

# Yeast

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## **Editorial**

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## **Erratum**

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In the December 2023 issue, page 83, I mistakenly reported the birth year of our late colleague Byron Johnson as 1924 when in fact it was 1928. A correction has been made in the online version of the issue. I apologize for this mistake.

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M.A. Lachance

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Recent publication.

- 1 Golubev W.I. Intraspecific heterogeneity of *Candida* in sensitivity to mycocins. *Current Mycology in Russia*. v. 10 p. 55.

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Recent publications.

- 1 Liu F, Hu Z-D, Yurkov A, et al. 2024. Saccharomycetaceae: delineation of fungal genera based on phylogenomic analyses, genomic relatedness indices and genomics-based synapomorphies. *Persoonia* 52:1–21 - <https://doi.org/10.3767/persoonia.2024.52.01>.
- 2 Liu F, Hu Z-D, Zhao X-M, et al. 2024. Phylogenomic analysis of the *Candida auris*-*Candida haemuli* clade and related taxa in the Metschnikowiaceae, and proposal of thirteen new genera, fifty-five new combinations and nine new species. *Persoonia* 52:22–43 - <https://doi.org/10.3767/persoonia.2024.52.02>.
- 3 Liu MM, Zhao YJ, Boekhout T, Wang QM. Exploring the antibiofilm efficacy of cinnamaldehyde against *Malassezia globosa* associated pityriasis versicolor. *Phytomedicine* - <https://doi.org/10.1016/j.phymed.2024.155542>.
- 4 Liu M, Ding RX, Zhang YX, Li HZ, Wang QM. 2024. *Wickerhamomyces corioli* f.a., sp. nov., a novel yeast species discovered in two mushroom species. *Int J Syst Evol Microbiol* 74:006333 - DOI 10.1099/ijsem.0.006333.
- 5 Liu M, Jiang YL, Zhang YX, Wang QM. 2024. *Nakazawaea tricholomae* f.a., sp. nov., a novel ascomycetous yeast species isolated from two mushroom species in China. *Curr Microbiol* 81(3):78 - doi: 10.1007/s00284-023-03600-w.

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**III VTT Technical Research Centre of Finland, Tietotie 2, P.O. Box 1000, 02044 VTT, Espoo, Finland. Communicated by Kristoffer Krogerus <[Kristoffer.Krogerus@vtt.fi](mailto:Kristoffer.Krogerus@vtt.fi)>.**

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Recent publications.

- 1 Li L, Zhong W, Liu H, Espinosa-Artiles P, Xu Y-m, Wang C, Verdugo Robles JM, Paz TA, Cascaes Inácio M, Chen F, Xu Y, Gunatilaka AAL, Molnár I. 2024. Biosynthesis of cytosporones in Leotiomycetous filamentous fungi. *J Am Chem Soc* 146:6189-6198 - DOI: 10.1021/jacs.3c14066
  - 2 Liu C, Choi B, Efimova E, Nygård Y, Santala S. 2024. Enhanced upgrading of lignocellulosic substrates by coculture of *Saccharomyces cerevisiae* and *Acinetobacter baylyi* ADP1. *Biotechnol Biofuels* 17:61 - <https://doi.org/10.1186/s13068-024-02510-8>
  - 3 Cámara E, Mormino M, Siewers V, Nygård Y. 2024. *Saccharomyces cerevisiae* strains performing similarly during fermentation of lignocellulosic hydrolysates show pronounced differences in transcriptional stress responses. *Appl Environ Microbiol* 90:e02330-23 - <https://doi.org/10.1128/aem.02330-23>
  - 4 Toivari M, Vehkomäki ML, Ruohonen L, Penttilä M, Wiebe MG. 2024. Production of d-glucaric acid with phosphoglucose isomerase-deficient *Saccharomyces cerevisiae*. *Biotechnology Letters* 46:69-83 - <https://link.springer.com/article/10.1007/s10529-023-03443-2>
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Recently published book. The preface follows.

- 1 Tofalo R., Alexandre H. 2024 New frontiers in sparkling wine production. Nova Science Publishers, Inc. DOI: <https://doi.org/10.52305/IYRF4658>

The consumption of sparkling wines has seen significant development over time. Sparkling wines, such as champagne, prosecco, cava and other sparkling wines, have gained popularity in many countries. They are no longer just



reserved for special occasions, but have become common drinks to celebrate or simply enjoy. The diversification of sparkling wines has also had an impact on consumption. Cheaper, but equally tasty, alternatives have emerged, expanding the market and reaching a wider audience. While sparkling wines were once associated primarily with celebrations and parties, their consumption has expanded to throughout the year. People now enjoy them at informal dinners, brunches and even as a drink of choice to accompany a regular meal. The demand for lighter sparkling wines, such as low-alcohol or no-alcohol versions, has increased. Consumers are also looking for healthier and organic alternatives, which has encouraged producers to diversify their offering. Consumption of sparkling wines has also increased in new markets, notably in Asia, where these wines are becoming increasingly popular. In short, the consumption of sparkling wines has evolved to become more diversified, more accessible and more frequent in daily life, going well beyond just festive occasions. Parallel to the

development of sparkling wines, scientists became interested by the product. Indeed, scientific research into sparkling wine is a fascinating field that encompasses many aspects, from production to tasting that helps producers to improve the quality of wine. Research focuses on different aspects of sparkling wine production such as the fermentation process to understand the specific yeasts used in the fermentation of sparkling wines, such as the champenoise method, traditional method, or closed tank fermentation. Understanding optimal conditions, temperatures, yeast strains, etc., can improve the quality of the final product. Sparkling Wine Chemistry is also of outmost importance. The study of chemical components, including sugars, acids, tannins, and volatile aromatic compounds, plays a crucial role in defining the sensory profile of wine. Understanding how these components interact during fermentation and aging helps improve taste and quality. Quality control constitutes another research field in which different analytical methods have been developed to assess the quality of sparkling wine at different stages of production, from harvest to bottling. This may include sensory analysis techniques, chromatography, spectroscopy, etc. Compared to other wines, sparkling wines have specific characteristics that have led researchers to focus on these singularities. The prise de mousse is a peculiar process specific to sparkling wine which need yeast adapted to harsh environment. After the prise de mousse, in order to facilitate disgorging, different strategies have been developed such as flocculant yeast or encapsulated yeast. The most emblematic example is all the research carried out into the physics of bubbles. When you open a bottle of champagne, the characteristic sound you hear is actually the sound of carbon dioxide bubbles escaping from the liquid at high speed. These areas of research are helping to improve the scientific understanding of sparkling wines, which can lead to advances in the production, quality and even consumer appreciation of these wines. Immerse yourself in the captivating world of prise de mousse, a field where science and technology meet to create unique sensory experiences. This book is the fruit of a meticulous and passionate exploration of this fascinating aspect of manufacturing. On these pages, you will discover the scientific basis of sparkling wine production, explore the complex mechanisms that govern bubble formation from a microbiological, chemical and physical point of view.

Genome sequences and high-throughput phenotypic data published for nearly every known species of Saccharomycotina

The Y1000+ Project has published a dataset containing genome sequences for 1,154 yeasts, quantitative growth data in 24 environmental conditions, and a novel hierarchical ontology of isolation environments in *Science* (Opulente/LaBella et al. 2024, see below). A newly revamped website (<http://y1000plus.org>) provides a curated gateway to the data, team members, and key publications.

Recent publications.

- 1 Harrison MC, Ubbelohde EJ, LaBella AL, Opulente DA, Wolters JF, Zhou X, Shen XX, Groenewald M, Hittinger CT, Rokas A. 2024. Machine learning enables identification of an alternative yeast galactose utilization pathway. *Proc Natl Acad Sci USA* 121: e2315314121 - <https://doi.org/10.1073/pnas.2315314121>

How genomic differences contribute to phenotypic differences is a major question in biology. The recently characterized genomes, isolation environments, and qualitative patterns of growth on 122 sources and conditions of 1,154 strains from 1,049 fungal species (nearly all known) in the yeast subphylum Saccharomycotina provide a powerful, yet complex, dataset for addressing this question. We used a random forest algorithm trained on these genomic, metabolic, and environmental data to predict growth on several carbon sources with high accuracy. Known structural genes involved in assimilation of these sources and presence/absence patterns of growth in other sources were important features contributing to prediction accuracy. By further examining growth on galactose, we found that it can be predicted with high accuracy from either genomic (92.2%) or growth data (82.6%) but not

from isolation environment data (65.6%). Prediction accuracy was even higher (93.3%) when we combined genomic and growth data. After the *GAL*actose utilization genes, the most important feature for predicting growth on galactose was growth on galactitol, raising the hypothesis that several species in two orders, Serinales and Pichiales (containing the emerging pathogen *Candida auris* and the genus *Ogataea*, respectively), have an alternative galactose utilization pathway because they lack the *GAL* genes. Growth and biochemical assays confirmed that several of these species utilize galactose through an alternative oxidoreductive D-galactose pathway, rather than the canonical *GAL* pathway. Machine learning approaches are powerful for investigating the evolution of the yeast genotype-phenotype map, and their application will uncover novel biology, even in well-studied traits.

