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C.T. Hittinger, Madison, Wisconsin, USA 2
J.P. Tamang, Gangtok, India. 6
D. Peris, Valencia, Spain 6
P. Buzzini, Perugia, Italy. 7
J. Carvajal Barriga, Quito, Ecuador 11
S. Nasr, Tehran, Iran 11
E.S. Naumova, Moscow, Russia. 12
S. Limtong & P. Kunnamwong, Bangkok, Thailand 13
A. Yurkov, Braunschweig, Germany 16
M.A. Lachance, London, Ontario, Canada 18
Obituary: Jovita Martínez Cruz 20
Forthcoming Meetings 22
Brief News Item 24
Fifty Years Ago. 25

Editorials

Jovita Martínez Cruz (1944-2019)

We were saddened to learn of the death of Profesora Jovita Martínez Cruz. Jovita was known in the community of yeast systematists and bioengineers for her contributions of the Microbial Collection of the Center for Research and Advanced Studies of the National Polytechnic Institute (CINVESTAV), in México City. Among other accomplishments was the organization of international courses on the taxonomy, conservation, and genetics of yeasts and their application to biotechnology. I had the privilege of attending the third course, held in Cuernavaca, México, of which I have fond memories. I thank Juan Carlos Estrada Mora for providing an obituary.

Email problems

Once again (see June 2017 issue) we have experienced difficulties in sending out the request for information due to idiosyncrasies of our email server. This only came to my attention on the day of the deadline, which was then extended by two weeks. I will do my utmost to avoid this kind of problem in the future. Thanks to all readers that have sent material on a shorter notice.

M.A. Lachance, Editor

I Lodz University of Technology, Faculty of Biotechnology and Food Sciences, Institute of Fermentation Technology and Microbiology, Wolczanska 171/173, 90-924 Lodz, Poland. Communicated by PhD, DSc Dorota Kregiel <dorota.kregiel@p.lodz.pl>.

The following papers have been published in 2019.

1 Pawlikowska E, Domanski J, Dziugan P, Berlowska J, Cieciura-Wloch W, Smigielski K, Kregiel D. 2019. Comparison of three deoxidation agents for ozonated broths used in anaerobic biotechnological processes. Processes 7,65.

Anaerobic fermentation of organic compounds is used in many biotechnological processes and has been the subject of much research. A variety of process conditions and different growth media can be used to obtain microbial metabolites. The media must be free from contamination before fermentation. Sterilization is most often achieved by applying heat or other treatments, such as ozonation. Sterilization of liquid media using ozone can be very beneficial, but this method introduces high concentrations of residual oxygen, which inhibit anaerobic processes. Deoxidation is therefore necessary to remove the oxygen from ozonated broths. This study evaluates the effectiveness of three deoxidation agents for two kinds of fermentation media based on malt or molasses: ultrasound, iron(II) sulfate, and *Metschnikowia* sp. yeast. The time needed for deoxidation varied, depending on the kind of broth and the deoxidation agent. In general, the dynamics of oxygen removal were faster in malt broth. A comparative analysis showed that yeast biomass was the most effective agent, achieving deoxidation in the shortest time. Moreover, the fully deoxidated broth was supplemented with yeast biomass, which is rich in biogenic substrates, expressed as a protein content of 0.13-0.73 g/L. Application of *Metschnikowia* sp. may therefore be considered as an effective strategy for simultaneous deoxidation and nutrient supplementation of broths used in anaerobic biotechnological processes.

2 Pawlikowska E, James SA, Breierova E, Antolak H, Kregiel D. Biocontrol capability of local *Metschnikowia* sp. isolates. Antonie van Leeuwenhoek. DOI: 10.1007/s10482-019-01272-w (in press).

This study set out to isolate and identify epiphytic yeasts producing pulcherrimin, and to evaluate their potential as biological control agents (BCAs). We isolated *Metschnikowia* sp. strains from flowers and fruits collected in Poland. The plant material had been collected between April to September 2017 from two small orchards where traditional organic management is employed. We identified the essential phenotypic features of the yeast, including assimilation and enzymatic profiles, stress resistance, adhesion properties, and antimicrobial activity against various fungi involved in crop and/or food spoilage. Yeast screening was performed using YPD agar supplemented with chloramphenicol and Fe(III) ions. Taxonomic classification was determined by sequence analysis of the D1/D2 domains of the large subunit rRNA gene. The isolates were identified as *Metschnikowia andauensis* and *M. sinensis*. The yeast isolates were further characterized based on their enzymatic and assimilation profiles, as well as their growth under various stress conditions. In addition, the hydrophobicity and adhesive abilities of the Metschnikowia isolates were determined using a MATH test and luminometry. Their antagonistic action against molds representing typical crop spoiling microflora was also evaluated. The assimilation profiles of the wild isolates were similar to those displayed by collection strains of *M. pulcherrima*. However, some of the isolates displayed more beneficial phenotypic properties, especially good growth under stress conditions. Several of the epiphytes grew well over a wider range of temperatures (8–30°C) and pH levels (3–9), and additionally showed elevated tolerance to ethanol (8%), glucose (30%), and peroxides (50 mM). The hydrophobicity and adhesion of the yeast cells were strain- and surface-dependent. The tested yeasts showed potential for use as BCAs, with some exhibiting strong antagonism against molds belonging to the genera *Alternaria, Botrytis, Fusarium, Rhizopus,* and *Verticillium*, as well as against yeasts isolated as food spoilage microbiota.

II Laboratory of Genetics, Genome Center of Wisconsin, DOE Great Lakes Bioenergy Research Center, Wisconsin Energy Institute, J. F. Crow Institute for the Study of Evolution, University of Wisconsin, Madison, WI 53706, USA. Communicated by Chris Todd Hittinger <cthittinger@wisc.edu>.

Recent publications.

1 Shen XX, Opulente DA, Kominek J, Zhou X, Steenwyk JL, Buh KV, Haase MAB, Wisecaver JH, Wang M, Doering DT, Boudouris JT, Schneider RM, Langdon QK, Ohkuma M, Endoh R, Takashima M, Manabe RI, Čadež N, Libkind D, Rosa CA, DeVirgilio J, Hulfachor AB, Groenewald M, Kurtzman CP, Hittinger CT, Rokas A. 2018. Tempo and mode of genome evolution in the budding yeast subphylum. Cell 175:1533-1545. https://doi.org/10.1016/j.cell.2018.10.023

Budding yeasts (subphylum Saccharomycotina) are found in every biome and are as genetically diverse as plants or animals. To understand budding yeast evolution, we analyzed the genomes of 332 yeast species, including 220 newly sequenced ones, which represent nearly one third of all known budding yeast diversity. Here, we establish a robust genus-level phylogeny comprising 12 major clades, infer the timescale of diversification from the Devonian period to the present, quantify horizontal gene transfer (HGT), and reconstruct the evolution of 45 metabolic traits and the metabolic toolkit of the budding yeast common ancestor (BYCA). We infer that BYCA was metabolically complex and chronicle the tempo and mode of genomic and phenotypic evolution across the subphylum, which is characterized by very low HGT levels and widespread losses of traits and the genes that control them. More generally, our results argue that reductive evolution is a major mode of evolutionary diversification.

2 Čadež N, Bellora N, Ulloa R, Hittinger CT, Libkind D. 2019. Genomic content of a novel yeast species *Hanseniaspora gamundiae* sp. nov. from fungal stromata (*Cyttaria*) associated with a unique fermented beverage in Andean Patagonia, Argentina. PLoS One 14: e0210792. https://doi.org/10.1371/journal.pone.0210792

A novel yeast species was isolated from the sugar-rich stromata of *Cyttaria hariotii* collected from two different *Nothofagus* tree species in the Andean forests of Patagonia, Argentina. Phylogenetic analyses of the concatenated sequence of the rRNA gene sequences and the protein-coding genes for actin and translational elongation factor-1α indicated that the novel species belongs to the genus *Hanseniaspora*. De novo genome assembly of the strain CRUB 1928T yielded a 10.2-Mbp genome assembly predicted to encode 4452 protein-coding genes. The genome sequence data were compared to the genomes of other *Hanseniaspora* species using three different methods, an alignment-free distance measure, Kr, and two model-based estimations of DNA-DNA homology values, of which all provided indicative values to delineate species of *Hanseniaspora*. Given its potential role in a rare indigenous alcoholic beverage in which yeasts ferment sugars extracted from the stromata of *Cytarria* sp., we searched for the genes that may suggest adaptation of novel *Hanseniaspora* species to fermenting communities. The *SSU1*-like gene encoding a sulfite efflux pump, which, among *Hanseniaspora*, is present only in close relatives to the new species, was detected and analyzed, suggesting that this gene might be one factor that characterizes this novel species. We also discuss several candidate genes that likely underlie the physiological traits used for traditional taxonomic identification. Based on these results, a novel yeast species with the name *Hanseniaspora gamundiae* sp. nov. is proposed with CRUB 1928^T (ex-types: ZIM 2545^T = NRRL Y-63793^T = PYCC 7262^T; MycoBank number MB 824091) as the type strain. Furthermore, we propose the transfer of the *Kloeckera* species, *K. hatyaiensis*, *K. lindneri* and *K. taiwanica* to the genus *Hanseniaspora* as *Hanseniaspora hatyaiensis* comb. nov. (MB 828569), *Hanseniaspora lindneri* comb. nov. (MB 828566) and *Hanseniaspora taiwanica* comb. nov. (MB 828567).

