasts found in fresh feces of street pigeons using the larval host model of *Tenebrio molitor*. The yeasts *Arxiozyma bovina* showed the highest pathogenicity, resulting in a significantly shortest median survival time — 24 h, followed by *Nakaseomyces glabratus* (4 days), *Candida albicans* and *C. tropicalis* (5 days), *Clavispora lusitaniae* (6 days), *C. parapsilosis* and *Pichia kudriavzevii* (7 days). The *T. molitor* model demonstrated the pathogenic potential and virulence differences of the ascomycetous yeasts observed in fresh pigeon droppings in the city. It provided a valuable, swift and cost-effective tool for preliminary virulence screening of clinically important yeasts spread by synanthropic birds in the anthropophized areas.

6 Kachalkin A, Bekkarevich A, Tomashevskaya M, Glushakova A. 2026. *Curvibasidium golubevii* sp. nov, a new dimorphic basidiomycetous fungus from different habitats. Biologia 81(1):1-1-8
DOI: 10.1007/s11756-025-02131-y

During the course of independent studies, three conspecific yeast strains were obtained from insect frass, berries and mosses in different regions of Russia. Phylogenetic analysis of two DNA-barcoding regions revealed that they belong to undescribed *Curvibasidium* species with basal position to other species. Mating tests of the strains revealed true mycelium with clamp connections and teliospores. The teliospore germination and basidia-like structures were also characterised, which is distinguished from other teleomorphic species of the genus. The new species differs genetically from other closely related *Curvibasidium* species by other genes studied and can also be distinguished from them by physiological characteristics. Based on these results, the new species *Curvibasidium golubevii* sp. nov. is formally described.

7 Poliakova AN, Cherdantsev IA, Glushakova AM, Wang Q-M, Karpov DS, Polyakov NB, Solovyev AI, Zhukhovitsky VG, Kachalkin AV. 2026. Three new yeast species of *Vishniacozyma* (*Bulleribasidiaceae, Tremellales*) from different habitats. MycoKeys 128:231-248 - DOI: 10.3897/mycokeys.128.175380

In this study, three new basidiomycetous yeast species of the genus *Vishniacozyma* are proposed for strains isolated from soil, *Scolytus scolytus* frass, fruits and kombucha tea. A complex analysis of the new isolates together with the described species by genetic, phylogenetic, MALDI-TOF MS profiling and phenotypic characterization revealed significant differences, allowing us to propose three new species: *V. pseudofoliicola*, *V. kombuchae*, and *V. fructicola* spp. nov. These descriptions contribute to the expansion of knowledge regarding species diversity of the genus *Vishniacozyma*.

8 Glushakova A, Kachalkin A. 2026. Post-brumation yeast mycobiota in *Vipera berus* (European adder): clinically relevant *Candida parapsilosis* oral dominance and diverse fecal communities compared with warmer-region snakes. Veterinary Research Communications 50(4):283
DOI: 10.1007/s11259-026-11233-0

Snakes may harbor clinically relevant yeasts, yet the culturable yeast mycobiota of temperate snake species remains poorly characterized. We surveyed culturable yeasts from 17 fecal samples and 5 oral swab samples of *Vipera berus* (European adder) collected in European Russia immediately after spring emergence from brumation. Oral communities were dominated by *Candida parapsilosis* (mean relative abundance ~ 84%), whereas fecal samples showed greater compositional diversity, with *Aureobasidium pullulans*, *Debaryomyces fabryi*, and *Tausonia pullulans* among the most abundant taxa. Psychrotolerant yeasts (e.g, *Aureobasidium subglaciale*, *Leucosporidium yakuticum*, *T. pullulans*) were detected in post-brumation samples. Aggregated presence/absence comparisons with published snake datasets indicated region-specific differences in culturable yeast assemblages.

VII VTT Technical Research Centre of Finland, Tietotie 2, P.O. Box 1000, 02044 VTT, Espoo, Finland. Communicated by Kristoffer Krogerus <Kristoffer.Krogerus@vtt.fi>.

Recent publications.

1 Blick E & Nygård Y. 2025. Expanding the yeast MoClo toolkit: gene expression control parts for *Saccharomyces cerevisiae* tested in industrially relevant conditions. Synth Biol ysaf018
https://doi.org/10.1093/synbio/ysaf018

2 Toivari M, Vehkomäki ML, Ruohonen L, Penttilä M & Wiebe M. 2025. Production of xylitol by yeast fed with formic/acetic acid organosolv treated wheat straw. Biores Technol Rep 32:102410
https://doi.org/10.1016/j.biteb.2025.102410

3 Kakko von Koch N, Tenkanen T, Castillo S, Vidgren V, Koponen T, Krogerus K, Penttilä M & Jouhten P. 2025. Model-guided chemical environment and metabolic network design to couple pathways with cell fitness. Metab Eng Comm 21: e00267 - https://doi.org/10.1016/j.mec.2025.e00267

4 Umashankar P, Choi B, Nygård Y. 2026. Towards the development of a CRISPR-Cas9 based kill switch for *Saccharomyces cerevisiae*. Microbial Cell Factories 25:62 https://doi.org/10.1186/s12934-026-02959-2

5 Rinta-Harri K, Koponen T, Mojzita D, Jouhten P, Liti G, Krogerus K. 2026. Influence of ploidy and genetic background on stress tolerance of intraspecific yeast hybrids. Microbial Biotechnology 19:e70337 https://doi.org/10.1111/1751-7915.70337

6 Nasuti C, Iannuzziello G, Papiani V, Tagliazucchi D, Krogerus K, Solieri L. 2026. Development of a GMO-free de novo lager yeast with reduced phenolic off-flavor production through interspecific hybridization and UV mutagenesis. International Journal of Food Microbiology 456:111786 https://doi.org/10.1016/j.ijfoodmicro.2026.111786

VIII National Collection of Agricultural and Industrial Microorganisms, Institute of Food Science and Technology, Hungarian University of Agriculture and Life Sciences, H-1118, Budapest, Somlói út 14-16, Hungary. Communicated by Gábor Péter <Peter.Gabor@uni-mate.hu>.

Recent publications.