- 2 Opulente DA, LaBella AL, Harrison MC, Wolters JF, Liu C, Li Y, Kominek J, Steenwyk JL, Stoneman HR, VanDenAvond J, Miller CR, Langdon QK, Silva M, Gonçalves C, Ubbelohde EJ, Li Y, Buh KV, Jarzyna M, Haase MAB, Rosa CA, Čadež N, Libkind D, DeVirgilio JH, Hulfachor AB, Kurtzman CP, Sampaio JP, Gonçalves P, Zhou X, Shen XX, Groenewald M, Rokas A, Hittinger CT. 2024. Genomic factors shape carbon and nitrogen metabolic niche breadth across Saccharomycotina yeasts. *Science* 384:eadj4503 - <https://doi.org/10.1126/science.adj4503>

Organisms exhibit extensive variation in ecological niche breadth, from very narrow (specialists) to very broad (generalists). Two general paradigms have been proposed to explain this variation: (i) trade-offs between performance efficiency and breadth and (ii) the joint influence of extrinsic (environmental) and intrinsic (genomic) factors. We assembled genomic, metabolic, and ecological data from nearly all known species of the ancient fungal subphylum Saccharomycotina (1154 yeast

strains from 1051 species), grown in 24 different environmental conditions, to examine niche breadth evolution. We found that large differences in the breadth of carbon utilization traits between yeasts stem from intrinsic differences in genes encoding specific metabolic pathways, but we found limited evidence for trade-offs. These comprehensive data argue that intrinsic factors shape niche breadth variation in microbes.

- 3 Sun L, David KT, Wolters JF, Karlen SD, Gonçalves C, Opulente DA, LaBella AL, Groenewald M, Zhou X, Shen XX, Rokas A, Hittinger CT. 2024. Functional and evolutionary integration of a fungal gene with a bacterial operon. *Mol Biol Evol* 41:msae045 - <https://doi.org/10.1093/molbev/msae045>

Siderophores are crucial for iron-scavenging in microorganisms. While many yeasts can uptake siderophores produced by other organisms, they are typically unable to synthesize siderophores themselves. In contrast, *Wickerhamiella/Starmerella* (W/S) clade yeasts gained the capacity to make the siderophore enterobactin following the remarkable horizontal acquisition of a bacterial operon enabling enterobactin synthesis. Yet, how these yeasts absorb the iron bound by enterobactin remains unresolved. Here, we demonstrate that *Enb1* is the key enterobactin importer in the W/S-clade species *Starmerella bombicola*. Through phylogenomic analyses, we show that *ENBI* is present in all W/S clade yeast species that retained the enterobactin biosynthetic genes. Conversely, it is absent in species that lost the *ent* genes, except for *Starmerella stellata*, making this species the only cheater in the W/S

clade that can utilize enterobactin without producing it. Through phylogenetic analyses, we infer that *ENBI* is a fungal gene that likely existed in the W/S clade prior to the acquisition of the *ent* genes and subsequently experienced multiple gene losses and duplications. Through phylogenetic topology tests, we show that *ENBI* likely underwent horizontal gene transfer from an ancient W/S clade yeast to the order Saccharomycetales, which includes the model yeast *Saccharomyces cerevisiae*, followed by extensive secondary losses. Taken together, these results suggest that the fungal *ENBI* and bacterial *ent* genes were cooperatively integrated into a functional unit within the W/S clade that enabled adaptation to iron-limited environments. This integrated fungal-bacterial circuit and its dynamic evolution determines the extant distribution of yeast enterobactin producers and cheaters.

- 4 David KT, Harrison MC, Opulente DA, LaBella AL, Wolters JF, Zhou X, Shen XX, Groenewald M, Pennell M, Hittinger CT, Rokas A. 2024. Saccharomycotina yeasts defy long-standing macroecological patterns. *Proc Natl Acad Sci USA* 121:e2316031121 - <https://doi.org/10.1073/pnas.2316031121>

The Saccharomycotina yeasts (“yeasts” hereafter) are a fungal clade of scientific, economic, and medical significance. Yeasts are highly ecologically diverse, found across a broad range of environments in every biome and continent on earth; however, little is known about what rules govern the macroecology of yeast species and their range limits in the wild. Here, we trained machine learning models on 12,816 terrestrial occurrence records and 96 environmental variables to infer global distribution maps at ~1 km<sup>2</sup> resolution for 186 yeast species (~15% of described species from 75% of orders) and to test environmental drivers of yeast biogeography and macroecology. We found that predicted yeast diversity hotspots occur in mixed montane forests in temperate climates. Diversity in vegetation type and topography were some of the greatest predictors of yeast species richness, suggesting

that microhabitats and environmental clines are key to yeast diversity. We further found that range limits in yeasts are significantly influenced by carbon niche breadth and range overlap with other yeast species, with carbon specialists and species in high-diversity environments exhibiting reduced geographic ranges. Finally, yeasts contravene many long-standing macroecological principles, including the latitudinal diversity gradient, temperature-dependent species richness, and a positive relationship between latitude and range size (Rapoport’s rule). These results unveil how the environment governs the global diversity and distribution of species in the yeast subphylum. These high-resolution models of yeast species distributions will facilitate the prediction of economically relevant and emerging pathogenic species under current and future climate scenarios.

- 5 Barros KO, Mader M, Krause DJ, Pangilinan J, Andreopoulos B, Lipzen A, Mondo SJ, Grigoriev IV, Rosa CA, Sato TK, Hittinger CT. 2024. Oxygenation influences xylose fermentation and gene expression in the yeast genera *Spathaspora* and *Scheffersomyces*. *Biotechnol Biofuels Bioprod* 17:20 - <https://doi.org/10.1186/s13068-024-02467-8>

Background: Cost-effective production of biofuels from lignocellulose requires the fermentation of D-xylose. Many yeast species within and closely related to the genera *Spathaspora* and *Scheffersomyces* (both of the

order Serinales) natively assimilate and ferment xylose. Other species consume xylose inefficiently, leading to extracellular accumulation of xylitol. Xylitol excretion is thought to be due to the different cofactor

requirements of the first two steps of xylose metabolism. Xylose reductase (XR) generally uses NADPH to reduce xylose to xylitol, while xylitol dehydrogenase (XDH) generally uses NAD<sup>+</sup> to oxidize xylitol to xylulose, creating an imbalanced redox pathway. This imbalance is thought to be particularly consequential in hypoxic or anoxic environments.

Results: We screened the growth of xylose-fermenting yeast species in high and moderate aeration and identified both ethanol producers and xylitol producers. Selected species were further characterized for their XR and XDH cofactor preferences by enzyme assays and gene expression patterns by RNA-Seq. Our data revealed that xylose metabolism is more redox balanced in some species, but it is strongly affected by oxygen levels. Under high aeration, most species switched from ethanol production to xylitol accumulation, despite the availability of ample oxygen to accept electrons from NADH. This switch was followed by decreases in enzyme activity and the

- 6 Pontes A, Paraíso F, Liu YC, Limtong S, Jindamorakot S, Jespersen L, Gonçalves C, Rosa CA, Tsai IJ, Rokas A, Hittinger CT, Gonçalves P, Sampaio JP. 2024. Tracking alternative versions of the galactose gene network in the genus *Saccharomyces* and their expansion after domestication. *iScience* 27: 108987 - <https://doi.org/10.1016/j.isci.2024.108987>

When *Saccharomyces cerevisiae* grows on mixtures of glucose and galactose, galactose utilization is repressed by glucose, and induction of the *GAL* gene network only occurs when glucose is exhausted. Contrary to reference *GAL* alleles, alternative alleles support faster growth on galactose, thus enabling distinct galactose utilization strategies maintained by balancing selection. Here, we report on new wild populations of *Saccharomyces cerevisiae* harboring alternative *GAL* versions and, for the first time, of *Saccharomyces paradoxus* alternative alleles. We also show that the non-

- 7 Wolters JF, LaBella AL, Opulente DA, Rokas A, Hittinger CT. Mitochondrial genome diversity across the subphylum Saccharomycotina. *Front Microbiol* 14:1268944 - <https://doi.org/10.3389/fmicb.2023.1268944>

Introduction: Eukaryotic life depends on the functional elements encoded by both the nuclear genome and organellar genomes, such as those contained within the mitochondria. The content, size, and structure of the mitochondrial genome varies across organisms with potentially large implications for phenotypic variance and resulting evolutionary trajectories. Among yeasts in the subphylum Saccharomycotina, extensive differences have been observed in various species relative to the model yeast *Saccharomyces cerevisiae*, but mitochondrial genome sampling across many groups has been scarce, even as hundreds of nuclear genomes have

expression of genes related to xylose metabolism, suggesting that bottlenecks in xylose fermentation are not always due to cofactor preferences. Finally, we expressed *XYL* genes from multiple *Scheffersomyces* species in a strain of *Saccharomyces cerevisiae*. Recombinant *S. cerevisiae* expressing *XYL1* from *Scheffersomyces xylosifermentans*, which encodes an XR without a cofactor preference, showed improved anaerobic growth on xylose as the primary carbon source compared to *S. cerevisiae* strain expressing *XYL* genes from *Scheffersomyces stipitis*.