3 Li XC, Peris D, Hittinger CT, Sia EA, Fay JC. Mitochondria-encoded genes contribute to evolution of heat and cold tolerance in yeast. Sci Adv 5: eaav1848. https://doi.org/10.1126/sciadv.aav1848

Genetic analysis of phenotypic differences between species is typically limited to interfertile species. Here, we conducted a genome-wide noncomplementation screen to identify genes that contribute to a major difference in thermal growth profile between two reproductively isolated yeast species, *Saccharomyces cerevisiae* and *Saccharomyces uvarum*. The screen identified only a single nuclear-encoded gene with a moderate effect on heat tolerance, but, in contrast, revealed a large effect of mitochondrial DNA (mitotype) on both heat and cold tolerance. Recombinant mitotypes indicate that multiple genes contribute to thermal divergence, and we show that protein divergence in *COX1* affects both heat and cold tolerance. Our results point to the yeast mitochondrial genome as an evolutionary hotspot for thermal divergence.

4 Baker EP, Peris D, Moriarty RV, Li XC, Fay JC, Hittinger CT. Mitochondrial DNA and temperature tolerance in lager yeasts. Sci Adv 5: eaav1869. https://doi.org/10.1126/sciadv.aav1869

A growing body of research suggests that the mitochondrial genome (mtDNA) is important for temperature adaptation. In the yeast genus *Saccharomyces*, species have diverged in temperature tolerance, driving their use in high- or low-temperature fermentations. Here, we experimentally test the role of mtDNA in temperature tolerance in synthetic and industrial hybrids (*Saccharomyces cerevisiae* × *Saccharomyces eubayanus* or *Saccharomyces pastorianus*), which cold-brew lager beer. We find that the relative temperature tolerances of hybrids correspond to the parent donating mtDNA, allowing us to modulate lager strain temperature preferences. The strong influence of mitotype on the temperature tolerance of otherwise identical hybrid strains provides support for the mitochondrial climactic adaptation hypothesis in yeasts and demonstrates how mitotype has influenced the world's most commonly fermented beverage.

5 Kominek J, Doering DT, Opulente DA, Shen XX, Zhou X, DeVirgilio J, Hulfachor AB, Groenewald M, Mcgee MA, Karlen SD, Kurtzman CP, Rokas A, Hittinger CT. 2019. Eukaryotic acquisition of a bacterial operon. Cell 176:1356-1366. https://doi.org/10.1016/j.cell.2019.01.034

Operons are a hallmark of bacterial genomes, where they allow concerted expression of functionally related genes as single polycistronic transcripts. They are rare in eukaryotes, where each gene usually drives expression of its own independent messenger RNAs. Here, we report the horizontal operon transfer of a siderophore biosynthesis pathway from relatives of *Escherichia coli* into a group of budding yeast taxa. We further show that the co-linearly arranged secondary metabolism genes are expressed, exhibit eukaryotic transcriptional features, and enable the sequestration and uptake of iron. After transfer, several genetic changes occurred during subsequent evolution, including the gain of new transcription start sites that were sometimes within protein-coding sequences, acquisition of polyadenylation sites, structural rearrangements, and integration of eukaryotic genes into the cluster. We conclude that the genes were likely acquired as a unit, modified for eukaryotic gene expression, and maintained by selection to adapt to the highly competitive, iron-limited environment.

6 Baker EP, Hittinger CT. 2019. Evolution of a novel chimeric maltotriose transporter in *Saccharomyces eubayanus* from parent proteins unable to perform this function. PLoS Genet 15: e1007786. https://doi.org/10.1371/journal.pgen.1007786

At the molecular level, the evolution of new traits can be broadly divided between changes in gene expression and changes in protein-coding sequence. For proteins, the evolution of novel functions is generally thought to proceed through sequential point mutations or recombination of whole functional units. In *Saccharomyces*, the uptake of the sugar maltotriose into the cell is the primary limiting factor in its utilization, but maltotriose transporters are relatively rare, except in brewing strains. No known wild strains of *Saccharomyces eubayanus*, the cold-tolerant parent of hybrid lager-brewing yeasts (*Saccharomyces cerevisiae x S. eubayanus*), are able to consume maltotriose, which limits their ability to fully ferment

malt extract. In one strain of *S. eubayanus*, we found a gene closely related to a known maltotriose transporter and were able to confer maltotriose consumption by overexpressing this gene or by passaging the strain on maltose. Even so, most wild strains of *S. eubayanus* lack native maltotriose transporters. To determine how this rare trait could evolve in naive genetic backgrounds, we performed an adaptive evolution experiment for maltotriose consumption, which yielded a single strain of *S. eubayanus* able to grow on maltotriose. We mapped the causative locus to a gene encoding a novel chimeric transporter that was formed by an ectopic recombination event between two genes encoding transporters that are unable to import maltotriose. In contrast to classic models of the evolution of novel protein functions, the recombination breakpoints occurred within a single functional domain. Thus, the ability of the new protein to carry maltotriose was likely acquired through epistatic interactions between independently evolved substitutions. By acquiring multiple mutations at once, the transporter rapidly gained a novel function, while bypassing potentially deleterious intermediate steps. This study provides an illuminating example of how recombination between paralogs can establish novel interactions among substitutions to create adaptive functions.

7 Opulente DA, Langdon QK, Buh KV, Haase MAB, Sylvester K, Moriarty RV, Jarzyna M, Considine SL, Schneider RM, Hittinger CT. 2019. Pathogenic yeasts isolated outside of clinical settings. FEMS Yeast Res 19: foz032. https://doi.org/10.1093/femsyr/foz032

Budding yeasts are distributed across a wide range of habitats, including as human commensals. However, under some conditions, these commensals can cause superficial, invasive, and even lethal infections. Despite their importance to human health, little is known about the ecology of these opportunistic pathogens, aside from their associations with mammals and clinical environments. During a survey of approximately 1000 non-clinical samples across the United States of America, we isolated 54 strains of budding yeast species considered opportunistic pathogens, including *Candida albicans* and *Candida (Nakaseomyces) glabrata*. We found that, as a group, pathogenic yeasts were positively associated with fruits and soil environments, whereas the species *Pichia kudriavzevii* (syn. *Candida krusei* syn. *Issatchenkia* orientalis) had a significant association with plants. Of the four species that cause 95% of candidiasis, we found a positive association with soil. These results suggest that pathogenic yeast ecology is more complex and diverse than is currently appreciated and raises the possibility that these additional environments could be a point of contact for human infections.

8 Steenwyk JL, Opulente DA, Kominek J, Shen XX, Zhou X, Labella AL, Bradley NP, Eichman BF, Čadež N, Libkind D, DeVirgilio J, Hulfachor AB, Kurtzman CP, Hittinger CT, Rokas A. Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. PLoS Biol 17: e3000255. https://doi.org/10.1371/journal.pbio.3000255

Cell-cycle checkpoints and DNA repair processes protect organisms from potentially lethal mutational damage. Compared to other budding yeasts in the subphylum Saccharomycotina, we noticed that a lineage in the genus *Hanseniaspora* exhibited very high evolutionary rates, low Guanine–Cytosine (GC) content, small genome sizes, and lower gene numbers. To better understand *Hanseniaspora* evolution, we analyzed 25 genomes, including 11 newly sequenced, representing 18/21 known species in the genus. Our phylogenomic analyses identify two *Hanseniaspora* lineages, a faster-evolving lineage (FEL), which began diversifying approximately 87 million years ago (mya), and a slower-evolving lineage (SEL), which began diversifying approximately 54 mya. Remarkably, both lineages lost genes associated with the cell cycle and genome integrity, but these losses were greater in the FEL. E.g., all species lost the cell-cycle regulator WHIskey 5 (*WHI5*), and the FEL lost components of the spindle checkpoint pathway (e.g., Mitotic Arrest-Deficient 1 [*MAD1*], Mitotic Arrest-Deficient 2 [*MAD2*]) and DNA-damage–checkpoint pathway (e.g., Mitosis Entry Checkpoint 3 [*MEC3*], RADiation sensitive 9 [*RAD9*]). Similarly, both lineages lost genes involved in DNA repair pathways, including the DNA glycosylase gene 3-MethylAdenine DNA Glycosylase 1 (*MAG1*), which is part of the base-excision repair pathway, and the DNA photolyase gene PHotoreactivation Repair deficient 1 (*PHR1*), which is involved in pyrimidine dimer repair. Strikingly, the FEL lost 33 additional genes, including polymerases (i.e., POLymerase 4 [*POL4*] and *POL32*)

and telomere-associated genes (e.g., Repressor/ activator site binding protein-Interacting Factor 1 [*RIF1*], Replication Factor A 3 [*RFA3*], Cell Division Cycle 13 [*CDC13*], Pbp1p Binding Protein [*PBP2*]). Echoing these losses, molecular evolutionary analyses reveal that, compared to the SEL, the FEL stem lineage underwent a burst of accelerated evolution, which resulted in greater mutational loads, homopolymer instabilities, and higher fractions of mutations associated with the common endogenously damaged base, 8-oxoguanine. We conclude that *Hanseniaspora* is an ancient lineage that has diversified and thrived, despite lacking many otherwise highly conserved cell-cycle and genome integrity genes and pathways, and may represent a novel, to our knowledge, system for studying cellular life without them.

9 Peris D, Moriarty RV, Alexander WG, Wrobel RL, Hittinger CT. 2019. Allododecaploid yeasts: synthetic hybrids of six species. bioRxiv under review. https://doi.org/10.1101/597633

Polyploidy generates diversity by increasing the number of copies of each chromosome. Many plants, animals, fungi, and other eukaryotes are ancient or recent polyploids, including some of the best-known evolutionary radiations, crops, and industrial organisms. Polyploidy facilitates differentiation and adaptation to new environments, but the tools to test its limits are lacking. Here we develop an iterative Hybrid Production (iHyPr) method to produce allododecaploid yeast strains with a base ploidy of 12n. Chromosomal instability increased dramatically as additional copies of the genome were added. These six-species hybrids rapidly improved their fitness during adaptive laboratory evolution. This new method for making synthetic hybrids will enable basic research on polyploidy, cancer, and chromosome biology, as well as more applied research on biofuels, bioproducts, and synthetic biology.