1 Wijayawardene NN, Hyde KD, Mikhailov KV, Péter G et al. 2024. Classes and phyla of the kingdom Fungi. Fungal Diversity - https://doi.org/10.1007/s13225-024-00540-z

Fungi are one of the most diverse groups of organisms with an estimated number of species in the range of 2–3 million. The higher-level ranking of fungi has been discussed in the framework of molecular phylogenetics since Hibbett et al., and the definition and the higher ranks (e.g., phyla) of the 'true fungi' have been revised in several subsequent publications. Rapid accumulation of novel genomic data and the advancements in phylogenetics now facilitate a robust and precise foundation for the higher-level classification within the kingdom. This study provides an updated classification of the kingdom Fungi, drawing upon a comprehensive phylogenomic analysis of *Holomycota*, with which we outline well-supported nodes of the fungal tree and explore more contentious groupings. We accept 19 phyla of *Fungi*, viz. *Aphelidiomycota*, *Ascomycota*, *Basidiobolomycota*, *Basidiomycota*, *Blastocladiomycota*, *Calcarisporiellomycota*, *Chytridiomycota*, *Entomophthoromycota*, *Entorrhizomycota*, *Glomeromycota*, *Kickxellomycota*, *Monoblepharomycota*, *Mortierellomycota*, *Mucoromycota*, *Neocallimastigomycota*, *Olpidiomycota*, *Rozellomycota*, *Sanchytriomycota*, and *Zoopagomycota*. In the phylogenies, *Caulochytriomycota* resides in *Chytridiomycota*; thus, the former is regarded as a synonym of the latter, while *Caulochytriomycetes* is viewed as a class in *Chytridiomycota*. We provide a description of each phylum followed by its classes. A new subphylum, *Sanchytriomycotina* Karpov is introduced as the only subphylum in *Sanchytriomycota*. The subclass *Pneumocystomycetidae* Kirk et al. in *Pneumocystomycetes*, *Ascomycota* is invalid and thus validated. Placements of fossil fungi in phyla and classes are also discussed, providing examples.

2 Dlauchy D, Álvarez-Pérez S, Tóbiás A and Péter G. 2024. *Vishniacozyma floricola* sp. nov., a flower-related tremellomycetous yeast species from Europe. Int J Syst Evol Microbiol. 74(10) - doi: https://doi.org/10.1099/ijsem.0.006555

During the course of two independent studies conducted in Hungary and Spain, four conspecific yeast strains were isolated from flowers of different plant species. DNA sequences of two barcoding regions, the D1/D2 domain of the LSU rRNA gene and the internal transcribed spacer (ITS) region (ITS1-5.8S rRNA gene-ITS2), revealed that the four strains represent an undescribed *Vishniacozyma* (family *Bulleribasidiaceae*, *Basidiomycota*) species. In terms of pairwise sequence similarities and according to our phylogenetic analyses of the concatenated DNA sequences of the ITS region and the D1/D2 domain of the LSU rRNA gene, the undescribed species is most closely related to *Vishniacozyma melezitolytica*, a yeast species of phylloplane origin. The novel species differs from the type strain of *V. melezitolytica* by 8 substitutions and 3 insertion/deletion (indels) and 11 substitutions and 5 indels along the D1/D2 domain of the LSU rRNA gene and the ITS region, respectively. In addition to the DNA sequence divergences, the two species differ in some physiological characters as well. We propose the species *Vishniacozyma floricola* sp. nov. to accommodate the above-noted strains (holotype, NCAIM Y.02320; isotype, CBS 18939; MycoBank number, 856028)

3 Dlauchy D, Kachalkin A, Glushakova A, Buda K, Fehér C, Péter G. 2025. Description of *Wickerhamia europaea* sp. nov. and revisitation of the ascospore number of *W. fluorescens*. Int Microbiol https://doi.org/10.1007/s10123-024-00622-7

During the course of two independent studies, six conspecific yeast strains were recovered from flowers, soil, bird faeces and wood of different geographical origins. The six strains share identical DNA sequences in two barcoding regions, the D1/D2 domain of the LSU rRNA gene and the internal transcribed spacer (ITS) region (ITS1-5.8S rRNA gene-ITS2). According to sequence comparisons and phylogenetic analysis, they represent an undescribed *Wickerhamia* species. The novel species is not only genetically distinct from *W. fluorescens*, the single species of the genus but can also be distinguished from it by some phenotypic characters. We propose *Wickerhamia europaea* sp. nov. (holotype: NCAIM Y.01938; isotype: CBS 18675; MycoBank no.: 856571) to accommodate the above noted strains. Under certain fermentation conditions, we detected the production of phenyllactic acid, a potential broad-spectrum antimicrobial compound against food-borne pathogens, by the type strain of the novel species, although in smaller concentrations than in the case of *W. fluorescens*. Comparing our observations on the formation and properties of the ascospores of *Wickerhamia europaea* sp. nov. and the ambiguous data on the number of ascospores per ascus of *W. fluorescens*, we suggest a possible explanation to reconcile the different data regarding the number of ascospores per ascus formed by *W. fluorescens*.

4 Thiyagaraja V, Hyde KD, Piepenbring M et al. 2025. Orders of *Ascomycota*. Mycosphere 16(1):536–1411 - https://doi.org/10.5943/mycosphere/16/1/8