Conclusion: Collectively, our data do not support the hypothesis that xylitol accumulation occurs primarily due to differences in cofactor preferences between xylose reductase and xylitol dehydrogenase; instead, gene expression plays a major role in response to oxygen levels. We have also identified the yeast *Sc. xylosifermentans* as a potential source for genes that can be engineered into *S. cerevisiae* to improve xylose fermentation and biofuel production.

functional *GAL* version found earlier in *Saccharomyces kudriavzevii* is phylogenetically related to the alternative versions, which constitutes a case of *trans*-specific maintenance of highly divergent alleles. Strains harboring the different *GAL* network variants show different levels of alleviation of glucose repression and growth proficiency on galactose. We propose that domestication involved specialization toward thriving in milk from a generalist ancestor partially adapted to galactose consumption in the plant niche.

become available.

Methods: By extracting mitochondrial assemblies from existing short-read genome sequence datasets, we have greatly expanded both the number of available genomes and the coverage across sparsely sampled clades.

Results: Comparison of 353 yeast mitochondrial genomes revealed that, while size and GC content were fairly consistent across species, those in the genera *Metschnikowia* and *Saccharomyces* trended larger, while several species in the order Saccharomycetales, which includes *S. cerevisiae*, exhibited lower GC content.

Extreme examples for both size and GC content were scattered throughout the subphylum. All mitochondrial genomes shared a core set of protein-coding genes for Complexes III, IV, and V, but they varied in the presence or absence of mitochondrially-encoded canonical Complex I genes. We traced the loss of Complex I genes to a major event in the ancestor of the orders Saccharomycetales and Saccharomycodales, but we also observed several independent losses in the orders Phaffomycetales, Pichiales, and Dipodascales. In contrast to prior hypotheses based on smaller-scale datasets, comparison of evolutionary rates in protein-coding genes showed no bias towards elevated rates among aerobically fermenting (Crabtree/Warburg-

positive) yeasts. Mitochondrial introns were widely distributed, but they were highly enriched in some groups. The majority of mitochondrial introns were poorly conserved within groups, but several were shared within groups, between groups, and even across taxonomic orders, which is consistent with horizontal gene transfer, likely involving homing endonucleases acting as selfish elements.

Discussion: As the number of available fungal nuclear genomes continues to expand, the methods described here to retrieve mitochondrial genome sequences from these datasets will prove invaluable to ensuring that studies of fungal mitochondrial genomes keep pace with their nuclear counterparts.

- 8 Opulente DA, Langdon QK, Jarzyna M, Buh KV, Haase MAB, Groenewald M, Hittinger CT. 2024. Taxogenomic analysis of a novel yeast species isolated from soil, *Pichia galeolata* sp. nov. *Yeast* 40:608-15 - <https://doi.org/10.1002/yea.3905>

A novel budding yeast species was isolated from a soil sample collected in the United States of America. Phylogenetic analyses of multiple loci and phylogenomic analyses conclusively placed the species within the genus *Pichia*. Strain yHMH446 falls within a clade that includes *Pichia norvegensis*, *Pichia pseudocactophila*, *Candida inconspicua*, and *Pichia cactophila*. Whole genome sequence data were analyzed for the presence of genes known to be important for carbon and nitrogen metabolism, and the phenotypic data from the novel

species were compared to all *Pichia* species with publicly available genomes. Across the genus, including the novel species candidate, we found that the inability to use many carbon and nitrogen sources correlated with the absence of metabolic genes. Based on these results, *Pichia galeolata* sp. nov. is proposed to accommodate yHMH446<sup>T</sup> (=NRRL Y-64187 = CBS 16864). This study shows how integrated taxogenomic analysis can add mechanistic insight to species descriptions.

- 9 Gonçalves C, Hittinger CT, Rokas A. 2024. Horizontal gene transfer in fungi and its ecological importance. In *Fungal Associations: The Mycota* vol 9, 3rd ed: 59-81. Springer: Cham, Switzerland - [https://doi.org/10.1007/978-3-031-41648-4\\_3](https://doi.org/10.1007/978-3-031-41648-4_3)

Fungi are one of the most diverse kingdoms in the tree of life, thrive in virtually every habitat on the planet, and are vital for a plethora of ecosystems and human-related activities. The advent of genomic technologies has revolutionized the study of fungal ecology and evolution. Surprisingly, evolutionary genomic investigations have revealed that horizontal gene transfer (HGT)—the movement of genetic material from one organism to another by means other than sexual reproduction—is an important factor influencing the ecology and evolution of fungal genomes. This chapter uses an evolutionary framework to discuss the extent and distribution of HGT across fungal ecologies and lifestyles, focusing on some of the best-supported cases to address fundamental questions such as frequencies,

barriers, and mechanisms for eukaryotic HGT. One important conclusion that can be drawn from studies of fungal HGT is that HGT rate varies extensively across lineages and that this variation can generally be associated with distinctive ecologies, lifestyles, or genetic backgrounds. Similarly, not all functional categories of genes are equally likely to result in successful transfers. The factors underlying both frequency and functional variations of HGT across fungi are thoroughly discussed. Advances in genomic and synthetic biology technologies will continue to shed light on these questions and bring many other still unanswered questions into focus. Some of these questions and directions for future research are highlighted at the end of this chapter.



- 10 Chavez CM, Groenewald M, Hulfachor AB, Kpurubu G, Huerta R, Hittinger CT, Rokas A. 2024. The cell morphological diversity of *Saccharomycotina* yeasts. *FEMS Yeast Res* 24:foad055 - <https://doi.org/10.1093/femsyr/foad055>

The ~1200 known species in subphylum Saccharomycotina are a highly diverse clade of unicellular fungi. During its lifecycle, a typical yeast exhibits multiple cell types with various morphologies; these morphologies vary across Saccharomycotina species. Here, we synthesize the evolutionary dimensions of variation in cellular morphology of yeasts across the subphylum, focusing on variation in cell shape, cell size, type of budding, and filament production. Examination of 332 representative species across the subphylum revealed that the most common budding cell shapes are ovoid, spherical, and ellipsoidal, and that their average length and width is 5.6  $\mu\text{m}$  and 3.6  $\mu\text{m}$ , respectively. 58.4% of

yeast species examined can produce filamentous cells, and 87.3% of species reproduce asexually by multilateral budding, which does not require utilization of cell polarity for mitosis. Interestingly, ~1.8% of species examined have not been observed to produce budding cells, but rather only produce filaments of septate hyphae and/or pseudohyphae. 76.9% of yeast species examined have sexual cycle descriptions, with most producing one to four ascospores that are most commonly hat-shaped (37.4%). Systematic description of yeast cellular morphological diversity and reconstruction of its evolution promises to enrich our understanding of the evolutionary cell biology of this major fungal lineage.

- 11 Zavala B, Dineen L, Fisher KJ, Opulente DA, Harrison MC, Wolters JF, Shen XX, Zhou X, Groenewald M, Hittinger CT, Rokas A, LaBella AL. Genomic factors shaping codon usage across the Saccharomycotina subphylum. *bioRxiv* - <https://doi.org/10.1101/2024.05.23.595506>

Codon usage bias, or the unequal use of synonymous codons, is observed across genes, genomes, and between species. The biased use of synonymous codons has been implicated in many cellular functions, such as translation dynamics and transcript stability, but can also be shaped by neutral forces. The Saccharomycotina, the fungal subphylum containing the yeasts *Saccharomyces cerevisiae* and *Candida albicans*, has been a model system for studying codon usage. We characterized codon usage across 1,154 strains from 1,051 species to gain insight into the biases, molecular mechanisms, evolution, and genomic features contributing to codon usage patterns across the subphylum. We found evidence of a general preference for A/T-ending codons and correlations between codon usage bias, GC content, and tRNA-ome size. Codon usage bias is also distinct between the 12 orders within the subphylum to such a degree that yeasts can be classified into orders with an accuracy greater than 90% using a machine learning algorithm trained on codon usage. We also characterized the degree to which codon usage bias is impacted by

translational selection. Interestingly, the degree of translational selection was influenced by a combination of genome features and assembly metrics that included the number of coding sequences, BUSCO count, and genome length. Our analysis also revealed an extreme bias in codon usage in the Saccharomycodales associated with a lack of predicted arginine tRNAs. The order contains 24 species, and 23 are computationally predicted to lack tRNAs that decode CGN codons, leaving only the AGN codons to encode arginine. Analysis of Saccharomycodales gene expression, tRNA sequences, and codon evolution suggests that extreme avoidance of the CGN codons is associated with a decline in arginine tRNA function. Codon usage bias within the Saccharomycotina is generally consistent with previous investigations in fungi, which show a role for both genomic features and GC bias in shaping codon usage. However, we find cases of extreme codon usage preference and avoidance along yeast lineages, suggesting additional forces may be shaping the evolution of specific codons.