10 Labella AL, Opulente DA, Steenwyk JL, Hittinger CT, Rokas A. 2019. Variation and selection on codon usage bias across an entire subphylum. bioRxiv under review. https://doi.org/10.1101/608042

Variation in synonymous codon usage is abundant across multiple levels of organization: between codons of an amino acid, between genes in a genome, and between genomes of different species. It is now well understood that variation in synonymous codon usage is influenced by mutational bias coupled with both natural selection for translational efficiency and genetic drift, but how these processes shape patterns of codon usage bias across entire lineages remains unexplored. To address this question, we used a rich genomic data set of 327 species that covers nearly one third of the known biodiversity of the budding yeast subphylum Saccharomycotina. We found that, while genome-wide relative synonymous codon usage (RSCU) for all codons was highly correlated with the GC content of the third codon position (GC3), the usage of codons for the amino acids proline, arginine, and glycine was inconsistent with the neutral expectation where mutational bias coupled with genetic drift drive codon usage. Examination between genes' effective numbers of codons and their GC3 contents in individual genomes revealed that nearly a quarter of genes (381,174/1,683,203; 23%), as well as most genomes (308/327; 94%), significantly deviate from the neutral expectation. Finally, by evaluating the imprint of translational selection on codon usage, measured as the degree to which genes' adaptiveness to the tRNA pool were correlated with selective pressure, we show that translational selection is widespread in budding yeast genomes (264/327; 81%). These results suggest that the contribution of translational selection and drift to patterns of synonymous codon usage across budding yeasts varies across codons, genes, and genomes; whereas drift is the primary driver of global codon usage across the subphylum, the codon bias of large numbers of genes in the majority of genomes is influenced by translational selection.

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The following paper was published during 2019.

1 Sha SP, Suryavanshi MS, Tamang JP. 2019. Mycobiome diversity in traditionally prepared starters for alcoholic beverages in India by high-throughput sequencing method. Frontiers in Microbiology 10:348. doi: 10.3389/fmicb.2019.003482237.

Chowan, dawdim, humao, hamei, khekhrii and *phut* are sun-dried starters used for preparation of alcoholic beverages in North East regions of India. We attempted to profile the mycobiome community in these starters by high-throughput sequencing (HTS) method. All fungal populations were found to be restricted to Ascomycota (67-99%), Zygomycota (0.7-29%), Basidiomycota (0.03-7%) and Chytridiomycota (0.0003%). We found 45 core operational taxonomic units (OTUs) which were universally present and were further weighed to 41 genera level and 22 species level taxonomy. Total number of 594 fungal species were detected by HTS including common species (224), unique species (133) and rare-species (237) in samples of starters. Unique species were recorded in *phut* (40 species), *khekhrii* (28), *hamei* (23), *dawdim* (21), *chowan* (13) and *humao* (8), respectively. Most of the fungal families were found to correlate to type of nutritional mode and growth morphologies of the community, where saprotrophic mode of mold species were more dominant, whereas morphotypes were more dominant in yeast species.

IV Institute of Agrochemistry and Food Technology (IATA), Centro Superior de Investigaciones Cientificas (CSIC), Calle Catedratico Agustin Escardino Benlloch, 7, Office 309, 46980 Paterna, Valencia, Spain. Communicated by David Peris <david.perisnavarro@gmail.com>.

Recent publications. See abstracts, as appropriate, under Dr. Hittinger's communication.

1 Li XC, Peris D, Hittinger CT, Sia EA, Fay JC. 2019. Mitochondria-encoded genes contribute to the evolution of heat and cold tolerance among *Saccharomyces* species. Science Advances 5(1):eaav1848.

2 Baker ECP, Peris D, Moriarty RV, Li XC, Fay JC, Hittinger CT. 2019. Mitochondrial DNA and temperature tolerance in lager yeasts. Science Advances 5(1): eaav1869

3 Langdon QK, Peris D, Kyle B, Hittinger CT. 2018. sppIDer: a species identification tool to investigate hybrid genomes with high-throughput sequencing. Mol Biol Evol 35(11): 2835-2849

The genomics era has expanded our knowledge about the diversity of the living world, yet harnessing high-throughput sequencing data to investigate alternative evolutionary trajectories, such as hybridization, is still challenging. Here we present sppIDer, a pipeline for the characterization of interspecies hybrids and pure species, that illuminates the complete composition of genomes. sppIDer maps short-read sequencing data to a combination genome built from reference genomes of several species of interest and assesses the genomic contribution and relative ploidy of each parental species, producing a series of colorful graphical outputs ready for publication. As a proof-of-concept, we use the genus *Saccharomyces* to detect and visualize both interspecies hybrids and pure strains, even with missing parental reference genomes. Through simulation, we show that sppIDer is robust to variable reference genome qualities and performs well with low-coverage data. We further demonstrate the power of this approach in plants, animals, and other fungi. sppIDer is robust to many different inputs and provides visually intuitive insight into genome composition that enables the rapid identification of species and their interspecies hybrids. sppIDer exists as a Docker image, which is a reusable, reproducible, transparent, and simple-to-run package that automates the pipeline and installation of the required dependencies (https://github.com/GLBRC/sppIDer).

4 Eizaguirre JI, Peris D, Rodríguez ME, Lopes CA, De Los Ríos P, Hittinger CT, Libkind D. 2018. Phylogeography of the wild Lager-brewing ancestor (*Saccharomyces eubayanus*) in Patagonia. Environ Microbiol 20(10):3732-3743

Saccharomyces eubayanus is the close relative of the Lager brewing yeast and was firstly found in North Patagonia associated with *Nothofagus* trees. In recent years additional strains were found in North America, Asia and New Zealand, and genomic analyses showed the existence of two main populations of this yeast, both of them present in Patagonia. Here, we performed the most comprehensive study of *S. eubayanus* in Patagonia natural environments (400 samples) and confirmed that this region has the highest isolation success rate for this species described worldwide (more than 10 fold). The genetic characterization of 200 isolates (*COX2*, *DCR1*, *intFR*) revealed five geographically structured subpopulations. We hypothesized that marine ingressions and glaciations, which shaped the Patagonian landscape, contributed on population differentiation. The first large screening of fermentation performance of 60 wild *S. eubayanus* strains indicated which subpopulations would be more suitable for beer production.

5 Peris D, Moriarty RV, Alexander WG, Wrobel RL, Hittinger CT. 2019. Allododecaploid yeasts: synthetic hybrids of six species. BioRxiv *Preprint*

National article.

6 Peris D. 2019. La domesticación de las levaduras cerveceras entendida desde la genética. Revista Alimentaria 502:40-42 (In Spanish).

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

Recent publications.

1 Trochine A, Turchetti B, Vaz AB, Brandao L, Rosa L, Buzzini P, Rosa C, Libkind D. 2017. Description of *Dioszegia patagonica* sp. nov., a novel carotenogenic yeast isolated from cold environments. Int J Syst Evol Microbiol 67: 4332-4339, doi: 10.1099/ijsem.0.002211.

During a survey of carotenogenic yeasts from cold and oligotrophic environments in Patagonia, several yeasts of the genus *Dioszegia* (Tremellales, Agaricomycotina) were detected, including three strains that could not be assigned to any known taxa. Analyses of internal transcribed spacer and D1/D2 regions of the large subunit rRNA gene showed these strains are conspecific with several other strains found in the Italian Alps and in Antarctica soil. Phylogenetic analyses showed that 19 of these strains represent a novel yeast species of the genus *Dioszegia*. The name *Dioszegia patagonica* sp. nov. is proposed to accommodate these strains and CRUB 1147T (UFMG 195T=CBMAI 1564T=DBVPG 10618T=CBS 14901T; MycoBank MB819782) was designated as the type strain. This *Dioszegia* species accumulates biotechnologically valuable compounds such as carotenoid pigments and mycosporines.

2 Selbmann L, Onofri S, Coleine C, Buzzini P, Canini F, Zucconi L. Effect of environmental parameters on biodiversity of the fungal component in lithic Antarctic communities. Extremophiles. 2017 21: 1069-1080, doi: 10.1007/s00792-017-0967-6.

A wide sampling of rocks, colonized by microbial epi-endolithic communities, was performed along an altitudinal gradient from sea level to 3600 m a.s.l. and sea distance from the coast to 100 km inland along the Victoria Land Coast, Antarctica. Seventy-two rock samples of different typology, representative of the entire survey, were selected and studied using denaturing gradient gel electrophoresis to compare variation in fungal diversity according to environmental conditions along this altitudinal and sea distance transect. Lichenized fungi were largely predominant in all the samples studied and the biodiversity was heavily influenced even by minimal local variations. The n-MDS analysis showed that

altitude and sea distance affect fungal biodiversity, while sandstone allows the communities to maintain high biodiversity indices. The Pareto-Lorenz curves indicate that all the communities analyzed are highly adapted to extreme conditions but scarcely resilient, so any external perturbation may have irreversible effects on these fragile ecosystems.

3 Forti L, Cramarossa MR, Filippucci S, Tasselli G, Turchetti B, Buzzini P. 2017. Non-conventional yeast-promoted biotransformation for the production of flavour compounds. In: Natural and Artificial Flavouring Agents and Food Dyes (Grumezescu AM, Holbaned AM eds.), Elsevier-Academic Press, Cambridge, USA, pp. 165-187, doi.org/10.1016/B978-0-12-811518-3.00006-5.