Ascomycota, the most speciose phylum of fungi, is a complex entity, comprising three diverse subphyla: *Pezizomycotina*, *Saccharomycotina*, and *Taphrinomycotina*. The largest and most diverse subphylum, *Pezizomycotina*, is a rich tapestry of 16 classes and 171 orders. *Saccharomycotina*, the second largest subphylum, is a diverse collection of seven classes and 12 orders, while *Taphrinomycotina*, the smallest, is a unique assembly of six classes and six orders. Over the past decade, numerous taxonomic studies have focused on the generic, family, and class classifications of Ascomycota. These efforts, well-documented across various databases, are crucial for a comprehensive understanding of the classification. However, the study of taxonomy at the ordinal level, a crucial tier in the taxonomic hierarchy, has been largely overlooked. In a global collaboration with mycologists and lichenologists, this study presents the first comprehensive information on the orders within *Pezizomycotina* and *Taphrinomycotina*. The recent taxonomic classification of *Saccharomycotina* has led to the exclusion of this subphylum from the present study, as an immediate revision is not necessary. Each order is thoroughly discussed, highlighting its historical significance, current status, key identification character-istics, evolutionary relationships, ecological and economic roles, future recommendations, and updated family-level classification. Teaching diagrams for the life cycles of several orders, viz. *Asterinales*, *Helotiales*, *Hypocreales*, *Laboulbeniales*, *Meliolales*, *Mycosphaerellales*, *Ophiostomatales*, *Pezizales*, *Pleosporales*, *Phyllachorales*, *Rhytismatales*, *Sordariales*, *Venturiales*, *Xylariales* (*Pezizomycotina*) and *Pneumocystidales*, *Schizosaccharomycetales* and *Taphrinales* (*Taphrinomycotina*) are provided. Each diagram is explained with a representative genus/genera of their sexual and asexual cycles of each order. Within *Pezizomycotina*, *Dothideomycetes* contains the highest number of orders, with 57, followed by *Sordario-mycetes* (52 orders), *Lecanoromycetes* (21 orders), *Eurotiomycetes* and *Leotiomycetes* (12 orders each), *Laboulbeniomycetes* (3 orders), and *Arthoniomycetes* and *Xylonomycetes* (2 orders each). *Candelariomycetes*, *Coniocybomycetes*, *Geoglossomycetes*, *Lichinomycetes*, *Orbiliomycetes*, *Pezizomycetes*, *Sareomycetes*, and *Xylobotryomycetes* each contain a single order, while *Thelocarpales* and *Vezdaeales* are treated as incertae sedis within *Pezizomycotina*. Notably, the classes *Candelariomycetes*, *Coniocybomycetes*, *Geoglossomycetes*, *Sareomycetes*, and *Xylonomycetes*, all recently grouped under *Lichinomycetes*, are treated as separate classes based on phylogenetic analysis and current literature. Within *Lecanoromycetes*, the synonymization of *Sporastatiales* with *Rhizocarpales* and *Sarrameanales* with *Schaereriales* is not supported in the phylogenetic analysis. These orders are retained separately, and the justifications are provided under each section as well as in the discussion. Within *Leotiomycetes*, the order *Medeolariales*, which was once considered part of *Helotiales*, is treated as a distinct order based on phylogenetic evidence. The classification of *Medeolariales* may change as more data becomes available from different gene regions. *Lahmiales* (*Leotiomycetes*) is not included in the phylogenetic analysis due to a lack of molecular data. *Sareomycetes* and *Xylonomycetes* are treated as separate classes. *Spathulospora* mixed with *Lulworthiales* and the inclusion of *Spathulosporales* within *Lulworthiomycetidae* is supported and extant molecular sampling is important to resolve the phylogenetic boundaries of members of this subclass. The majority of the classes of *Pezizomycotina* and *Taphrinomycotina* formed monophyletic clades in the phylogenetic analysis conducted based on SSU, LSU, 5.8S, TEF and RPB2 sequence data. However, *Arthoniomycetes* nested with the basal lineage of *Dothideomycetes* and formed a monophyletic clade also known as the superclass, *Dothideomyceta*. In *Taphrinomycotina*, a single order is accepted within each class.

5 Acs-Szabo L, Pfliegler WP, Kovács S, Adácsi C, Rácz HV, Horváth E, Papp LA, Murvai KP, Király S, Miklós I, Péter G, Pusztahelyi T, Pócsi I. 2025. Striking mycotoxin tolerance and zearalenone elimination capacity of the decaying wood associated yeast *Sugiyamaella novakii* (*Trichomonascaceae*). BMC Microbiology 25:422 - https://doi.org/10.1186/s12866-025-04145-7

Background. Mycotoxin-producing fungal species and their mycotoxins pose a global threat for crop production and for human and animal health. Given the increasing demand for healthier food and feed, alternative non-pesticide approaches for reducing fungal infections in crops and eliminating mycotoxin contamination in feedstock are becoming more prevalent. For such purposes, yeast species can be good candidates. Thus, the present study examined the mycotoxin tolerance and mycotoxin elimination ability of several yeast strains belonging to the *Trichomonascaceae* family. **Results**. While none of the tested yeasts inhibited the growth of different *Fusarium* species, several yeast strains exhibited tolerance to *Fusarium* mycotoxins such as deoxynivalenol, zearalenone, T-2 toxin, and fumonisin B1. *Sugiyamaella novakii* strains displayed exceptional tolerance for the tested mycotoxins. Besides, phylogenetic analyses suggested that tolerant species clustered more closely to each other than to the sensitive species. Although whole genome sequencing of *S. novakii* NCAIM Y.00986 revealed several enzyme-coding genes that may have a role in mycotoxin elimination, significant mycotoxin elimination was not achieved in the case of deoxynivalenol, T-2 toxin, and fumonisin B1. However, *S. novakii* successfully eliminated zearalenone, likely due to cell wall adsorption rather than enzymatic degradation. **Conclusions**. This study highlights the potential of *S. novakii* for zearalenone detoxification and emphasizes the role of yeast cell walls in mycotoxin mitigation strategies.

6 Liu M-M, Zhao X-M, Bai J, Boekhout T, Yurkov A, Péter G, Bensch K, Liu F, Cui T-X, Liu Z-Q, Zhao Y-J, Zhang Y-X, Zhang X-H, Liu J-H, Wang J-C, Li H-Z, Bai F-Y, Blackwell M, Wang Q-M (2026) Taxogenomic reclassification of *Candida* and related genera in *Saccharomycotina*. Fungal Diversity136:136006 - https://doi.org/10.65390/fdiv.2026.136006

The genus *Candida* in the *Saccharomycotina* has long reflected the historical practice of yeast classification based on phenotypic characteristics, retaining remnants of dual nomenclature even after its abandonment in 2011. Following this shift, many *Candida* species were reclassified into existing or newly proposed genera; yet, *Candida* itself remained heterogeneous and phylogenetically divergent. This heterogeneity is also true for genera like *Ogataea*, *Starmerella*, and *Wickerhamomyces*. While this heterogeneity has been demonstrated in previous studies, including several recent proposals for new genera, the inclusion of reclassified *Candida* species in these genera will make them more phylogenetically diverse. Despite widespread recognition of the polyphyletic nature of *Candida*, confusion persists due to the continued use of this single generic name for species belonging to lineages distantly related to that of the generic type species, *Candida vulgaris*, a current synonym under *Candida tropicalis*. In this study, we aim to reduce the genetic heterogeneity of the genus *Candida* by (i) focusing on lineages distantly related to its nomenclature type and (ii) assessing the diversity and composition of genera into which former *Candida* species have been reassigned. Phylogenomic analyses were conducted to determine the positions of Candida species and several genomic metrics, including average amino acid identity (AAI), percentage of conserved proteins (POCP), and presence-absence patterns of orthologs (PAPO), in order to quantify genetic divergence in genera and clades, were calculated to assist the reclassification decisions as complementary approaches. In addition to phylogenomic analyses, comprehensive phylogenetic analyses using ITS and LSU D1/D2 rDNA sequence data were performed to include species that are not represented in the genome-scale analyses and to assist species recognition in future studies. This framework led to an updated classification of Candida species and related taxa, proposing 25 new genera to accommodate reclassified species and validating 4 genera, along with 175 new combinations and 87 newly recognized species.