- 12 Rojas J, Hose J, Auguste Dutcher H, Place M, Wolters JF, Hittinger CT, Gasch AP. Comparative modeling reveals the molecular determinants of aneuploidy fitness cost in a wild yeast model. *bioRxiv* - <https://doi.org/10.1101/2024.04.09.588778>

Although implicated as deleterious in many organisms, aneuploidy can underlie rapid phenotypic evolution. However, aneuploidy will only be maintained if the benefit outweighs the cost, which remains incompletely understood. To quantify this cost and the

molecular determinants behind it, we generated a panel of chromosome duplications in *Saccharomyces cerevisiae* and applied comparative modeling and molecular validation to understand aneuploidy toxicity. We show that 74-94% of the variance in aneuploid

strains' growth rates is explained by the additive cost of genes on each chromosome, measured for single-gene duplications using a genomic library, along with the deleterious contribution of snoRNAs and beneficial effects of tRNAs. Machine learning to identify properties of detrimental gene duplicates provided no support for

the balance hypothesis of aneuploidy toxicity and instead identified gene length as the best predictor of toxicity. Our results present a generalized framework for the cost of aneuploidy with implications for disease biology and evolution.

13 Gonçalves C, Harrison MC, Steenwyk JL, Opulente DA, LaBella AL, Wolters JF, Zhou X, Shen XX, Groenewald M, Hittinger CT, Rokas A. Diverse signatures of convergent evolution in cacti-associated yeasts. bioRxiv - <https://doi.org/10.1101/2023.09.14.557833>

Many distantly related organisms have convergently evolved traits and lifestyles that enable them to live in similar ecological environments. However, the extent of phenotypic convergence evolving through the same or distinct genetic trajectories remains an open question. Here, we leverage a comprehensive dataset of genomic and phenotypic data from 1,049 yeast species in the subphylum Saccharomycotina (Kingdom Fungi, Phylum Ascomycota) to explore signatures of convergent evolution in cactophilic yeasts, ecological specialists associated with cacti. We inferred that the ecological association of yeasts with cacti arose independently ~17 times. Using machine-learning, we further found that cactophily can be predicted with 76% accuracy from functional genomic and phenotypic data. The most informative feature for predicting cactophily was thermotolerance, which is likely associated with

duplication and altered evolutionary rates of genes impacting the cell envelope in several cactophilic lineages. We also identified horizontal gene transfer and duplication events of plant cell wall-degrading enzymes in distantly related cactophilic clades, suggesting that putatively adaptive traits evolved through disparate molecular mechanisms. Remarkably, multiple cactophilic lineages and their close relatives are emerging human opportunistic pathogens, suggesting that the cactophilic lifestyle—and perhaps more generally lifestyles favoring thermotolerance—may preadapt yeasts to cause human disease. This work underscores the potential of a multifaceted approach involving high throughput genomic and phenotypic data to shed light onto ecological adaptation and highlights how convergent evolution to wild environments could facilitate the transition to human pathogenicity.

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**VI 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](mailto:lenna_naumova@yahoo.com)>.**

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The following are papers for 2024 or in press.

1 Tellini N, De Chiara M, Mozzachiodi S, Tattini L, Vischioni C, Naumova E.S, Warringer J, Bergström A, Liti G. 2024. Ancient and recent origins of shared polymorphisms in yeast. *Nature Ecology and Evolution* 8(4):761–776 - <https://doi.org/10.1038/s41559-024-02352-5>

Shared genetic polymorphisms between populations and species can be ascribed to ancestral variation or to more recent gene flow. Here, we mapped shared polymorphisms in *Saccharomyces cerevisiae* and its sister species *Saccharomyces paradoxus*, which diverged 4–6 million years ago. We used a dense map of single-nucleotide diagnostic markers (mean distance 15.6 base pairs) in 1,673 sequenced *S. cerevisiae* isolates to catalogue 3,852 sequence blocks ( $\geq 5$  consecutive markers) introgressed from *S. paradoxus*, with most being recent and clade-specific. The highly diverged wild Chinese *S. cerevisiae* lineages were depleted of introgressed blocks but retained an excess of individual ancestral polymorphisms derived from incomplete

lineage sorting, perhaps due to less dramatic population bottlenecks. In the non-Chinese *S. cerevisiae* lineages, we inferred major hybridization events and detected cases of overlapping introgressed blocks across distinct clades due to either shared histories or convergent evolution. We experimentally engineered, in otherwise isogenic backgrounds, the introgressed PAD1-FDC1 gene pair that independently arose in two *S. cerevisiae* clades and revealed that it increases resistance against diverse antifungal drugs. Overall, our study retraces the histories of divergence and secondary contacts across *S. cerevisiae* and *S. paradoxus* populations and unveils a functional outcome.

- 2 Tuaveva AYU, Ponomareva AM, Livshits VA, Naumova ES. In press. Yeast microflora of dairy products sold in Russia. *Microbiology (Moscow)* 93 (5).

Using restriction analysis of the 5.8S-ITS rDNA fragment and sequencing of the D1/D2 domain of 26S rDNA, the yeast microflora of various dairy products sold in Russia was studied. Most of the fermented milk products studied were dominated by lactose-utilizing yeasts *Kluyveromyces* and *Debaryomyces*, as well as lactose-negative yeasts *Saccharomyces*, *Monosporozyma*, *Pichia*, *Geotrichum* and *Yarrowia*. The yeast *Kluyveromyces marxianus* was present in most of the fermented milk products studied, while the related species *K. lactis* was found only in some samples of

ayran, curds and cheese. The dominance of *K. marxianus* is apparently associated with their physiological characteristics (thermo- and osmotolerance), which provide these yeasts with better adaptation to industrial fermentation conditions. The dominant species in mixed-fermentation dairy products, *Saccharomyces cerevisiae* and *Monosporozyma unispora*, were completely absent in cheeses and lactic acid fermentation products. In general, the species composition of yeast largely depended on the fermented milk product, the type of milk and the specific manufacturer.

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**VII Medical Mycology Group, Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT, Utrecht, The Netherlands. Communicated by F. Hagen <[f.hagen@wi.knaw.nl](mailto:f.hagen@wi.knaw.nl)>.**

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We recently described the basidiomycetous yeast species *Trichosporon austroamericanum*, which we first observed among a set of Brazilian strains that were previously identified as *Trichosporon inkin*. Until now, *Trichosporon* species are not well covered in the MALDI-TOF mass spectrometry

databases which hampers species-level identification in clinical diagnostics. Hence, we provided the reference profile for the Bruker MALDI-TOF platform to the open access identification platform MicrobeNet. For more information about *T. austroamericanum*, please see the publication:

- 1 Francisco EC, Desnos-Ollivier M, Dieleman C, Boekhout T, Santos DWCL, Medina-Pestana JO, Colombo AL, Hagen F. 2024. Unveiling *Trichosporon austroamericanum* sp. nov.: A novel emerging opportunistic basidiomycetous yeast species. *Mycopathologia* 189(3):43 - doi: 10.1007/s11046-024-00851-4.

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After many years, an update on the global guideline for the diagnosis and management of cryptococcosis has been published, an initiative led by the European Confederation of Medical Mycology societies and the International Society for Human and Animal Mycology, in cooperation with the American Society for Microbiology. The current version is the 'online ahead of print' version, but the

supplementary material, <https://www.sciencedirect.com/science/article/pii/S1473309923007314?via%3Dihub#sec1> contains the full document that forms the fundament for the outline paper by Chang and co-workers that is online available via The Lancet Infectious Diseases, see [https://doi.org/10.1016/S1473-3099\(23\)00731-4](https://doi.org/10.1016/S1473-3099(23)00731-4)