The rising consumer demand for "natural" foodstuffs has encouraged a growing part of both the academic and industrial scientific communities to develop novel biocatalysts for producing flavoring molecules. In this context, nonconventional yeasts (NCYs) have attracted increasing interest due to their biochemical characteristics and potential applications, being able to produce aroma compounds from a variety of carbon sources, including sugars, alkanes, plant oils, starch hydrolysates, ethanol, and glycerol. Apart from classical fermentation processes (de novo synthesis), bioconversion of appropriate precursor compounds is also being developed to produce food aromas. An overview on the potential of NCYs' whole cell for producing food flavors by biotransformation is illustrated in this chapter by a discussion of the production of different class of compounds, namely alcohols, aldehydes, ketones, lactones, terpenes, and terpenoids, alkenes, phenols, and sulfur compounds.

4 Buzzini P, Turchetti B, Yurkov A. 2018. Extremophilic yeasts: the toughest yeasts around? Yeast 35: 487–497, doi.org/10.1002/yea.3314

Microorganisms are widely distributed in a multitude of environments including ecosystems that show challenging features to most life forms. The combination of extreme physical and chemical factors contributes to the definition of extreme habitats although the definition of extreme environments changes depending on one's point of view: anthropocentric, microbial centric or zymo centric. Microorganisms that live under conditions that cause hard survival are called extremophiles. In particular organisms that require extreme conditions are called true extremophiles while organisms that tolerate them to some extent are termed extremotolerant. Deviation of temperature, pH, osmotic stress, pressure and radiation from the common range delineates extreme environments. Yeasts are versatile eukaryotic organisms that are not frequently considered the toughest microorganisms in comparison with prokaryotes. Nevertheless extremophilic or extremotolerant species are present also within this group. Here a brief description is provided of the main extreme habitats and the metabolic and physiological modifications adopted by yeasts depending on their adverse conditions. Additionally, the main extremophilic and extremotolerant yeast species associated with a few extreme habitats are listed.

5 Borruso L, Sannino C, Selbmann L, Battistel D, Zucconi L, Azzaro M, Turchetti B, Buzzini P, Guglielmin. 2018. A thin ice layer segregates two distinct fungal communities in Antarctic brines from Tarn Flat (Northern Victoria Land). Sci Rep 8: 6582, doi:10.1038/s41598-018-25079-3.

Brines are hypersaline solutions which have been found within the Antarctic permafrost from the Tarn Flat area (Northern Victoria Land). Here, an investigation on the possible presence and diversity of fungal life within those peculiar ecosystems has been carried out for the first time. Brines samples were collected at 4- and 5-meter depths (TF1 and TF2, respectively), from two brines separated by a thin ice layer. The samples were analyzed via Illumina MiSeq targeting the ITS region specific for both yeasts and filamentous fungi. An unexpected high alpha diversity was found. Beta diversity analysis revealed that the two brines were inhabited by two phylogenetically diverse fungal communities (Unifrac value: 0.56, p value < 0.01; Martin's P-test p-value < 0.001) characterized by several specialist taxa. The most abundant fungal genera were *Candida* sp., *Leucosporidium* sp., *Naganishia* sp. and *Sporobolomyces* sp. in TF1, and *Leucosporidium* sp., *Malassezia* sp., *Naganishia* sp. and *Sporobolomyces* sp. in TF2. A few hypotheses on such differentiation have been done: i) the different chemical and physical

composition of the brines; ii) the presence in situ of a thin layer of ice, acting as a physical barrier; and iii) the diverse geological origin of the brines.

6 Turchetti B, Selbmann L, Gunde-Cimerman N, Buzzini P, Sampaio JP, Zalar P. 2018. *Cystobasidium alpinum* sp. nov. and *Rhodosporidiobolus oreadorum* sp. nov. from European cold environments and arctic region. Life 2018, 8: 9, doi:10.3390/life8020009.

Over 80% of the Earth's environments are permanently or periodically exposed to temperatures below 5°C. Cold habitats harbour a wide diversity of psychrophilic and psychrotolerant yeasts. During ecological studies of yeast communities carried out in cold ecosystem in the Italian Alps, Svalbard (Norway, Arctic region), and Portugal, 23 yeast strains that could not be assigned to any known fungal taxa were isolated. In particular, two of them were first identified as *Rhodotorula* sp., showing the highest degree of D1/D2 sequence identity with *Cystobasidum laryngis* accounted to only 97% with the type strain *C. laryngis* CBS 2221). The other 21 strains, exhibiting identical D1/D2 sequences, had low identity (97%) with *Rhodosporidiobolus lusitaniae* and *Rhodosporidiobolus colostri*. Similarly, ITS sequences of the type strains of the most closely related species (93–94%). In a 2-genes multilocus D1/D2 and ITS ML phylogenetic tree, the studied strains pooled in two well separated and supported groups. In order to classify the new 23 isolates based on phylogenetic evidences, we propose the description of two novel species *Cystobasidium alpinum* sp. nov. and *Rhodosporidiobolus oreadorum* sp. nov.

7 Tasselli G, Filippucci S, Borsella E, D'Antonio S, Gelosia M, Cavalaglio G, Turchetti B, Sannino C, Onofri A, Mastrolitti S, De Bari I, Cotana F, Buzzini P. 2018. Yeast lipids from cardoon stalks, stranded driftwood and olive tree pruning residues as possible extra sources of oils for producing biofuels and biochemicals. Biotechnol Biofuels 11: 147, doi: 10.1186/s13068-018-1142-8.

Some lignocellulosic biomass feedstocks occur in Mediterranean Countries. They are still largely unexploited and cause considerable problems due to the lack of cost-effective harvesting, storage and disposal technologies. Recent studies found that some basidiomycetous yeasts are able to accumulate high amount of intracellular lipids for biorefinery processes (i.e., biofuels and biochemicals). Accordingly, the above biomass feedstocks could be used as carbon sources (after their pre-treatment and hydrolysis) for lipid accumulation by oleaginous yeasts. Cardoon stalks, stranded driftwood and olive tree pruning residues were pre-treated with steam-explosion and enzymatic hydrolysis for releasing free mono- and oligosaccharides. Lipid accumulation tests were performed at two temperatures (20 and 25 °C) using *Leucosporidium creatinivorum* DBVPG 4794, *Naganishia adeliensis* DBVPG 5195 and *Solicoccozyma terricola* DBVPG 5870. *S. terricola* grown on cardoon stalks at 20 °C exhibited the highest lipid production (13.20 g/l), a lipid yield (28.95%) close to the maximum theoretical value and a lipid composition similar to that found in palm oil. On the contrary, *N. adeliensis* grown on stranded driftwood and olive tree pruning residues exhibited a lipid composition similar to those of olive and almonds oils. A predictive evaluation of the physical properties of the potential biodiesel obtainable by lipids produced by tested yeast strains has been reported and discussed. Lipids produced by some basidiomycetous yeasts grown on Mediterranean lignocellulosic biomass feedstocks could be used as supplementary sources of oils for producing biofuels and biochemicals.

8 Rossi S, Turchetti B, Sileoni V, Marconi O, Perretti G. 2018. Evaluation of *Saccharomyces cerevisiae* strains isolated from non-brewing environments in beer production. J Inst Brewing 124: 381–388, doi.org/10.1002/jib.503.

This study sought to select novel *Saccharomyces cerevisiae* strains not previously used in the production of beer. Twelve strains isolated from grape must, bakery, wine and apple stillage were compared through laboratory scale fermentation. Yeast from the grape must exhibited a superior fermentative capability (comparable with that of two commercial strains). Some of the strains produced appreciable concentrations of esters and higher alcohols, suggesting their potential as novel yeasts for beer characterised by distinct flavours. The most suitable strain for beer production, based on fermentative ability and volatile profile, was a baker's yeast which was subject to pilot plant scale-up. The standard quality attributes, amino acids, volatile and sensory profiles were monitored during the primary

fermentation and after bottle conditioning. These were aligned with those of a standard ale, suggesting that the selected yeast strain could be used for beer production. Interestingly, some esters were above the sensory threshold.

9 De Francesco G, Sannino C, Sileoni V, Marconi O, Filippucci S, Tasselli G, Turchetti B. 2018. *Mrakia gelida* in brewing process: an innovative production of low alcohol beer using a psychrophilic yeast strain. Food Microbiology 76: 354–362, doi.org/10.1016/j.fm.2018.06.018

Due to the increasing consumer demand, the production of low alcoholic and non-alcoholic beer is the new goal of the present brewing producers. Although the beer with reduced alcohol content is currently obtained by physical methods, the use of non-*Saccharomyces* yeast, with low fermentations capacities, may represent an interesting biological approach. In this study the ethanol content and the volatile profile of a beer obtained using the basidiomycetous psychrophilic yeast strain *Mrakia gelida* DBVPG 5952 was compared with that produced by a commercial starter for low alcohol beers, *Saccharomycodes ludwigii* WSL17. The two beers were characterized by a low alcohol content (1.40% and 1.32% v/v) and by a low diacetyl production (5.04 and 5.20 µg/L). However, the organoleptic characteristics of the beer obtained using M. gelida are more appreciated by the panelists, in comparison to the analogous produced with the commercial strain of *S. ludwigii*.

10 Kulikova-Borovikova D, Lisi S, Dauss E, Alamäe T, Buzzini P, Hallsworth JE, Rapoport A. 2018. Activity of the α-glucoside transporter Agt1 in *Saccharomyces cerevisiae* cells during dehydration-rehydration events. Fungal Biol 122: 613-620, doi.org/10.1016/j.funbio.2018.03.006.