IX VIB Lab for Systems Biology, Center for Microbiology, KU Leuven | Laboratory for Genetics and Genomics Leuven Institute for Beer Research, LIBR Bio-Incubator Gaston Geenslaan 1. 3001 Heverlee-Leuven, Belgium

https://www.kuleuven.be/verstrepen, https://verstrepenlab.sites.vib.be/en.

Communicated by L. Vermeersch <verstrepenlab@kuleuven.be>.

The following articles and reviews have recently come out from the Verstrepen lab.

1 Bircham PW, Del Cortona A, Garsholm LM,. Tawfeeq MT, Herrera-Malaver B, Mannaerts S, Cortebeeck J, Nolmans R, Gallone B, Gorkovskiy A, Abrouk M, Steensels J, Verstrepen KJ. 2026. Distinctive domestication of farmhouse beer yeasts preserved pre-industrial genetic and phenotypic diversity. Current Biology 36(8) - https://doi.org/10.1016/j.cub.2026.03.030

Since its inception over 10,000 years ago, beer brewing has transformed from a domestic activity based on uncontrolled spontaneous fermentations into a highly optimized industrial process that uses pure single-strain starter cultures of Saccharomyces yeasts. Along with the storage of frozen yeast stocks, this shift halted the domestication process of beer yeasts and led to a massive loss of beer yeast biodiversity. However, a few traditional farmhouse brewers in Northern and Eastern Europe still rely on artisanal fermentation methods, using mixed cultures of yeasts that are passed on from one fermentation to the next. We genetically and phenotypically analyzed 1,760 isolates from 44 traditional European farmhouse ale yeast cultures from Norway, Latvia, Lithuania, and Russia. We find that farmhouse cultures harbor remarkable genetic diversity, from near-monocultures to intricate communities of over 30 different S. cerevisiae variants. Farmhouse yeast genomes exhibit clear geographic structuring but also reveal signs of admixture alongside lineage-specific genomic features, such as a horizontally transferred gene cluster in Baltic strains. Large-scale phenotyping reveals that farmhouse yeasts harbor domestication signatures that are distinct from those of industrial beer yeasts, including maintenance of a sexual cycle, higher stress tolerance, and more diverse flavor profiles. Together, our study reveals the complex structure and diversity of farmhouse cultures and provides a reservoir of new yeast strains that can propel the next wave of beer innovation.

A blog written about this paper: VIB | The lost world of farmhouse brewing

2 Tawfeeq MT, Konstantinidis D, Rocha Iraizos AL, Van Genechten W, Vreys J, Vermeersch L, Voordeckers K, Van Dijck P, Verstrepen KJ. 2026. Gim3 buffers and potentiates de novo mutations that affect fluconazole susceptibility in yeast. 2026. EMBO Reports 27:1510–1539 https://doi.org/10.1038/s44319-026-00702-x

Reviews:

3 Keil A, Woestenborghs J, Lyzak O, Vlaeminck E, Uitterhaegen E, De Winter K, Verstrepen KJ, Soetaert W. 2026. High cell density fermentation of *Yarrowia lipolytica* on n-hexadecane for the valorization of pyrolyzed plastic waste. Int J Mol Sci (MDPI) 27(2):1107 - https://doi.org/10.3390/ijms27021107

4 Yogiswara S, Verstrepen KJ. 2026. Recent advances in microbial 3-methyl-1- butanol production. Front Microbiol 16:2025 - https://doi.org/10.3389/fmicb.2025.1753983

X Portuguese Yeast Culture Collection, Life Sciences Department, NOVA School of Science and Technology, UNL, 2829-516 Caparica, Portugal. Communicated by J.P. Sampaio <jss@fct.unl.pt>.

The following papers, authored by PYCC members, were recently published.

1 Pontes A, Silva MR, Rutkowski D, Carvalho C, Coito J, Capela N, Groenewald M, Brito PH, Gonçalves C, Vannette RL, Sampaio JP. 2025. *Zygosaccharomyces progenitor* sp. nov a new yeast species associated with bees of the genera *Apis* and *Bombus*. Int J Syst Evol Microbiol 75:006957 - http://dx.doi.org/10.1099/ijsem.0.006957

2 Avesani M, Carvalho C, Conacher CG, Steffen HC, Botha A, Zapparoli G and Sampaio JP. 2025. *Kwoniella olivae* f.a. sp. nov a novel basidiomycetous yeast species associated with olive ecosystems. Int J Syst Evol Microbiol 75:006916 - http://dx.doi.org/10.1099/ijsem.0.006916

3 Ryan APR, Carvalho C, Zhao Y, Decuseara J, Osborne M, Heneghan PG, Byrne KP, Cróinín TÓ, Wolfe KH, Sampaio jP and Butler G. 2025. *Cyberlindnera hibernica* sp. nov. and *Barnettozyma discipulorum* sp. nov isolated from forest soil in Ireland. Int J Syst Evol Microbiol 75:006898 - http://dx.doi.org/10.1099/ijsem.0.006898

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

Recent publication.