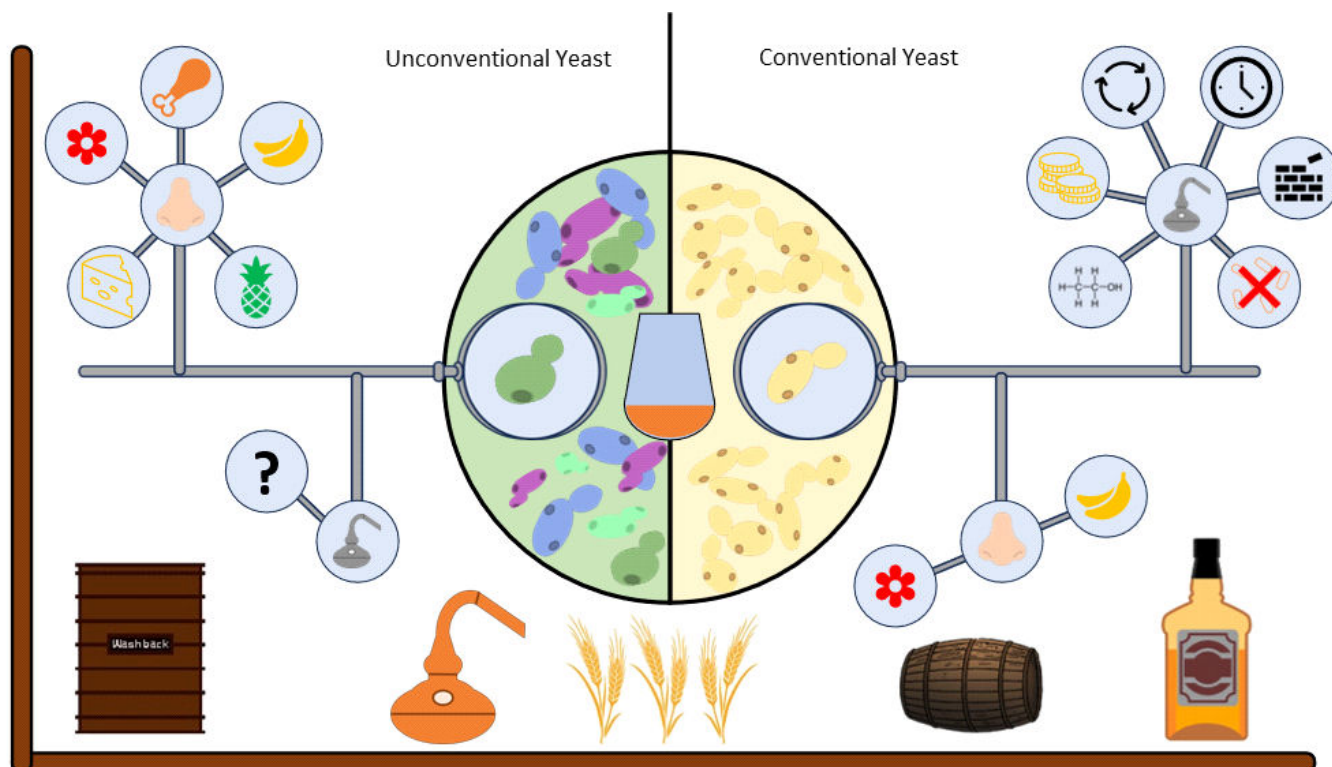
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In December 2023 a proposal for a conceptual framework for nomenclature stability and validity of medically important fungi was published in the *Journal of Clinical Microbiology* (de Hoog et al. 2023). A conceptual framework for nomenclatural stability and validity of medically important fungi: a proposed global consensus guideline for fungal name changes supported by ABP, ASM, CLSI, ECMM, ESCMID-EFISG, EUCAST-AFST, FDLC, IDSA, ISHAM, MMSA and MSGERC. *J Clin Microbiol* 61:e00873-23. doi: <https://doi.org/10.1128/jcm.00873-23>).

However, others observed some inconsistencies within the proposed framework which risks further confusion about fungal nomenclature, hence this was published as a Letter to the Editor (Kidd et al. *J Clin Microbiol.* 2024;62(4):e0157023. <https://doi.org/10.1128/jcm.01570-23>). This Letter was followed by a response from the authors of the original paper which can be found in the same April issue of the *Journal of Clinical Microbiology* (de Hoog et al., 2024;62(4):e0162523. <https://doi.org/10.1128/jcm.01625-23>).

Recent publication.

- 1 Daute M, Jack F, Walker G. 2024. The potential for scotch malt whisky flavour diversification by yeast. FEMS Yeast Res foae017 - <https://doi.org/10.1093/femsyr/foae017>



Scotch Whisky, a product of high importance to Scotland, has gained global approval for its distinctive qualities derived from the traditional production process which is defined in law. However, ongoing research continuously enhances Scotch Whisky production and is fostering a diversification of flavour profiles. To be classified as Scotch Whisky, the final spirit needs to retain the aroma and taste of “Scotch”. While each production step contributes significantly to whisky flavour - from malt preparation and mashing to fermentation, distillation, and maturation - the impact of yeast during fermentation is crucially important. Not only does the yeast convert the sugar to alcohol, it also

produces important volatile compounds, for example esters and higher alcohols, that contribute to the final flavour profile of whisky. The yeast chosen for whisky fermentations can significantly influence whisky flavour, so the yeast strain employed is of high importance. This review explores the role of yeast in Scotch Whisky production and its influence on flavour diversification. Furthermore, an extensive examination of non-conventional yeasts employed in brewing and winemaking is undertaken to assess their potential suitability for adoption as Scotch Whisky yeast strains, followed by a review of methods for evaluating new yeast strains.

Recent publications.

- 1 Maza DD, Barros JM, Guillamón JM, Aybar MJ and Viñarta SC. 2024. Valorization of sugarcane vinasse and crude glycerol for single-cell oils production by *Rhodotorula glutinis* R4: a preliminary approach to the integration of biofuels industries for sustainable biodiesel feedstock. *Fermentation* (MDPI) 10(4):178 - <https://doi.org/10.3390/fermentation10040178>

Single-cell oils (SCOs) offer a promising alternative to conventional biodiesel feedstocks. The main objective of this work was to obtain SCOs suitable for biodiesel production from the oleaginous yeast *Rhodotorula glutinis* R4 using sugarcane vinasse from a local sugar-derived alcohol industry as the substrate. Additionally, crude glycerol from the local biodiesel industry was evaluated as a low-cost carbon source to replace expensive glucose and as a strategy for integrating the bioethanol and biodiesel industries for the valorization of both agro-industrial wastes. R4 achieved a high lipid accumulation of 88% and 60% (w/w) in vinasse-based culture media, containing 10% and 25% vinasse with

glucose (40 g L<sup>-1</sup>), respectively. When glucose was replaced with crude glycerol, R4 showed remarkable lipid accumulation (40%) and growth (12.58 g L<sup>-1</sup>). The fatty acids profile of SCOs showed a prevalence of oleic acid (C18:1), making them suitable for biodiesel synthesis. Biodiesel derived from R4 oils exhibits favorable characteristics, including a high cetane number (CN = 55) and high oxidative stability (OS = 13 h), meeting international biodiesel standards (ASTMD6751 and EN14214) and ensuring its compatibility with diesel engines. *R. glutinis* R4 produces SCOs from vinasse and crude glycerol, contributing to the circular economy for sustainable biodiesel production.

- 2 Angelicola MV, Fernández PM, Aybar MJ, Van Nieuwenhove CP, Figueroa LIC, and Viñarta SC. 2023. Bioconversion of commercial and crude glycerol to single-cell oils by the Antarctic yeast *Rhodotorula glutinis* R4 as a biodiesel feedstock. *Biocatalysis and Agricultural Biotechnology* 47(1):102544 - <https://doi.org/10.1016/j.bcab.2022.102544>

Ability of the oleaginous yeast *Rhodotorula glutinis* R4 to produce single-cell oils (SCO) using different concentrations (25–100 g L<sup>-1</sup>) of commercial and crude glycerol as substrate was evaluated. *R. glutinis* R4 reached 44–57% and 41–52% (w/w) of lipid accumulation when grown with 25–100 g L<sup>-1</sup> of crude and commercial glycerol, respectively. R4 grown with 35 and 50 g L<sup>-1</sup> of crude glycerol reached a lipid accumulation of 44–45% (w/w) at 120 h corresponding to 6 g L<sup>-1</sup> of lipid concentration, with a yield  $Y_{LX} \sim 0.45$  g g<sup>-1</sup>, lipid productivity (Q<sub>L</sub>) of 0.05 g L<sup>-1</sup>h<sup>-1</sup>, and a glycerol consumption of 31 and 37.2 g L<sup>-1</sup>, respectively. Regarding the volumetric productivities at the different concentrations, the Q<sub>L</sub> (0.05 g L<sup>-1</sup> h<sup>-1</sup>) and Q<sub>X</sub> (0.11 g L<sup>-1</sup> h<sup>-1</sup>), did not differ statistically from the control

(glucose). Lipid accumulation was higher at 216 h of culture using 100 g L<sup>-1</sup> of glycerol (51 and 57% for commercial and crude, respectively), but a significant decrease of Q<sub>L</sub> (from 0.05 to 0.03 g L<sup>-1</sup> h<sup>-1</sup>) and Q<sub>X</sub> (0.11 to 0.09 g L<sup>-1</sup> h<sup>-1</sup>) was observed. A negative effect on yield, Q<sub>X</sub> and Q<sub>L</sub> was observed at glycerol concentrations above 50 g L<sup>-1</sup>. R4 SCO showed a fatty acid profiles rich in oleic acid and suitable for biodiesel production, and were efficiently transformed into biodiesel with yields above 90% by acid transesterification. Biodiesels derived from R4 using crude glycerol are fully complies with international biodiesel standards. This allows advance in a process of circular economy for biodiesel industry.