Microbial cells can enter a state of anhydrobiosis under desiccating conditions. One of the main determinants of viability during dehydration-rehydration cycles is structural integrity of the plasma membrane. Whereas much is known about phase transitions of the lipid bilayer, there is a paucity of information on changes in activity of plasma membrane proteins during dehydration-rehydration events. We selected the α-glucoside transporter Agt1 to gain insights into stress mechanisms/responses and ecophysiology during anhydrobiosis. As intracellular water content of *S. cerevisiae* strain 14 (a strain with moderate tolerance to dehydration-rehydration) was reduced to 1.5 g water/g dry weight, the activity of the Agt1 transporter decreased by 10–15 %. This indicates that functionality of this trans-membrane and relatively hydrophobic protein depends on water. Notably, however, levels of cell viability were retained. Prior incubation in the stress protectant xylitol increased stability of the plasma membrane but not Agt1. Studies were carried out using a comparator yeast which was highly resistant to dehydration-rehydration (*S. cerevisiae* strain 77). By contrast to *S. cerevisiae* strain 14, there was no significant reduction of Agt1 activity in *S. cerevisiae* strain 77 cells. These findings have implications for the ecophysiology of *S. cerevisiae* strains in natural and industrial systems.

11 Coleine C, Stajich JE, Zucconi L, Onofri S, Pombubpa N, Egidi E, Franks AE, Buzzini P, Selbmann L. 2018. Antarctic cryptoendolithic fungal communities are highly adapted and dominated by Lecanoromycetes and Dothideomycetes. Frontiers Microbiol 9: 1392, doi.org/10.3389/fmicb.2018.01392.

Endolithic growth is one of the most spectacular microbial adaptations to extreme environmental constraints and the predominant life-form in the ice-free areas of Continental Antarctica. Although Antarctic endolithic microbial communities are known to host among the most resistant and extreme-adapted organisms, our knowledge on microbial diversity and composition in this peculiar niche is still limited. In this study, we investigated the diversity and structure of the fungal assemblage in the cryptoendolithic communities inhabiting sandstone using a meta-barcoding approach targeting the fungal Internal Transcribed Sequence region 1 (ITS1). Samples were collected from 14 sites in the Victoria Land, along an altitudinal gradient ranging from 1,000 to 3,300 m a.s.l. and from 29 to 96 km distance to coast. Our study revealed a clear dominance of a 'core' group of fungal *taxa* consistently present across all the samples, mainly composed of lichen-forming and Dothideomycetous fungi. Pareto-Lorenz curves

indicated a very high degree of specialization (F_0 approximately 95%), suggesting these communities are highly adapted but have limited ability to recover after perturbations. Overall, both fungal community biodiversity and composition did not show any correlation with the considered abiotic parameters, potentially due to strong fluctuations of environmental conditions at local scales.

12 G. Khroustalyova, G. Giovannitti, D. Severini, R. Scherbaka, B. Turchetti, P. Buzzini, A. Rapoport. 2019. Anhydrobiosis in yeasts: psychrotolerant yeasts are highly resistant to dehydration. Yeast 2019: 1-5, doi: 10.1002/yea.3382.

Yeast cells are able to transition into a state of anhydrobiosis (temporary reversible suspension of metabolism) under conditions of desiccation. One of the most efficient approaches for understanding the mechanisms underlying resistance to dehydration–rehydration is to identify yeasts, which are stable under such treatments, and compare them with moderately resistant species and strains. In the current study, we investigated the resistance to dehydration–rehydration of six psychrotolerant yeast strains belonging to two species. All studied strains of *Solicoccozyma terricola* and *Naganishia albida* were found to be highly resistant to dehydration–rehydration. The viability of S. terricola strains was close to 100%. Such results have not been previously reported in studies of anhydrobiosis in yeasts. The plasma membrane changes, revealed by determining its permeability under various rehydration conditions, were also surprisingly minimal. Thus, the high level of resistance of psychrotolerant yeast strains might be related to the chemical composition and molecular organisation of their plasma membranes. Aside from plasma membrane characteristics, other important factors may also influence the maintenance of yeast cell viability under conditions of dehydration–rehydration.

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Recent publication.

1 Lascano Demera L, Portero Barahona P, and Carvajal Barriga EJ. 2019. Production, extraction and characterization of lipases from the Antarctic yeast *Guehomyces pullulans*. Amer J Biochem Biotechnol DOI: 10.3844/ajbbsp.2019.

The production of extracellular lipases from the Antarctic yeast *Guehomyces pullulans* is induced using an olive oil medium as an inductor substrate and a first characterization of its enzyme, using the protein extract obtained from the medium, is described. For this, the effect of pH and temperature on the lipase activity are evaluated and the enzyme kinetic for the lipase is determined. Lipase production was 0.27 U/mL, a high value compared to lipolytic activities in non-optimized media. However, this value can be increased by optimizing the culture medium. The lipase of *G. pullulans* has maximum activity at pH 8.0 and 40°C (thermal stability 40-50°C). Regarding the kinetic parameters, a $K_M = 3.7\times10^{-4}$ M was obtained, a value located in the range of industrial lipases. In addition, its kinetics presented the phenomenon of interfacial activation. The results presented in this work show the biotechnological potential of the lipase due its biochemical properties and are useful for later work directed to study other factors that affect the enzyme activity and potential biotechnological applications of the *Guehomyces pullulans* lipase.

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Recent publication.

1 Nasr S, Lutz M, Amoozegar MA, Eparvier V, Stien D, Fazeli SAS, Yurkov A. *Graphiola fimbriata*: the first species of Graphiolaceae (Exobasidiales, Basidiomycota) described only based on its yeast stage. Mycological Progress - https://doi.org/10.1007/s11557-018-1450-1

The systematic position of three yeast strains isolated from a plant cell culture, a piece of termite nest, or as a foliar endophyte of *Coffea arabica*, respectively, is evaluated using morphological, physiological, and phylogenetical characteristics. In culture, all three isolates produced white, pale orange to pink colored colonies of cylindrical cells with monopolar budding and pseudohyphae. Standard phenotypic, biochemical, physiological characterization, and phylogenetic analyses of the combined 26S rRNA gene (D1/D2 domains) and ITS region sequences showed the conspecificity of these isolates and suggest their placement within the Exobasidiales (Ustilaginomycotina) as a sister lineage of the sampled and sequenced *Graphiola* species. Here, we describe this species as *Graphiola fimbriata* sp. nov. MycoBankMB825077 (holotype: PC1T; ex-type cultures: IBRCM30158^T = CBS 13945^T = DSM 104832^T). This is the first species described in the genus *Graphiola* for which only the asexual, saprobic developmental phase is known. The description of the genus *Graphiola* is therefore emended to allow species known only from a saprobic state.

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The following are papers for 2018 and 2019 or in press.

1 Naumov GI, Shalamitskyi MYu, Naumova ES, Ch-F Lee. 2018. Phylogenetics, biogeography, and ecology of methylotrophic yeasts of the heterogeneous genus *Ogataea*: achievements and prospects. Microbiology (Moscow) 87 (4) 443–452.

Analysis of the literature and GenBank data showed that the genus *Ogataea* is heterogeneous and includes at least five non-described genera. Comprehensive phylogenetic analysis of the present genus *Ogataea* may be conducted only based on multigene analysis of all the known species. Possibilities of molecular species identification in biogeographical and ecological studies of yeasts are discussed.

2 Naumov GI, Naumova ES., Boundy-Mills KL. 2018. Description of *Komagataella mondaviorum* sp. nov., a new sibling species of *Komagataella* (*Pichia*) *pastoris*. Antonie van Leeuwenhoek. 111 (7):1197–1207.

3 Shalamitskiy MYu, Naumov GI. 2018. Phylogenetic analysis of pectinases of ascomycetous yeasts. Applied Biochemistry and Microbiology 54 (7): 723–729.

4 Naumov GI., Borovkova AN, Shnyreva AV, Naumova ES. 2019. Phylogenetic origin of the MAL and IMA alpha-glucosidases of the international genetic line of *Saccharomyces cerevisiae* S288C. Microbiology (Moscow) 88 (1): 39–45.

Taking into account the accepted concept of the ancient whole genome duplication (WGD) in the yeast genus *Saccharomyces*, comparative analysis of the multiple α-glucosidases MAL and IMA of the genetic line *Saccharomyces cerevisiae* S288C and α-glucosidases of protoploid yeasts *Kluyveromyces* and *Lachancea*, which have not experienced genome duplication, was carried out. Only certain isoforms of MAL and IMA of the latter two genera were shown to be in a close phylogenetic relationship to α-glucosidases MAL12. MAL32 and IMA1-IMA4 of the yeast *S. cerevisiae* S288C, while others are closer to the divergent IMA5. The results obtained are consistent with the WGD concept, according to which the yeast *Saccharomyces*, *Kluyveromyces* and *Lachancea* originated from the common protoploid ancestor and, therefore, may have common closely related α-glucosidases MAL and IMA. The identity of the amino acid sequences of isomaltases IMA1-IMA4 of *S. cerevisiae* S288C and *L. dasiensis*, *L. fantastica*, *L. fermentati*, *L. lanzarotensis*, *L. meyersii*, *L. quebecensis*, *L. thermotolerans* is 75-100%, the maltases MAL of the same species are identical by 75-99%. Note that the α-glucosidases MAL and IMA diverged in each genus, species and even strain.

5 Naumova ES, Shalamitskiy MYu, Naumov GI. Molecular polymorphism of pectinase genes *PGU* of *Saccharomyces bayanus* var. *uvarum* yeast. Applied Biochemistry and Microbiology 55 (9) (in press).

A molecular genetic study of the pectinase *PGU* genes from 74 strains of the yeast *Saccharomyces bayanus* var. *uvarum* isolated from various fermentation processes and natural sources in different regions of Europe and in the USA has been performed. Unlike the *S. cerevisiae* yeasts each having a single *PGU* gene, the *S. bayanus* var. *uvarum* strains have three divergent genes *PGU1b*, *PGU2b* and *PGU3b*, located respectively on chromosomes X, I and XIV. The high pectinolytic activity of these yeasts appears to be related to the presence of several *PGU* polymeric genes in their genomes.

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The following are our publications so far for 2015-2018.