1 Tironi APO, Barros KO, Santana LFA, Souza DL, Santos ARO, Ávila1 GR, Batista TM, Franco GR, Pimenta RS, Morais PB, Lachance MA, Rosa CA, Johann S. 2026. *Candidozyma cisalpinoae* sp. nov., a genomically distinct, flower-associated yeast, resistant to azoles and exhibiting pathogenicity-related traits. Yeast 43(1-2):25-37 - https://doi.org/10.1002/yea.70012

Six yeast isolates were recovered from Ipomoea flowers collected in the Cerrado biome of Tocantins, Brazil. Sequence analyses of the ITS–5.8S region and the D1/D2 domains of the large subunit (LSU) rRNA gene indicated that these isolates represent a novel species of the genus *Candidozyma*, phylogenetically related to *Candidozyma auris* and *Ca. ruelliae*. A phylogenomic analysis based on 2116 single copy orthologs from *Candidozyma* species with available whole genome sequences showed that the new species, represented by strain UFMG CM Y6065, is a sister species to *Ca. ruelliae*. The name *Candidozyma cisalpinoae* sp. nov. (MycoBank no. 861366) is proposed to accommodate the new species. The holotype is CBS16108. Sporulation or other evidence of sexual reproduction was not observed, although the genome sequence showed the presence of a functional mating type locus (MATa) and functional pheromone peptides, indicating that the species is haplontic and heterothallic. The species exhibited resistance to multiple antifungals, growth at 42°C, biofilm formation, adhesion to buccal epithelial cells, and expression of efflux pumps, traits of clinical relevance that have been reported for other species in the genus *Candidozyma*.

2 Santos ARO, Vianei DO, Lopes MR, Barros KO, Morais PB, Della Torre OHP, Pompéia SL, Santa-Brígida R, Martins MB, Souza DL, Franco GR, Lachance MA, Rosa CA. 2026. Description of *Deakozyma peteri* sp. nov., a yeast isolated from substrates of neotropical regions. Int J Syst Evol Microbiol (accepted May 2026).

Seven isolates of a candidate of a novel yeast species were isolated from various substrates in three neotropical countries. The substrates included rotting wood, fruit, soil and mushrooms in Brazil, an agave necrosis in Mexico, and an oak sap flux in Costa Rica. Analysis of barcode sequences showed that the novel species is related to *Candida bentonensis* but a divergence of 16-19 substitutions in the D1/D2 domains of the LSU rRNA gene shows that the two are distinct species. Phylogenomic studies have shown that *C. bentonensis* belongs to the *Deakozyma* clade. The novel species is polymorphic and heterogeneous at several sites in the D1/D2 domains. Our taxogenomic analysis confirmed both that the novel species should be assigned to the genus *Deakozyma* and that it is distinct from *C. bentonensis.* The name *Deakozyma peteri* sp. nov. (MycoBank MB862524) is proposed for the novel species. The holotype of *D. peteri* sp. nov. is CBS 14242 (isotype UFMG-CM-Y2876).

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YEAST HUNTER CLUB

In 2025, the Faculty of Biotechnology at the University of Rzeszów (Poland) launched a bold international initiative to map a "hidden" world: the **Yeast Hunter Club (YHC)**.

What is the Yeast Hunter Club?

The YHC is a global community of scientists, researchers, and enthusiasts dedicated to advancing yeast biotechnology and microbiology. Its mission is simple yet ambitious: to foster international collaboration and drive innovation through the study of yeasts. The Yeast Hunter Club pursues its objectives through supporting scientific development in the fields of biology, genetics, biotechnology, and microbiology of yeast, including its industrial and medical applications; facilitating international cooperation between scientists, students, and experts by organizing conferences, workshops, and seminars; and supporting work on new methods of using yeast in the production of biofuels, food, pharmaceuticals, and other areas of biotechnology. Furthermore, the club organizes educational activities, lectures, and programmes to promote the importance of yeast in biotechnology and microbiology while creating a platform for the presentation of young researchers' work, promoting their achievements and supporting their scientific career development. Finally, the initiative aims to integrate experts from different countries and institutions involved in yeast-related research and biotechnology in order to build an international scientific network, while promoting sustainable and ethically responsible research and technological development.

Empowering the Next Generation

The initiative brings together experienced researchers alongside early-career scientists and students, fostering intergenerational exchange of knowledge and ideasA vital part of the community is the **Young Yeast Hunters**—a dedicated platform for students and high school learners interested in yeast science. By providing young researchers with opportunities to present their work and interact with established experts, the YHC supports the development future leaders in biotechnology.

Expanding Horizons

The Yeast Hunter Club continues to grow as a powerhouse of international scientific collaboration, bringing together top-tier experts from a vast geographical spectrum to foster innovation across borders. With members hailing from **19+ countries and territories**—including Poland, USA, Canada, Chile, Brazil, UK, Germany, France, Sweden, Italy, Slovakia, Ireland, Belgium, South Korea, Japan, Peru, Costa Rica, Colombia, Iceland, and the Faroe Islands—the network successfully bridges expertise across **four continents**: Europe, North America, South America, and Asia. Beyond academia, this initiative includes several R&D private sector partners, creating a robust ecosystem of dozens of specialized units dedicated to the advancement of yeast research.

Our Distinguished Partners

We are proud to collaborate with these distinguished scientists and their respective institutions: Francisco A. Cubillos – iBio, Universidad de Santiago de Chile (Chile); Chris Todd Hittinger – University of Wisconsin-Madison (USA); Paul A. Rowley – University of Idaho (USA); Lubomir Tomaska & Jozef Nosek – Comenius University in Bratislava (Slovakia); John Morrissey – University College Cork (Ireland); Marc-André Lachance – University of Western Ontario (Canada); Vivien Measday – University of British Columbia (Canada); Carlos Augusto Rosa – Federal University of Minas Gerais (Brazil); Matthias Sipiczki – University of Debrecen (Hungary); Duccio Cavalieri – University of Florence (Italy); Rike Stelkens – Stockholm University (Sweden); Sonja Billerbeck – Imperial College London (UK) & University of Groningen (Netherlands); Kevin Verstrepen – KU Leuven, VIB Center for Microbiology (Belgium); Hyun Ah Kang – Chung-Ang University (South Korea); Alejandra Calderón Hernández – Universidad Nacional (Costa Rica); Masaki Mizunuma – Hiroshima University (Japan); Milan Certik – Slovak University of Technology (Slovakia); Primrose Boynton – Wheaton College (USA); Jérôme Mounier – ESIAB, Université de Bretagne Occidentale (France); Andre Rodrigues – São Paulo State University (UNESP) (Brazil); Volkmar Passoth – Swedish University of Agricultural Sciences (Sweden); Jorge Ronny Díaz-Valderrama – Univ. Nacional Toribio Rodríguez de Mendoza (Peru); Geraldine Butler – University College Dublin (Ireland); Mathias Hutzler & Juan Ignacio Eizaguirre – Technical University of Munich (Germany); Mauricio Ramírez Castrillón – Universidad Industrial de Santander (Colombia); Gustavo Graciano Fonseca – University of Akureyri (Iceland); Anni Djurhuus – University of the Faroe Islands (Faroe Islands); The YHC Teams – Faculty of Biotechnology and Faculty of Biology, University of Rzeszów (Poland).