- 3 Sineli PE, Maza DD, Aybar MJ, Figueroa LIC and Viñarta SC. 2022. Bioconversion of sugarcane molasses and waste glycerol on single cell oils for biodiesel by the red yeast *Rhodotorula glutinis* R4 from Antarctica. *Energy Conversion and Management X*, 16(1):100331 - <https://doi.org/10.1016/j.ecmx.2022.100331>

In the context of the global energy crisis and the constant demand for biofuels, this work explored the biodiesel production from single-cell oils (SCO) produced by the Antarctic oleaginous yeast *Rhodotorula*

*glutinis* R4 from low-cost local agro-industrial by-products (sugarcane molasses and waste glycerol). The lipid accumulation reached 46.8% and 40.7% at 120 h of culture using glycerol and molasses, respectively, which

correspond to 5.72 and 8.68 g L<sup>-1</sup> of final lipid concentration. *R. glutinis* R4 yielded 0.172 and 0.185 gram of lipids per gram of substrate consumed grown in molasses or glycerol medium, respectively. These amounts being higher than the ones obtained in glucose medium (0.126 g g<sup>-1</sup>). At 120 h of culture, lipid volumetric productivities were 0.048 and 0.072 g L<sup>-1</sup> h<sup>-1</sup> using glycerol and molasses, respectively, and 0.043 g L<sup>-1</sup> h<sup>-1</sup> in the glucose yeast extract (GYM) medium. Oleic acid is the predominant fatty acid in the oils from *R. glutinis* R4, reaching 67.5% with molasses, thus

indicating that it is adequate for biodiesel synthesis. This is the first study where SCO produced by *R. glutinis* R4 were converted into biodiesel by acid transesterification with an efficiency above 90%. The biodiesel produced by *R. glutinis* R4 grown on culture media containing molasses or waste glycerol is fully compliant with the international standards for biodiesel. SCO obtained from *R. glutinis* R4 using molasses and waste-glycerol can be effectively used as sources of triacylglycerols for biodiesel production.

Book chapter.

- 4 Viñarta SC, Angelicola MV, Garolera B, Fernández PM. 2024. Harnessing microbial recycling of organic wastes in a circular waste management system for greenhouse gas reduction (Chapter 14). In: Kumar V, Bhat SA, Kumar S, Verma P (Eds). Environmental Engineering and Waste Management: Recent Trends and Perspectives. Springer Nature Switzerland AG. ISBN: 978-3-031-58440-4 - [https://doi.org/10.1007/978-3-031-58441-1\\_14](https://doi.org/10.1007/978-3-031-58441-1_14)

The circular waste management system and the reduction of greenhouse gas emissions are critical aspects for achieving environmental sustainability goals and mitigating environmental challenges. Microbial recycling of organic wastes represents a promising approach to address these challenges. Microorganisms play a vital role in the recycling process by decomposing and transforming organic materials, offering a sustainable perspective for waste management. This chapter provides an overview of the microbial recycling of organic wastes in achieving a circular waste management system and reducing greenhouse gas emissions. It explores the role of microorganisms in the decomposition and transformation of organic wastes, with a focus on their ability to convert waste materials into valuable resources. The chapter also discusses the

different types of organic wastes involved and the microbial processes employed in the recycling process. Moreover, it delves into the opportunities, challenges, and future perspectives in this field, drawing upon recent scientific research. The chapter emphasizes the environmental benefits associated with microbial recycling, including the mitigation of greenhouse gas emissions, nutrient cycling, and resource recovery. Understanding the significance of microorganisms in organic waste recycling can pave the way for sustainable development practices, contributing to a cleaner and healthier environment. By harnessing the potential of microorganisms, we can advance towards a more efficient circular waste management system and achieve substantial reductions in greenhouse gas emissions.

Doctoral thesis.

- 5 Cruz, Elías Leonardo. 2023. Supervisor: PM Fernandez. Co-Supervisor: HF Pajot, National University of Tucumán, Argentina. Study of cultivation systems for the removal of Cr(VI) using yeast isolates from contaminated and uncontaminated environments.

Environmental pollution is one of the major challenges humanity currently faces due to technological advancements and population growth. Specifically, Cr(VI) contamination is a global problem. Among the remediation strategies used to address this issue, bioremediation with microorganisms, including yeasts, is notable due to their unique metabolic characteristics. This study focuses on the biotechnological processes using yeasts isolated from both contaminated and pristine environments for the removal of hexavalent chromium (Cr(VI)) from industrial effluents. Initially, the tolerance of seven Antarctic yeast isolates was

studied, from which two were selected based on their tolerance and removal capacity at 52 µg/mL of Cr(VI). The most suitable medium for their growth was also identified and compared with strains from contaminated environments. The removal mechanism was studied using Atomic Absorption Spectroscopy and Electron Microscopy, with results indicating that the predominant mechanism is the reduction of Cr(VI) to Cr(III). The interaction of the four strains under study was evaluated to create mixed cultures, revealing no negative interactions among them. However, the removal efficiency of all evaluated combinations was not superior

to that of *Wickerhamomyces anomalus* M10 in pure culture. Therefore, this strain was selected for scaling up in an instrumented bioreactor. Various conditions in a batch system were studied to optimize the reduction of 1 mM of the metal, modifying pH and aeration/agitation levels using the medium previously optimized for the M10 strain. The results indicated complete Cr(VI) reduction within 20 hours when oxygen control was set at 40% and pH at 5.5. Under these conditions, the yeast achieved a 90% reduction of the metal following an additional pulse of Cr(VI). Additionally, a continuous system was proposed, which effectively achieved complete reduction of 25 µg/mL of Cr(VI). As an additional strategy, yeast immobilization was pursued. Various supports were studied, with calcium alginate showing the highest efficiency due to its consistent integrity throughout the process, good cell retention, and observed reduction levels. Different ratios between the medium volume and the volume occupied by the beads (Vp/Vm) were evaluated, demonstrating that Cr(VI) was reduced by 92.36% within 24 hours at Vp/Vm=1, while similar values were achieved in 48 hours at a lower ratio

(0.5). The immobilization process was scaled up in a 3L Airlift reactor under the batch conditions that were most favorable and at Vp/Vm=0.5.

In parallel, an effluent from the decorative chrome plating industry was characterized, with a Cr(VI) concentration (87.2 µg/mL) slightly exceeding that studied in previous tests, and was completely removed within 28 hours. The biologically treated effluent in batch was used for Cr(III) adsorption studies with three types of clays, with Montmorillonite at 5 g/L being able to adsorb 73.65% of the residual metal in its trivalent form. Finally, to assess the toxicity of the biologically and clay-treated effluent, germination bioassays with *Lactuca sativa* were conducted, showing a marked reduction in toxicity in the effluent subjected to both treatments.

The results obtained thus far successfully demonstrate that various technologies can be applied for effluent treatment and serve as a starting point for the construction of an integrated system with potential biotechnological transfer.

Conference.

- 6 Viñarta SC. 2023. Microbial lipids for biodiesel production: biotechnological potential, role of oleaginous yeasts, challenges, and opportunities. Conference at the Biotechnology and Bioprocesses Symposium, XVIII Argentine Congress of General Microbiology (SAMIGE 2023). Organized by the Argentine Society for General Microbiology, SAMIGE. Chapadmalal, Buenos Aires, Argentina, October 4, 2023.

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Communicated by M.A. Lachance <[lachance@uwo.ca](mailto:lachance@uwo.ca)>.**

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Recent publications.

- 1 Rosa CA, Santos ARO, Palmier K, Duell M, Carvalho AOS, Fernandez NV, Pimenta RS, Morais PB, Araya M, Cubillos FA, Pontes A, Aires A, Gonçalves C, Gonçalves P, Sampaio JP, Lachance MA. 2024. Taxogenomic analyses of *Starmerella gilliamiae* f.a. sp. nov. and *Starmerella monicapupuae* f.a., sp. nov., two novel species isolated from plant substrates and insects. *Int J Syst Evol Microbiol* 74(2):006270.

Four yeast isolates collected from flowers from different ecosystems in Brazil, one from fruit of *Nothofagus alpina* in Argentina, three from flowers of *Neltuma chilensis* in Chile and one obtained from the proventriculus of a female bumblebee in Canada were demonstrated, by analysis of the sequences of the internal transcribed spacer (ITS) region and D1/D2 domains of the large subunit rRNA gene, to represent two novel species of the genus *Starmerella*. These species are described here as *Starmerella gilliamiae* f.a. sp. nov. (CBS 16166<sup>T</sup>; Mycobank MB 851206) and *Starmerella monicapupuae* f.a., sp. nov. (PYCC 8997<sup>T</sup>; Mycobank

MB 851207). The results of a phylogenomic analysis using 1037 single-copy orthogroups indicated that *S. gilliamiae* is a member of a subclade that contains *Starmerella opuntiae*, *Starmerella aceti* and *Starmerella apicola*. The results also indicated that *S. monicapupuae* is phylogenetically related to *Starmerella riodocensis*. The two isolates of *S. monicapupuae* were obtained from flowers in Brazil and were probably vectored by insects that visit these substrates. *Starmerella gilliamiae* has a wide geographical distribution having been isolated in flowers from Brazil and Chile, fruit from Argentina and a bumblebee from Canada.