Yeast Taxonomy

1 Khunnamwong P, Jindamorakot S & Limtong S. 2018. Endophytic yeasts diversity in leaf tissue of rice, corn and sugarcane cultivated in Thailand assessed by a culture-dependent approach. Fungal Biol 122(8): 785-799.

Endophytic yeasts are yeasts that can colonize healthy plant tissues without causing any damage to the host plant. Although a number of investigations on endophytic microorganisms have been carried out, few have focused on endophytic yeasts. Therefore, this work aimed to explore the diversity of endophytic yeasts in leaf tissue of rice, corn and sugarcane, which are main agricultural crops in Thailand, by a culture-dependent approach. A total of 311 leaf samples, consisting of rice leaf (n=100), corn leaf (n=109) and sugarcane leaf (n=102), were collected from their cultivation fields. From the tissue of surface sterilized leaves of rice (n=92), corn (n=76) and sugarcane (n=78) leaf samples, 117, 118 and 123 yeast strains were respectively isolated and identified based on the D1/D2 region of the large subunit (LSU) rRNA gene sequence analysis to be yeast species in both the phyla Basidiomycota and Ascomycota. Higher numbers of basidiomycetous yeast than ascomycetous yeast were detected in the leaf tissue of the three crops. *Pseudozyma* (*Dirkmeia*) *churashimaensis* (Ustilaginales) was the most prevalent yeast species in the rice and corn leaves with relative frequencies (RF) of 35.9% and 17.8%, respectively. Whereas the predominant species in the sugarcane leaves was *Meyerozyma caribbica* (Saccharomycetales) with an RF of 14.6%. In addition, in this study, six new yeast species and one new yeast genus were proposed. Therefore, our findings suggest that these three plant species are good sources from which new yeast species may be isolated.

2 Khunnamwong P, Surussawadee J, Srisuk N, Boonmak C & Limtong S. 2018. *Papiliotrema phichitensis* f.a., sp. nov., a novel yeast species isolated from sugarcane leaf in Thailand. Antonie van Leeuwenhoek 111 (12): 2455-2461.

3 Kaewkrajay C & Limtong S. 2018. *Spencerozyma siamensis* sp. nov., a novel anamorphic basidiomycetous yeast species in Puccinomycotina isolated from coral in Thailand. Int J Syst Evol Microbio. 68: 3611-3614.

4 Kaewwichian R, Khunnamwong P, Jindamorakot S, Lertwattanasakul N & Limtong S. 2018. *Cryptotrichosporon siamensis* sp. nov., a ballistoconidium-forming yeast species in Trichosporonales isolated from natural habitats in Thailand. Int J Syst Evol Microbiol 68: 2473-2477.

5 Nitiyon S, Khunnamwong P, Lertwattanasakul N & Limtong S. 2018. *Candida kantuleensis* sp. nov., a D-xylose-fermenting yeast species isolated from peat in a tropical swamp forest. Int J Syst Evol Microbiol 68: 2313-2318.

6 Into P, Pontes A, Jacques N, Casaregola S, Limtong S & Sampaio JP. 2018. *Papiliotrema plantarum* sp. nov., a novel tremellaceous sexual yeast species. J Syst Evol Microbiol 68: 1937-1941.

7 Khunnamwong P & Limtong S. 2018. *Saturnispora kantuleensis* f.a., sp. nov., a novel yeast species isolated from peat in a tropical peat swamp forest in Thailand. Int J Syst Evol Microbiol 68(4): 1160-1164.

8 Kim JY, Jang JH, Park JH, Jung HY, Park JS, Cho SJ, Lee HB, Limtong S, Subramani G, Sung GH & Kim MK. 2018. Cellulose degrading basidiomycetes yeast isolated from the gut of grasshopper in Korea. The Microbiological Society of Korea. 54 (4):362-368.

9 Khunnamwong P, Ribeiro JRA, Garcia KM, Hagler AN, Takashima M, Ohkuma M, Endoh R, Sugita T, Jindamorakot S & Limtong S. 2017. *Occultifur plantarum* f.a., sp. nov., a novel cystobasidiomycetes yeast species. Int J Syst Evol Microbiol 67: 2628–2633.

10 Limtong S, Polburee P, Chamnanpa T, Khunnamwong P& Limtong P. 2017. *Meira siamensis* f.a., sp. nov., a novel anamorphic ustilaginomycetous yeast species isolated from the vetiver grass phylloplane in Thailand. Int J Syst Evol Microbiol 67: 2418–2422.

11 Polburee P, Lertwattanasakul N, Limtong P, Groenewald M & Limtong S. 2017. *Nakazawaea todaengensis* f.a., sp. nov., a novel yeast isolated from a peat swamp forest in Thailand. Int J Syst Evol Microbiol 67: 2377–2382.

12 Boontham W, Limtong S, Rosa CA, Lopes MR, Vital MJS & Srisuk N. 2017. *Cyberlindnera tropicalis* f.a., sp. nov., a novel yeast isolated from tropical regions. Int J Syst Evol Microbiol 67: 2569–2573.

13 Nasanit R, Jaibangyang S, Tantirungkij M & Limtong S. 2016. Yeast diversity and novel yeast D1/D2 sequences from corn phylloplane obtained by a culture-independent approach. Antonie van Leeuwenhoek 109:1615-1634.

14 Jaiboon K, Lertwattanasakul N, Limtong P & Limtong S. 2016. Yeasts from peat in a tropical peat swamp forest in Thailand and their ability to produce ethanol, indole-3-acetic acid and extracellular enzymes. Mycol Progress 15: 755–770.

15 Khunnamwong P & Limtong S. 2016. *Yamadazyma endophytica* f.a. sp. nov., an ascomycetous yeast species isolated from leaf tissue in Thailand. Int J Syst Evol Microbiol 66: 2717-2723.

16 Khunnamwong P, Lertwattanasakul N, Jindamorakot S, Limtong S, & Lachance MA. 2015. The genus *Diutina*, description of *Diutina siamensis*, f.a. sp. nov., and reassignment *of Candida catenulata*, C. mesorugosa, *C. neorugosa*, *C. pseudorugosa*, *C. ranongensis*, *C. rugosa* and *C. scorzettiae* to the genus *Diutina*. Int J Syst Evol Microbiol 65: 4701-4709.

17 Nasanit R, Tangwong-o-thai A, Tantirungkij M & Limtong S. 2015. The assessment of epiphytic yeast diversity in sugarcane phyllosphere in Thailand by culture independent method. Fungal Biol 119: 1145-1157.

18 Tantirungkij M, Nasanit R & Limtong S. 2015. Assessment of endophytic yeast diversity in rice leaves by a culture-independent approach. Antonie van Leeuwenhoek 108 3):633-647.

19 Surussawadee J, Jindamorakot S, Nakase T, Lee CF & Limtong S. 2015. *Hannaella phyllophila* sp. nov., a novel basidiomycetous yeast species associated with plants in Thailand and Taiwan. Int J Syst Evol Microbiol 65 (7): 2135-2140.

20 Khunnamwong P, Surussawadee J, Jindamorakot S, Ribeiro JRA, Hagler AN & Limtong S. 2015. *Occultifur tropicalis* f.a., sp. nov., a novel Cystobasidiomycetous yeast species isolated from tropical regions. Int J Syst Evol Microbiol 65(5): 1578-1582.

21 Nasanit R, Krataithong K, Tantirungkij M & Limtong S. 2015. Assessment of epiphytic yeast diversity in rice (*Oryza sativa*) phyllosphere in Thailand by a culture-independent approach. Antonie van Leeuwenhoek 107:1475-1490.

22 Kaewwichian R, Jindamorakot S, Am-In S, Sipiczki M & Limtong S. 2015. *Hannaella siamensis* sp. nov. and *Hannaella phetchabunensis* sp. nov., two new anamorphic basidiomycetous yeast species isolated from plants. Int J Syst Evol Microbiol 65: 1297-1303.

23 Jindamorakot S, Am-In S, Kaewwichian R & Limtong S. 2015. *Yamadazyma insecticola* f.a., sp. nov. and *Yamadazyma epiphylla* f.a., sp. nov., two novel yeast species. Int J Syst Evol Microbiol 65: 1290-1296.

24 Limtong S & Kaewwichian R. 2015. The diversity of culturable yeasts in the phylloplane of rice in Thailand. Ann Microbiol 65(2): 667-675.

Yeast Technology

25 Wu CC, Tsai YY, Ohashi T, Misaki R, Limtong S & Fujiyama K. 2018. Isolation of a thermotolerant *Rhodosporidium toruloides* DMKU3-TK16 mutant and its fatty acid profile at high temperature. FEMS Microbiol Lett 365 (21): fny203.

26 Poontawee R, Yongmanitchai W & Limtong S. 2018. . Lipid production from a mixture of sugarcane top hydrolysate and biodieselderived crude glycerol by the oleaginous red yeast, *Rhodosporidiobolus uvialis*. Process Biochemistry 66: 150-161.

27 Polburee P, Ohashi T, Tsai YY, Sumyai T, Lertwattanasakul N, Limtong S, & Fujiyama K. 2018. Molecular cloning and overexpression of DGA1, an acyl-CoA dependent diacylglycerol acyltransferase, in the oleaginous yeast *Rhodosporidiobolus fluvialis* DMKU-RK253. Microbiology 164: 1-10.

28 Poontawee R, Yongmanitchai W & Limtong S. 2017. Efficient oleaginous yeasts for lipid production from lignocellulosic sugars and effects of lignocellulose degradation compounds on growth and lipid production. Process Biochem 53: 44-60.

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X Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Inhoffenstraße 7B, 38124 Braunschweig, Germany – http://www.dsmz.de. Communicated by AM Yurkov <andrey.yurkov@dsmz.de>.

Recently published papers.