Why Join the YHC?

Being a member of the Yeast Hunter Club offers invaluable benefits, including exclusive access to specialized equipment and state-of-the-art facilities that empower cutting-edge research. Members also gain unique opportunities to represent the YHC at prestigious international events, enhancing their professional visibility while becoming part of a vast global network of world-class experts and institutional partners.

Explore our network: yeasthunterclub.webnode.page

Contact Information:
Faculty of Biotechnology, University of Rzeszów, Pigonia Street 1, Rzeszów, Poland.
Phone: +48 17 851 86 20
Email: mwnuk@ur.edu.pl

Beyond the Classroom: Cultivating the Next Generation of Scientists through Exploration

As an academic teachers we believe that the heart of modern education lies in fueling the fire of discovery through unconventional methods. To truly engage the younger digital generation, we must move beyond traditional lectures and seek innovative ways to spark curiosity. One of the most vital aspects of nurturing the next generation of scientists is developing their passion for field expeditions, venturing into the unknown to master the art of environmental sampling. It is through these hands-on journeys and immersive experiences that students learn to track down elusive conventional and non-conventional yeast strains that hold the key to future biotechnological breakthroughs. By replacing static learning with active exploration, we transform science from a subject into a lifelong calling. In this spirit, the Yeast Hunter Club continues to thrive, particularly through its Young Yeast Hunters section, which brings together ambitious university students and high school enthusiasts eager to push the boundaries of microbiology.

This commitment to real-world exploration was put into practice on March 26th, when the Young Yeast Hunters conducted an extraordinary research expedition to the historic Wieliczka Salt Mine (https://www.wieliczka-saltmine.com/).

This venture was made possible through the graciousness of the Mine's Management, allowing our team to access unique biological environments deep underground. While the standard Tourist Route concludes at 135 meters, our team descended to a depth of 200 meters to secure samples from one of the most extreme environments on Earth. Under the expert guidance of Deputy Manager of the Surveying and Geological Department and Chief Mining Geologist, the team secured nearly 50 environmental samples, including brines, subsurface soil, and various salt precipitates. For our researchers, this extreme site serves as a living laboratory. Preliminary screening has already identified several hardy species thriving in these high-salinity conditions. Specifically, the team isolated halophilic strains belonging to the genera *Candida*, *Debaryomyces*, *Meyerozyma*, *Metschnikovia*, *Pichia*, and *Yarrowia*. Their presence in these subterranean saline niches is consistent with previous observations of hypersaline ecosystems, where specialized fungal communities are shaped primarily by low water activity and high ionic stress.

Notably, studies on hypersaline fungi have demonstrated that black yeast-like species such as *Hortaea wernecki*i can tolerate near-saturated NaCl concentrations and serve as important eukaryotic models for salt adaptation (Gostinčar C, Gunde-Cimerman N. Black yeasts in hypersaline conditions. Appl Microbiol Biotechnol. 2024 Mar 5;108(1):252
doi: 10.1007/s00253-024-13052-2).

Current evidence suggests that survival under such conditions depends on coordinated osmoadaptive responses, including activation of the HOG signaling pathway, intracellular accumulation of compatible solutes such as glycerol, and extensive remodeling of cellular membranes and melanized cell walls, which collectively stabilize cellular integrity under chronic osmotic stress. The presence of phylogenetically diverse halotolerant yeasts in the Wieliczka underground system therefore supports the view that deep saline environments may constitute stable ecological reservoirs for highly specialized fungal microbiota adapted to long-term hypersaline conditions.

These expeditions are by far the best way to educate a new generation of scientists. By stepping out of the classroom and into a historic Wieliczka Salt Mine, students don't just study science – they live it. Importantly, participation in such projects allows young participants to acquire real-world research skills—from experiment planning, through working in challenging field conditions, to analyzing and interpreting results. This experience significantly exceeds the standard model of academic education. Such trips are essential for developing professional passions and offer a genuine opportunity to discover unique, 'wild' strains with previously unseen properties. Through the "Young Yeast Hunters" programme, we are not only discovering microscopic life forms; we believe that in this way, the younger generation has the chance to shape the future of biotechnology, step by step, on every expedition.

Justyna Ruchała, Maciej Wnuk, and Magdalena Słowik-Borowiec, Dean's Council, Faculty of Biotechnology, University of Rzeszów.

Science Meets Sound: A Musical Journey into Yeast Research

We believe that science shouldn't be confined to the laboratory—it should be heard. While traditional scientific publications remain essential, music offers a unique medium for knowledge exchange. This track explores the hidden world of yeast, transforming complex biological processes into a narrative of growth, fermentation, and discovery.

Art and science are both attempts to understand our world. By combining them, we make the microscopic visible—and the invisible audible.

Listen to the track here: https://youtu.be/okL55iQ3TCo?si=I3tbiIdP6VMBbEQ6

Maciej Wnuk, Justyna Ruchała

Sixty Years of the International Commission on Yeasts

I am honored to have the possibility, every ten years, to remind the yeast research community, especially to its younger segment, of the foundation of the International Commission on Yeasts (ICY). The role of this international body is "to establish effective liaison between persons and organizations concerned in yeast investigations, and between them and the practical users of results of investigations, including yeast culture collections". The reason is perhaps that I served for more than a decade as one of the associate editors of the Yeast Newsletter and that the foundation of the ICY is linked to my country, Slovakia. This year we commemorate the 60th anniversary of the existence of the Commission. The creation of this body is linked to the second International Symposium on Yeasts which was held in July 1966, in Bratislava, Czechoslovakia, now the capital of Slovakia. The meeting was attended by 145 participants from 21 countries. During the Symposium the Czechoslovak representatives initiated the creation of an international organization which would stimulate communication and scientific collaboration among people working with yeasts all over the world. A Council for International Collaboration in Yeast Science was founded.