- 2 Garcia-Acero AM, Morais CG, Souza GFL, Santos ARO, Lachance MA, Velásquez-Lozano ME, Rosa CA. 2024. *Ogataea nonmethanolica* f.a, sp. nov., a novel yeast species isolated from rotting wood in Brazil and Colombia. *Int J Syst Evol Microbiol* 74(2) - doi: 10.1099/ijsem.0.006273.

Three yeast isolate candidates for a novel species were obtained from rotting wood samples collected in Brazil and Colombia. The Brazilian isolate differs from the Colombian isolates by one nucleotide substitution in each of the D1/D2 and small subunit (SSU) sequences. The internal transcribed spacer (ITS) and translation elongation factor 1- $\alpha$  gene sequences of the three isolates were identical. A phylogenetic analysis showed that this novel species belongs to the genus *Ogataea*. This novel species is phylogenetically related to *Candida nanaspora* and *Candida nitratophila*. The novel species differs from *C. nanaspora* by seven nucleotides and two

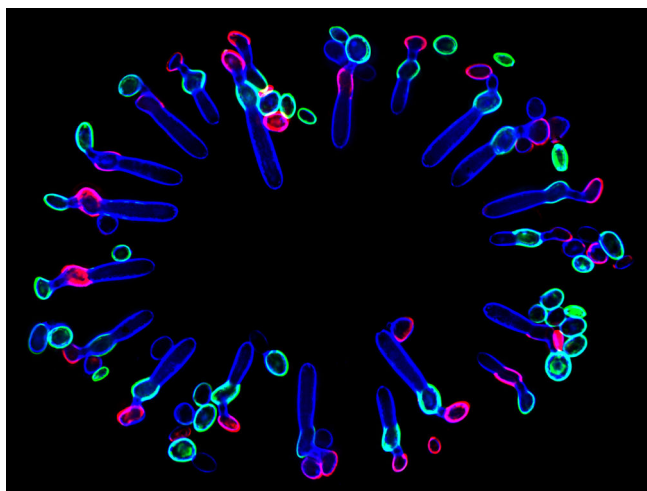
indels, and by 17 nucleotides and four indels from *C. nitratophila* in the D1/D2 sequences. The ITS sequences of these three species differ by more than 30 nucleotides. Analyses of the sequences of the SSU and translation elongation factor 1- $\alpha$  gene also showed that these isolates represent a novel species of the genus *Ogataea*. Different from most *Ogataea* species, these isolates did not assimilate methanol as the sole carbon source. The name *Ogataea nonmethanolica* sp. nov. is proposed to accommodate these isolates. The holotype of *Ogataea nonmethanolica* is CBS 13485<sup>T</sup>. The MycoBank number is MB 851195.

- 3 Barros KO, Batista TM, Soares RCC, Lopes MR, Alvarenga FBM, Souza GFL, Abegg MA, Santos ARO, Hilário HO, Moreira RG, Franco GR, Lachance MA, Rosa CA. 2024. *Spathaspora marinasilvae* sp. nov., a xylose-fermenting yeast isolated from galleries of passalid beetles and rotting wood in the Amazonian rainforest biome. *Yeast* (in press).

Four yeast isolates were obtained from rotting wood and galleries of passalid beetles collected in different sites of the Brazilian Amazonian Rainforest in Brazil. This yeast produces unconjugated allantoid asci each with a single elongated ascospore with curved ends. Sequence analysis of the ITS-5.8S region and the D1/D2 domains of the large subunit rRNA gene showed that the isolates represent a novel species of the genus *Spathaspora*. The novel species is phylogenetically related to a subclade containing *Sp. arborariae* and *Sp. suhii*. Phylogenomic analysis based on 1,884 single-copy

orthologs for a set of *Spathaspora* species whose whole genome sequences are available confirmed that the novel species represented by strain UFMG-CM-Y285 is phylogenetically close to *Sp. arborariae*. The name *Spathaspora marinasilvae* sp. nov. is proposed to accommodate the novel species. The holotype of *Spathaspora marinasilvae* is CBS 13467<sup>T</sup>. The novel species was able to accumulate xylitol and produce ethanol from D-xylose, a trait of biotechnological interest common to several species of the genus *Spathaspora*.

- 4 Lachance MA, Burke C, Nygard K, Courchesne M, Timoshenko AV. 2024. Yeast sexes: mating types do not determine the sexes in *Metschnikowia* species. *FEMS Yeast Research* 24:foae014.



Although filamentous Ascomycetes may produce structures that are interpreted as male and female gametangia, ascomycetous yeasts are generally not considered to possess male and female sexes. In haplontic yeasts of the genus *Metschnikowia*, the sexual cycle begins with the fusion of two morphologically identical cells of complementary mating types. Soon after conjugation, a protuberance emerges from one of the conjugants, eventually maturing into an ascus. The originating cell can be regarded as an ascus mother cell, hence as female. We tested the hypothesis that the sexes, female or male, are determined by the mating types. There were good reasons to hypothesize further that mating type  $\alpha$  cells are male. In a conceptually simple experiment, we observed the early stages of the mating reaction of mating types differentially labeled with



fluorescent concanavalin A conjugates. Three large-spored *Metschnikowia* species, *M. amazonensis*, *M. continentalis*, and *M. matae*, were examined. In all

three, the sexes were found to be independent of mating type, cautioning that the two terms should not be used interchangeably.

- 5 Lachance MA. 2024. Entry 23. *Kluyveromyces* Van der Walt, Antonie van Leeuwenhoek 22: 271. 1956. In: CS Bhunjun et al. What are the 100 most cited fungal genera? *Studies in Mycology* 108, 409 pp. (In press).
- 6 Lachance MA. 2024. Entry 47. *Metschnikowia* T. Kamiński, Trudy Obshch. Estestvoisp. 30: 364. 1900. In: CS Bhunjun et al. What are the 100 most cited fungal genera? *Studies in Mycology* 108, 409 pp. (In press).

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## Forthcoming Meetings

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### International Mycological Congress (IMC12) Maastricht, Netherlands, 11-15 August 2024

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On behalf of all Dutch mycologists, we are delighted and very honoured to host the 12th edition of the International Mycological Congress (IMC12), one of the most prestigious international mycological meetings. The congress will be held in the city of Maastricht, Netherlands, from 11-15 August 2024.

This World Congress represents a unique opportunity for mycologists from around the world to get together and enjoy excellent science in one of Europe's most impressive cities. We hope you will

join us in creating an inspiring and diverse scientific programme.

This four-day meeting will include keynote lectures by scientific leaders, bridging sessions and workshops in seven themes: Cell biology, biochemistry and physiology; Environment, ecology and interactions; Evolution, biodiversity and systematics; Fungal pathogenesis and disease control; Genomics, genetics and molecular biology; Applied Mycology and Nomenclature.

For additional information: <https://imc12.org/>

Wieland Meyer, President of the International Mycological Association  
Pedro Crous, Chair of IMC12

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### 16<sup>th</sup> International Congress on Yeasts Cape Town, South Africa, September 29<sup>th</sup> to October 3<sup>rd</sup> 2024

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The 16th International Congress on Yeasts is the premier gathering of local and international academic and researchers, industry scientists and students working in the field of yeast biodiversity and biotechnology. It is intended to share the latest developments in fundamental yeast research linked to biotechnological applications as well as to enable more interaction between African and international partners.



Join us at the Cape Town International Convention Centre in South Africa, from 29 September to 03 October 2024 for this groundbreaking in-person event, where the contribution of yeast science and technology will be of great value to the continent, region, the local industry, academic scholars, innovators as well as the Southern African

industry sectors of food and beverage, health and medicine, energy and environment.

The program is available [here](#). See also the conference website: [www.icy2024.com](http://www.icy2024.com).

The congress will be managed by Eastern Sun Events <[yeasts@easternsun.co.za](mailto:yeasts@easternsun.co.za)>.



The 18th Congress of the International Union of Microbiological Societies (IUMS) will be held in Florence (Italy) on October 23-25, 2024. The meeting, which will take place in one of the most beautiful cities of the world, will be a unique opportunity to bring together scientists working on Bacteriology, Virology, and Mycology worldwide, to share and discuss the most recent advances and future perspectives in microbiology.

The topics that will be discussed include microbial genetics, molecular biology, gene

regulation, proteomics, and the applied aspects of microbiology, including biotechnology, clinical, medical, industrial, and environmental applications.

In addition, the 2024 IUMS meeting will be an opportunity to increase awareness of the importance of microbes for the society and for the planet by discussing how we can actively work together to promote sustainable solutions to preserve microbial diversity and maximize global well-being. Special attention will be provided to facilitate the participation of young people.