1 Nasr, S., Lutz, M., Amoozegar, M.A., Eparvier, V., Stien, D., Fazeli, S.A.S., Yurkov, A. 2019. *Graphiola fimbriata*: the first species of Graphiolaceae (Exobasidiales, Basidiomycota) described only based on its yeast stage. Mycological Progress 18: 359-368.

See abstract under Dr. Nasr's communication.

2 Streletskii RA, Kachalkin AV, Glushakova AM, Yurkov AM, Demin VV. 2019. Yeasts producing zeatin. PeerJ 7: e6474.

The present paper describes the first screening study of the ability of natural yeast strains to synthesize in culture the plant-related cytokine hormone zeatin, which was carried out using HPLC-MS/MS. A collection of 76 wild strains of 36 yeast species (23 genera) isolated from a variety of natural substrates was tested for the production of zeatin using HPLC-MS/MS. Zeatin was detected in more than a half (55%) of studied strains and was more frequently observed among basidiomycetous than ascomycetous species. The amount of zeatin accumulated during the experiment varied among species and strains. Highest zeatin values were recorded for basidiomycete *Sporobolomyces roseus* and ascomycete *Taphrina* sp. that produced up to 8,850.0 ng and 5,166.4 ng of zeatin per g of dry biomass, respectively. On average, the ability to produce zeatin was more pronounced among species isolated from the arctic-alpine zone than among strains from tropical and temperate climates. Our study also demonstrated that epiphytic strains and pigmented yeast species, typically for phyllosphere, are able to more often produce a plant hormone zeatin than other yeasts.

3 Yurkov AM, Kurtzman CP. 2019. Three new species of Tremellomycetes isolated from maize and northern wild rice. FEMS Yeast Research 19: foz004.

The present work studied novel basidiomycetous yeasts from maize and northern wild rice plants. From comparisons of ribosomal internal transcribed spacer region (ITS) and large subunit (LSU) (D1 and D2 domains), and subsequent phylogenetic analyses, the following species were resolved and described: *Papiliotrema zeae* Yurkov & Kurtzman sp. nov. (ex-type cultures DSM 104035, NRRL Y-63980, MB 827356, GenBank MH718306), *Solicoccozyma zizaniae* Yurkov & Kurtzman sp. nov. (ex-type cultures DSM 104031, NRRL Y-7649, MB 827354, GenBank MH718302) and *Vishniacozyma kurtzmanii* Yurkov sp. nov. (ex-type cultures DSM 104032, NRRL Y-63981, MB 827355, GenBank MH718303). A search among environmental sequences showed that all three yeasts were previously detected, but not reliably assigned to a genus or clade. *Papiliotrema zeae* from maize and *S. zizaniae* from northern wild rice were previously found in agricultural soils under maize and rice, respectively.

4 Heege, F, Bourne EC, Baschien C, Yurkov A, Bunk B, Spröer C, Overmann J, Mazzoni CJ, Monaghan MT. 2018. Long read DNA metabarcoding of ribosomal RNA in the analysis of fungi from aquatic environments. Molecular Ecology Resources 18: 1500-1514.

DNA metabarcoding is widely used to study prokaryotic and eukaryotic microbial diversity. Technological constraints limit most studies to marker lengths below 600 base pairs (bp). Longer sequencing reads of several thousand bp are now possible with third generation sequencing. Increased marker lengths provide greater taxonomic resolution and allow for phylogenetic methods of classification, but longer reads may be subject to higher rates of sequencing error and chimera formation. In addition, most bioinformatics tools for DNA metabarcoding were designed for short reads and are therefore unsuitable. Here, we used Pacific Biosciences circular consensus sequencing (CCS) to DNA metabarcode environmental samples using a ca. 4,500 bp marker that included most of the eukaryote SSU and LSU rRNA genes and the complete ITS region. We developed an analysis pipeline that reduced error rates to levels comparable to short read platforms. Validation using a mock community indicated that our pipeline detected 98% of chimeras de novo. We recovered 947 OTUs from water and sediment samples from a natural lake, 848 of which could be classified to phylum, 397 to genus and 330 to species. By allowing for the simultaneous use of three databases (Unite, SILVA and RDP LSU), long read DNA metabarcoding provided better taxonomic resolution than any single marker. We foresee the use of long reads enabling the cross validation of reference sequences and the synthesis of ribosomal rRNA gene databases. The universal nature of the rRNA operon and our recovery of >100 nonfungal OTUs indicate that long read DNA metabarcoding holds promise for studies of eukaryotic diversity more broadly.

Papers accepted for publication.

5 Passer AR, Coelho MA, Billmyre RB, Nowrousian M, Mittelbach M, Yurkov AM, Averette, AF, Cuomo CA, Sun S, Heitman J. 2019. Genetic and genomic analyses reveal boundaries between species closely related to *Cryptococcus* pathogens. mBio: in press.

6 Kachalkin AV, Turchetti B, Inácio J, Carvalho C, Mašínová T, Pontes A, Röhl O, Glushakova AM, Akulov A, Baldrian P, Begerow D, Buzzini P, Sampaio JP, Yurkov AM. 2019. Rare and undersampled dimorphic basidiomycetes. Mycological Progress: in press.

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

The following have been published since the last issue of the Yeast Newsletter.

1 Gordon Z, Soltysiak MPM, Leichthammer C, Therrien JA, Meaney RS, Lauzon C, Adams M, Lee DK, Janakirama P, Lachance MA, Karas BJ. 2019. Development of a transformation method for *Metschnikowia borealis* and other CUG-serine yeasts. Genes 10:78, 11 pp.

Yeasts belonging to the *Metschnikowia* genus are particularly interesting for the unusual formation of only two needle-shaped ascospores during their mating cycle. Presently, the meiotic process that can lead to only two spores from a diploid zygote is poorly understood. The expression of fluorescent nuclear proteins should allow the meiotic process to be visualized in vivo; however, no large-spored species of *Metschnikowia* has ever been transformed. Accordingly, we aimed to develop a transformation method for *Metschnikowia borealis*, a particularly large-spored species of *Metschnikowia*, with the goal of enabling the genetic manipulations required to study biological processes in detail. Genetic analyses confirmed that *M. borealis*, and many other *Metschnikowia* species, are CUG-Ser yeasts. Codon-optimized selectable markers lacking CUG codons were used to successfully transform *M. borealis* by electroporation and lithium acetate, and transformants appeared to be the result of random integration. Mating experiments confirmed that transformed-strains were capable of generating large asci and undergoing recombination. Finally, random integration was used to transform an additional 21 yeast strains, and all attempts successfully generated transformants. The results provide a simple method to transform many yeasts from an array of different clades and can be used to study or develop many species for various applications.

2 Lopes MR, Santos ARO, Moreira JD, Santa-Brígida R, Martins MB, Pinto FO, Valente P, Morais PB, Jacques N, Grondin C, Casaregola S, Lachance MA, Rosa CA. 2019. Description of *Kurtzmaniella hittingeri* f.a., sp. nov., isolated from rotting wood and fruits, and transfer of three *Candida* species to the genus *Kurtzmaniella* as new combinations. Int J Syst Evol Microbiol 69: 1504-1508,.

Twelve strains of a novel yeast species were isolated from rotting wood, mushrooms and fruit samples in Brazil and French Guiana. Analysis of the sequences of the internal transcribed spacer region and the D1/D2 domains of the large subunit rRNA gene showed that the novel species belongs to the *Kurtzmaniella* clade. The novel species differed from its closest relative, *Candida natalensis*, by 12 substitutions in the D1/D2 sequences. The novel species could be distinguished from C. natalensis by its inability to assimilate cellobiose and salicin, and growth at 50 % (w/w) glucose. The name *Kurtzmaniella hittingeri* f.a., sp. nov. is proposed for the novel species. The type strain of *K. hittingeri* sp. nov. is CBS 13469T (=UFMG CM-Y272T). The MycoBank number is 827183. We also propose the transfer of *Candida fragi*, *Candida quercitrusa* and *Candida natalensis* to the genus *Kurtzmaniella* as new combinations.

3 Tang JM, Jimenez Padilla Y, Lachance MA, Sinclair B 2019 Gut yeasts do not improve desiccation survival in *Drosophila melanogaster*. J Insect Physiol doi: 10.1016/j.jinsphys.2019.103893. [Epub ahead of print]

A healthy gut microbiota generally improves the performance of its insect host. Although the effects can be specific to the species composition of the microbial community, the role of gut microbiota in determining water balance has not been well-explored. We used axenic and gnotobiotic (reared with a known microbiota) *Drosophila melanogaster* to test three hypotheses about the effects of gut yeasts on the water balance of adult flies: 1) that gut yeasts would improve desiccation survival in adult flies; 2) that larval yeasts would improve adult desiccation survival; 3) that the effects would be species-specific, such that yeasts closely associated with *D. melanogaster* in nature are more likely to be beneficial than those rarely found in association with *D. melanogaster*. We used *Saccharomyces cerevisiae* (often used in *Drosophila* cultures, but rarely associated with D. melanogaster in nature), *Lachancea kluyveri* (associated with some species of *Drosophila*, but not *D. melanogaster*), and *Pichia kluyveri* (associated with *D. melanogaster* in nature). Adult inoculation with yeasts had no effect on survival of desiccating conditions. Inoculation with *P. kluyveri* as larvae, did not change desiccation survival in adults; however, rearing with *L. kluyveri* or *S. cerevisiae* reduced adult desiccation survival. We conclude that adult inoculation with gut yeasts has no impact on desiccation survival, but that rearing with yeasts can have either no or detrimental effect. The effects appear to be species-specific: *P. kluyveri* did not have a negative impact on desiccation tolerance, suggesting some level of co-adaptation with *D. melanogaster*. We note that *S. cerevisiae* may not be an appropriate species for studying the effects of gut yeasts on *D. melanogaster*.