Dr. Anna Kocková-Kratochvílová (1915-1992)

Dr. Erich Minárik (1924-2007)

The late Dr. Anna Kocková-Kratochvílová was appointed Chair and the Dr. Erich Minárik, Secretary of the Council. Both were from Czechoslovakia. The other founding members of the Council were: K Beran (Czechoslovakia), A. Eddy (UK), P. Elinov (USSR), H. Klaushoffer (Austria), N.I. Kudrjavcev (USSR), U. Leopold (Switzerland), R. Muller (GDR), S. Nagai (Japan), O. Necas (Czechoslovakia), H.J. Phaff (USA), C.F. Robinow (Canada), H. Soumalainen (Finland), T. Tsuchiya (Japan), L.J. Wickerham (USA), T. Wikén (Holland) and S. Windisch (GFR), all well-recognized yeast researchers at the time. During the meeting it was also agreed that the existing Yeast Newsletter, edited by H.J. Phaff at the University of California, would serve as the official publication of the Council. Thanks to Prof. Phaff and later to Prof. M.A. Lachance, current editor, the Yeast Newsletter is still alive and bringing important information to our groups. In the early years after its foundation, the Council underwent changes in names and affiliations. In 1970, under the new name, International Commission on Yeasts and Yeast-like Microorganisms (ICY), it became a part of the Microbiology Division of the International Union of Biological Sciences (IUBS). In 1981 ICY also joined the Mycology Division of the International Union of Microbiological Societies (IUMS).

Dr. Kocková-Kratochvílová and Dr. Minárik also founded a tradition of national annual yeast conferences (originally Czechoslovak, and since 1993, Czech and Slovak), which are open to foreign scientists. The conferences, among the oldest scientific events in Slovakia and Central Europe, are held in the spring in a beautiful venue, the popular Smolenice Castle, near Bratislava. In May of this year the Slovak scientists held the 50th anniversary yeast conference (https://yeastconference.sk), which became also an opportunity to celebrate this traditional meeting and recall its best memories.

Smolenice Castle

Peter Biely,
Emeritus of the Institute of Chemistry, Slovak Academy of Science, and former Associate Editor of Yeast Newsletter.

Obituary

Graham Stewart (1942-2026)

With the passing of Emeritus Professor Graham Stewart on May 1st the global yeast community lost a great scientist and true friend. For over 50 years, Graham dedicated himself to research and education and his contributions to both were immense. His numerous seminal publications on yeast biochemistry, genetics, and physiology led to several innovative practices in the brewing sector (flocculation control, high-gravity fermentations, ice beer etc). Graham was also passionate about education and after 38 years leading research at Labatt brewing company in Canada, in 1994 he became Director of the International Centre for Brewing and Distilling at Heriot-Watt University in Edinburgh. During his academic tenure in Scotland, he became very interested in distilling yeasts and fermentation, and one of his final published contributions was on the merits of Scotch whisky! Whilst he was Professor, many students and researchers, including myself, benefitted greatly from his guidance and wisdom and we owe him a huge debt of gratitude. I first met Graham in 1980 at the ISY held at the University of Western Ontario in Canada which he organised. My abiding memories from his engaging presentations at this meeting, and numerous other scientific conferences, was his booming voice – no matter the size of the audience or auditorium, he had no need for a microphone! To Graham's family, friends and yeast colleagues, my sincere condolences. Thank you Graham for your friendship and support over the years, may you rest in peace.

Graeme Walker

Forthcoming Meetings

Yeast

Genetics Meeting

June 13–17, 2026

Asilomar Conference Grounds

Pacific Grove, CA

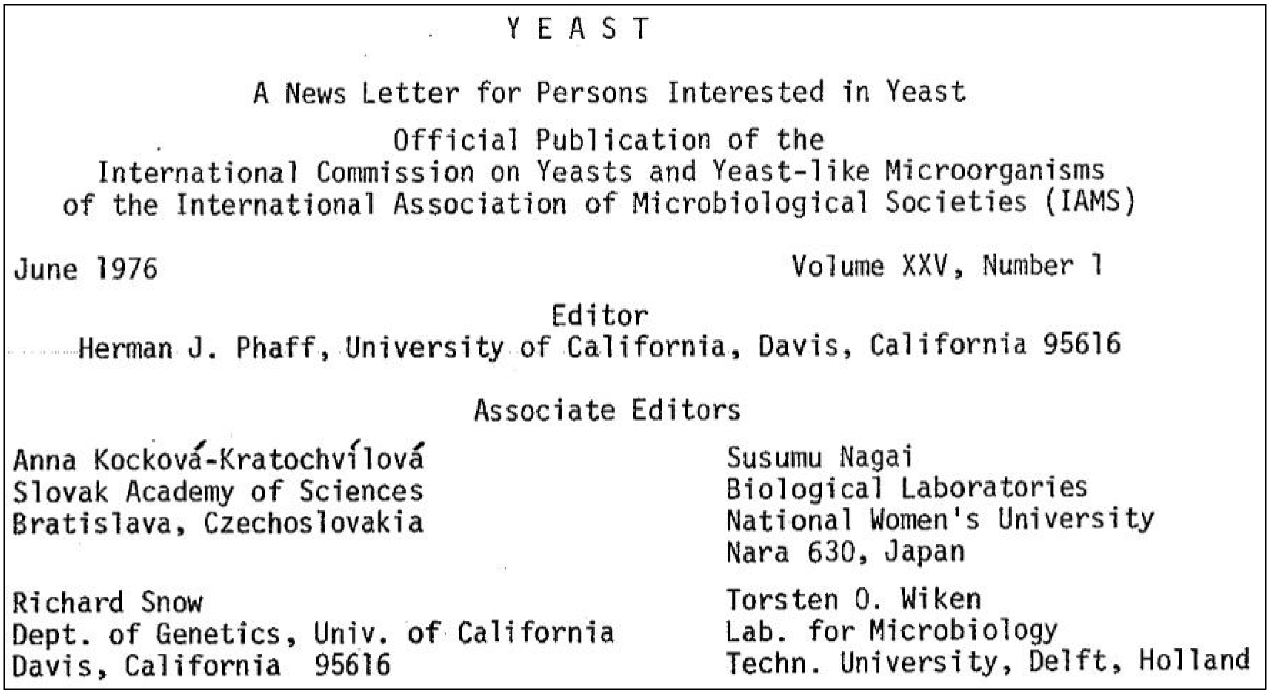
genetics-gsa.org/yeast

GSA

https://genetics-gsa.org/yeast-2026/

https://www.issy39.org/html/

50 Years Ago



YEAST

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Editor
Herman J. Phaff, University of California, Davis, California 95616