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### **International Workshop on Brewing Yeasts 16-17<sup>th</sup> of November 2024 in Bariloche, Patagonia, Argentina**

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The International Workshop on Brewing Yeasts is planned for 16-17<sup>th</sup> of November 2024 in Bariloche, Patagonia, Argentina. Stay tuned for news! Check the latest update at <https://iwoby.com.ar>



**International Workshop on  
Brewing Yeasts**  
16 - 17th November 2024  
Bariloche, PATAGONIA, ARGENTINA

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**Brief News Items**

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**Postdoctoral Position(s) Available  
in Yeast Evolutionary Genomics and/or Synthetic Biology**

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Please send a CV, p/reprints, and contact information for 2 references to [cthittinger@wisc.edu](mailto:cthittinger@wisc.edu). Specifically mention why you are interested in this training position in your email. Apply by 30<sup>th</sup> June 2024 for full consideration, but strong applications may be considered sooner.

C.T. Hittinger

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**Yeast Art, Agar, and a Forgotten Woman**

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This image of Fanny Angelina Hesse is an example of *Yeast Art*, executed by Alexandra Wudzinska and Jeff Boeke at NYU Langone upon my suggestion. More *Yeast Art* can be seen at <https://www.yeastart.org/art>. Hesse (1850-1934) is responsible for bringing agar to the attention of the early microbiological community. Without her, yeast research would be very different.

With a fantastic team of creatives, science communicators, science comic illustrators, and bioartists we are currently developing a graphic novel about her and this story, and we will go public with a kickstarter campaign soon. I'd be very happy to provide a link and more information if there is interest. We to elicit some support from YNL readers and the yeast community at large. For additional information, feel free to contact me.

Corrado Nai

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## Fifty Years Ago

Y E A S T

A News Letter for Persons Interested in Yeast

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

June 1974

Volume XXIII, Number 1

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Microbiology Research Group of the South African Council for Scientific and Industrial Research. P. O. Box 395, Pretoria, South Africa.  
Communicated by J. P. van der Walt.

The yeast genus Wickerhamiella gen. nov. (Ascomycetes). J. P. van der Walt and N. v.d. W. Liebenberg; Antonie van Leeuwenhoek, Vol. 39 (1973), pp. 121-128.

The perfect state of Torulopsis magnoliae. J. P. van der Walt and Elzbieta Johannsen; Antonie van Leeuwenhoek, Vol. 39 (1973), pp. 635-647.

The dangeardien and its significance in the taxonomy of the ascomycetous yeasts. J. P. van der Walt and Elzbieta Johannsen; Antonie van Leeuwenhoek, Vol. 40 (1974), pp. 185-192.

Dr. Marie-Claire Pignal from the Département Biologie Végétale of The Université Claude Bernard in Lyons spent four weeks in our laboratories. Apart from looking at yeasts, Mile Pignal also had the opportunity of observing the wild-life of the Kruger National Park.

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

Lysis of Yeast Cell Walls: Glucanases from Bacillus circulans WL-12

Graham H. Fleet and Herman J. Phaff

Journal of Bacteriology, in press (July issue 1974)

Demonstration of a Fibrillar Component

In the Cell Wall of the Yeast

Saccharomyces cerevisiae and its chemical nature

Marie Kopecká (Department of General Biology, Faculty of Medicine, J. E. Purkyne, University Brno, Czechoslovakia), H. J. Phaff, and G. H. Fleet.

The Jour. Cell Biology. In press (July issue 1974)

Cryptococcus cereanus a new species of the genus Cryptococcus

H. J. Phaff, M. W. Miller and Mary Miranda

W. B. Heed, and W. T. Starmer

Submitted to: Intern. Jour. Svst. Bacteriol.

Karl-Marx University, Klinik für Hautkrankheiten, Liebigstr. 21. 701 Leipzig, DDR. Communicated by Christina Schönborn.

We have determined the sodium chloride tolerance of about 200 freshly isolated yeast strains from the human microflora. The salt concentration in the nutrient medium (glucose-peptone-agar) was the limiting factor for growth in this medium, and the various species showed different sensitivities to increasing NaCl concentrations. Growth-limiting NaCl values below 8% were observed for strains of Candida krusei, Candida pseudotropicalis, and Cryptococcus neoformans. A maximal tolerance for NaCl (14.8%) was observed for Candida parapsilosis and C. guilliermondii. Average values are given in the following table:

Species	Number of Strains	Limiting NaCl concentrations for growth
<u>Cryptococcus neoformans</u>	2	5.4
<u>Candida krusei</u>	16	8.4
<u>Candida pseudotropicalis</u>	16	8.8
<u>Candida humicola</u>	9	9.7
<u>Trichosporon cutaneum</u>	17	10.1
<u>Rhodotorula mucilaginosa</u>	12	10.3
<u>Torulopsis glabrata</u>	9	10.8
<u>Candida albicans</u>	20	10.9
<u>Candida tropicalis</u>	20	11.7
<u>Candida lipolytica</u>	12	11.9
<u>Candida guilliermondii</u>	20	13.7
<u>Candida parapsilosis</u>	20	14.2

National Research Council Canada. Division of Biological Sciences  
Ottawa, Canada K1A 0R6. Communicated by Byron Johnson.

CELL DIVISION IN YEASTS. II. TEMPLATE CONTROL OF CELL  
PLATE BIOGENESIS IN *SCHIZOSACCHAROMYCES POMBE*

Byron F. Johnson Bong Y. Yoo G. C. Calleja

On the Nature of the Forces Involved in the Sex-directed  
Flocculation of a Fission Yeast

G. B. Calleja

In Press: Can. J. Microbiol.

National Institutes of Health, National Institute of Arthritis,  
Metabolism, and Digestive Diseases, Building 4, Room 116, Bethesda,  
Maryland 20014. Communicated by Reed Wickner.

Chromosomal and Nonchromosomal Mutations Affecting the "Killer  
Character" of *Saccharomyces cerevisiae*.

Genetics, March 1974.

Institut für Physiologische Chemie der Ruhr-Universität Bochum.  
Communicated by W. Duntze.

Purification and Partial Characterization  
of  $\alpha$ -Factor, a Mating-Type Specific Inhibitor  
of Cell Reproduction from *Saccharomyces cerevisiae*

Wolfgang Duntze, Dieter Stötzler, Elizabeth Bücking-Throm, and Sigrid  
Kalbitzer

Cells of *Saccharomyces cerevisiae* exhibiting the  $\alpha$  mating type excrete into the culture medium a low-molecular-weight substance, termed  $\alpha$  factor. This factor, which specifically inhibits DNA replication in cells of the opposite mating type  $a$ , has been purified more than 100,000-fold from culture filtrates of  $\alpha$  cells. Purified  $\alpha$  factor appears to be homogeneous as judged from thin-layer chromatography and thin-layer electrophoresis in different systems. It shows a positive ninhydrin reaction and, upon hydrolysis, gives rise to several ninhydrin-positive substances of which the amino acids leucine, glycine, proline, glutamic acid, tyrosine, tryptophan and possibly histidine have been identified. The presence of tryptophan and tyrosine is also confirmed by the ultraviolet absorption spectrum of the factor. In addition, purified  $\alpha$  factor contains cupric ions which can be separated from the ninhydrin-positive material by thin-layer electrophoresis at pH 3.6. Gel filtration on Sephadex G-25 in 8 M urea indicates a molecular weight in the range of 1400. The properties of the purified  $\alpha$  factor are consistent with those of a low-molecular-weight peptide.

National Research Council Canada. Division of Biological Sciences  
Ottawa, Canada K1A 0R6. Communicated by Byron Johnson.

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In Press: Can. J. Microbiol.

University of Rochester, School of Medicine, Rochester, N.Y. 14642.  
Communicated by Fred Sherman.

Excerpt from: F. Sherman and C. W. Lawrence, *Saccharomyces*  
In "Handbook of Genetics" vol. 1, edited by R. C. King, Plenum  
Pub. Corp. in press.

GENETIC NOMENCLATURE

A recommendation for the nomenclature used in yeast genetics  
was published as the November 1969 supplement to the Microbial  
Genetics Bulletin, and except for the persistence of a few of  
the older notations, these proposals are usually followed. For  
the sake of clarity and convenience, a few minor changes appear  
appropriate and these are included in the following rules of  
nomenclature which have been expanded and updated:

1. The two mating type alleles are designated, respectively  
by  $\underline{a}$  and  $\alpha$ . (In the old system, the italicized  $\underline{a}$ , in contrast  
to the bold face  $\underline{a}$ , was sometimes difficult to differentiate  
from  $\alpha$ .)

Fimbriae, fusion and flocculation in yeasts. A. W. Day and N. H. Poon,  
Department of Plant Sciences, University of Western Ontario, London,  
Canada.

We have recently discovered that the cells of several species of  
yeasts and yeast-like fungi produce large numbers of fine hairs on  
the cell wall. These hairs have been termed fimbriae, because of their  
close developmental & morphological similarity to bacterial fimbriae  
(or pili).