Associate Editors

Anna Kocková-Kratochvílová
Slovak Academy of Sciences
Bratislava, Czechoslovakia

Richard Snow
Dept. of Genetics, Univ. of California
Davis, California 95616

Susumu Nagai
Biological Laboratories
National Women's University
Nara 630, Japan

Torsten O. Wiken
Lab. for Microbiology
Techn. University, Delft, Holland

D. Yarrow of the Centraalbureau voor Schimmelcultures listed newly accessioned species including *Bullera piricola*, *Candida podzolica*, *Pichia lindneri*, *Sterigmatomyces nectairii*, *Torulopsis sonorensis*, and *Pichia burtonii*. Several represented newly described taxa or teleomorph-anamorph relationships.

Douglas S. King and **Sally A. Meyer** of the American Type Culture Collection reported dozens of newly accessioned yeast strains, including species of *Candida, Cryptococcus, Pichia,* Rhodotorula, Saccharomyces, and Lipomyces. Sally Meyer and Ruth Brown also used DNA reassociation studies to clarify relationships among species of Hanseniaspora and Kloeckera, demonstrating that Hanseniaspora uvarum and Kloeckera apiculata represented perfect-imperfect counterparts.

Maudy Th. Smith and colleagues at CBS described the new genus Stephanoascus to accommodate the perfect state of the yeast formerly known as Candida ciferrii.

D. G. Ahearn of Georgia State University summarized studies of hydrocarbon-utilizing yeasts, especially Candida maltosa and Yarrowia lipolytica (then Candida lipolytica). Researchers examined fungal utilization of hexadecane in the presence of the pesticide heptachlor and evaluated commercial clinical yeast identification systems.

Researchers in the laboratory of **Herman Phaff** at the University of California Davis published studies on yeast cell wall glucanases, carbohydrate-degrading enzymes, yeast ecology, and taxonomy. One major ecological study examined yeasts associated with cacti and *Drosophila* species in the Sonoran Desert, demonstrating close associations between particular yeasts, insect hosts, and cactus species. *Pichia membranaefaciens* was the dominant yeast recovered from these habitats.

- **H.J. Phaff, M.W. Miller,** and **M. Miranda** also described *Pichia scutulata* as a new yeast species isolated from tree exudates in Hawaii, Washington State, and British Columbia.
- **C. W. Price** and **H.J. Phaff** summarized extensive DNA comparison studies among species of *Debaryomyces*, *Pichia*, *Saccharomyces*, and *Schwanniomyces*. Their work argued that many traditional taxonomic criteria based on sugar fermentation did not accurately reflect evolutionary relationships. DNA sequence relatedness, ascospore ultrastructure, and ubiquinone composition were proposed as more reliable tools for yeast systematics.

C. P. Kurtzman of the USDA Northern Regional Research Center published work on ascospore ultrastructure in Debaryomyces melissophilus, sporulation in Pichia spartinae, and yeasts isolated from the traditional Mexican fermented maize food pozol.

K. J. Kwon-Chung of the National Institutes of Health used electron microscopy to characterize dolipore septa in Filobasidiella neoformans, the sexual state of Cryptococcus neoformans.

Myung Sam Park of Chonnam National University, South Korea studied yeasts associated with seaweeds and marine environments near Mok-po, Korea. Species of *Rhodotorula*, *Torulopsis*, and *Debaryomyces* were common in estuarine waters and on marine algae.

Heikki Suomalainen and colleagues at Alko in Finland investigated plasma membrane structure, lipid composition, nutrient utilization, carbon dioxide assimilation, glycerol production, and respiratory metabolism in Saccharomyces cerevisiae. Their studies linked membrane lipid composition with permeability and metabolic regulation under aerobic and anaerobic growth conditions.

Audrey Bersten at the University of Sydney studied morphogenesis in *Trigonopsis variabilis* using chemostat culture techniques. She showed that triangular cell morphology depended on temperature, oxygen availability, growth rate, and membrane lipid composition.

Researchers at NASA Ames Research Center purified and characterized acetyl-CoA synthetase from Saccharomyces cerevisiae, showing that the enzyme was composed of three similar subunits and inhibited by palmityl-CoA.

Akira Kimura of Kyoto University described methods for producing cytidine coenzymes such as CDP-choline using respiration-deficient yeast mutants and detergent-treated yeast cells.

N. van Uden and colleagues in Portugal investigated the effects of temperature, antibiotics, starch utilization, cyanide-resistant respiration, and chemostat energetics in Saccharomyces cerevisiae.

Eric Zeuthen of the Carlsberg Foundation studied synchronized cell cycles in Schizosaccharomyces pombe, demonstrating that some enzyme activity changes resulted directly from heat shock treatments rather than the cell cycle itself.

Mortimer Starr and colleagues at the University of Californa, Davis identified astaxanthin as the major carotenoid pigment of the newly described yeast *Phaffia rhodozyma*. They demonstrated that the astaxanthin stereochemistry differed from that of previously studied natural sources.

J. Schwencke in France characterized transport of S-adenosyl-L-methionine into yeast vacuoles, demonstrating that vacuolar and plasma membrane transport systems differed in pH optimum, inhibitor sensitivity, and energy requirements.

A. Martini of the University of Perugia, Italy, published studies on amino acid composition as a taxonomic tool, production of indole-3-acetic acid by yeasts, improved methods for isolating fruit-surface yeasts, and evaluation of yeast species as single-cell protein sources.

Note:
The June 1976 issue of the Yeast Newsletter reflects a period when yeast research was becoming increasingly molecular, ecological, and interdisciplinary. Many studies combined classical microbiology with emerging techniques such as DNA reassociation, electron microscopy, chemostat physiology, and biochemical enzyme analysis. At the same time, scientists continued expanding yeast culture collections and discovering new species that remain important today in biotechnology, ecology, food science, and medicine.

Kyria Boundy-Mills, Curator, Phaff Yeast Culture Collection