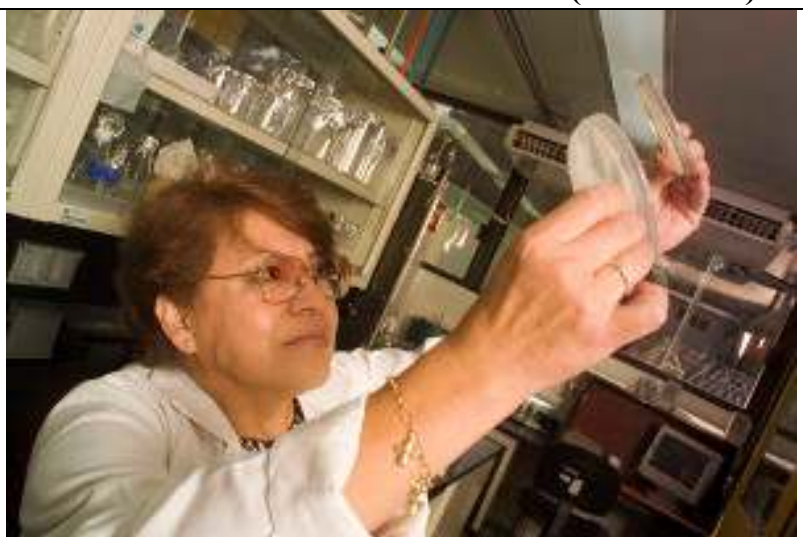
Conference presentation.

4 Lachance MA, Lee DK, Hsiang T. 2019. Mating pheromone sequences predict some but not all mating compatibilities in species of the yeast *Metschnikowia*. Great Lakes-St Lawrence Mycology Workshop, Brock University, St. Catharines, Ontario.

Species of the genus *Metschnikowia* share the intriguing property of producing asci with only two meiotic ascospores, assembled in parallel with the first meiotic division. In many heterothallic species, the asci are much larger than the budding cells, making easy to assess mating competence in large numbers of cultures. We have mined draft genomes of these species to document many genes involved in mating compatibility, including the mating loci themselves, pheromone-coding genes, and pheromone receptor protein genes. The mating type locus and its flanking genes are conserved across the family Metschnikowiaceae and bear some similarities with those of the neighbouring Debaryomycetaceae. Genes coding for mating pheromones vary across species in number of loci and number of coding regions per locus. **a**-Pheromone sequences are highly conserved across a broad phylogenetical range, whereas α-pheromones reflect mating compatibility more closely. Pheromone similarity or divergence among species made it possible to predict mating compatibility in some, but not all cases. We attempted to correlate α-pheromone-mediated G1 arrest with variations in key amino acids using synthetic pheromones, but the variation observed is more difficult to explain. The emerging conclusion is that pheromone interactions are complex and that speciation in haplontic *Metschnikowia* species begins with genetic divergence between isolated populations and is only accompanied by prezygotic isolation much later in evolutionary time.

Obituary

Profesora Jovita Martínez Cruz (1944-2019)



Jovita Martínez Cruz was born in México City December 1st, 1944. She studied chemical bacteriology and parasitology (1962-1966) at the National School of Biological Sciences of the National Polytechnic Institute and obtained a Master of Science in Ecological Biotechnology at the Biotechnology and Bioengineering Department of the Center for Research and Advanced Studies of the National Polytechnic Institute (CINVESTAV) (1975-1978). She later obtained a specialty in Aquatic Microbiology at Cornell's University, Ithaca, New York, USA (1975-1976).

During three decades, she worked as a teacher in the Master of Science in Biotechnology program of the department of Biotechnology and Bioengineering at CINVESTAV-Mexico.

She was a member of the Mexican Society of Mycology, the American Society of Microbiology, the Mexican Society of Microbiology, the National Academy of Pharmaceutical Sciences, the World Federation of Culture Collections (WFCC) and Latin American Federation of Collections (FELACC).

As a professor at the department of Biotechnology and Bioengineering in CINVESTAV she was responsible for over-seeing the Microbial Culture Collection, in 1974, founded by Dr. Carlos Casas Campillo, Head of the Department at CINVESTAV at that time, a task that she fulfilled till 2017. Due to its research and service activities, in 2000, the collection became part of the General Services Coordination under the responsibility of Dr. Jose Tapia Ramírez.

Prof. Martinez's expertise in the area of microbial collections was enhanced by her participation in training courses on techniques of management and maintenance of microbial cultures at international institutions such as the Department of Microbiology of the University of Queensland in Brisbane, Australia (1977) and her participation in several International Conferences on Microbiological Collections organized by WFCC worldwide. The World Data Centre for Microorganisms (WDCM) recognized the CINVESTAV Collection in 1977. The collection was identified by the acronym CDBB-500 (Collection of Biotechnology and Bioengineering Department). In 1981, it was affiliated to WFCC and continues to be.

The academic dedication of Prof. Martinez and the need to make Mexico's scientific community aware of the importance of

microbial collections led her coordinate and participate in a large number of relevant events in this field. She organized, coordinated and taught in the 1st, 2nd and 3rd International Theoretical-Practical Courses on the Taxonomy, Genetics, and Conservation of Yeasts and their applications to Biotechnology, which were hosted by the Graduate Center of the Technological Institute of Merida in 1984, CINVESTAV in 1986, and the UNAM Research Centre for Genetic Engineering and Biotechnology in 1989. The first National Conference on Collections of Microorganisms and their importance in teaching, research and Biotechnology and the first National Theoretical-Practical Course on Conservation of Microbial Cultures were held at the Faculty of Biological Sciences, Universidad Autónoma de Nuevo León, Monterrey, in 1992.

Another of her great achievements was the invitation by the National Commission for Knowledge and Use of Biodiversity, Mexico (CONABIO), in 1994, to develop, through an inter institutional project, a database system to generate a catalogue of microbial strains as a generator of microbial information in México.

Prof. Martínez's Research activities on yeasts led to establish professional relationships in México and abroad. Nationally, she collaborated with Dr. Ricardo Vazquez Juarez of the Biological Research Northwest Center of Baja California, MSc Miriam Cortes Noh of the Oaxaca Technological Institute, and Dra. Patricia Lappe Oliveras of the Biology Institute of UNAM just to mention a few. International collaborators in yeast taxonomy included the late Dr. Cletus Kurtzman of the ARS Culture Collection (NRRL), USDA, USA, Dr. Jack W Fell of the University of Miami, Florida, Dr. Marc-André Lachance of the University of Western Ontario, Canada, and Dr. Sally A. Meyer of the Biology Department of Georgia State University, USA, who were all great colleagues and close friends.

Her influence through advisory activities with different companies where microorganisms play a primary role created an awareness of the need to protect cultures that serve as inoculum in fermentation processes used by the food industry and the production of alcoholic beverages, in particular tequila.

As a professor at CINVESTAV, Prof. Jovita Martinez Cruz always showed her full willingness to support research and teaching in institutions across different Mexican states and as a friend, she always supported and assisted those in need. She was always ready to offer her knowledge and mentorship to young microbiologists.

Professor Jovita Martínez Cruz died on 10 February 2019.

As a legacy of Prof. Jovita Martinez Cruz, the National Collection of Microbial Strains and Cell Cultures continues, now under the direction of Biol. Juan Carlos Estrada Mora, Research Assistant who since 1991 collaborated in the service and research activities offered by the unit. Regarded as a microbial collection of importance for the development of biotechnology in Mexico, CDBB currently holds more than 2000 strains of filamentous fungi, yeast, bacteria, and microalgae. Some of these strains have been isolated in our country and others were acquired through exchanges with scientists within and outside Mexico. The collection will continue to offer strains and information to the scientific community, educational institutions, research centers, and industry in Mexico and the world.

Juan Carlos Estrada Mora

Forthcoming Meetings

29th International Conference on Yeast Genetics and Molecular Biology (ICYGMB) Gothenburg, Sweden, August 18th-22nd 2019.

The "Yeast Genetics Conferences" started in the 1960s with a handful of delegates and since then have become THE most important event in yeast research. Many yeast researchers still remember the meeting in Gothenburg 2003 with over 1,100 delegates, a truly memorable event. Now the yeast meeting returns to Gothenburg, Sweden, August 18th-22nd 2019. The Life Sciences are changing and yeast research remains at their forefront. Advancements in genome sequencing and genome editing just make yeast more exciting as model organism in basic cell biological research, genome evolution and as a tool for synthetic biology and biotechnology. We incorporate the present excitement in yeast research in the programme. Featuring 55 confirmed speakers including keynote lectures by Susan Gasser, Roger Kornberg and Frederick Roth, this conference will contain important news and information for all yeast researchers. The 29th ICYGMB will provide an up-to-date overview in yeast research and it will set the scene for years to come.

Registration and abstract submission is now open at http://yeast2019.org

Looking forward to seeing you in Gothenburg this summer!

Stefan Hohmann, Chair of the Organizing Committee
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37th Small Meeting on Yeast Transport and Energetics, Nove Hrady, Czech Republic 11th to 15th of September 2019

The organizers would like to invite you to the 37th SMYTE in the new castle Nove Hrady, Czech Republic from 11th to 15th of September 2019. The meeting gathers scientists interested in transport and energetics mainly in yeast, but also in other fungi and model organisms. SMYTE37 will cover many aspects of transmembrane transport, such as structure, function, regulation, evolution, role in signaling, homeostasis and physiology. SMYTE traditionally has been a meeting allowing students and young scientists to present and discuss their work among each other and with more experienced colleagues. Therefore, students and Postdocs are especially encouraged to register at a reduced fee. Registration fee including participation, excursion to the medieval town of Cesky Krumlov (world cultural heritage), all meals from dinner at 11th and breakfast at 15th is 232 EUR for regular participants and 192 EUR for students and postdocs. Accommodation can be organized for 48 EUR (dormitory) to 160 EUR (single room in the conference center Chateau Nove Hrady) for the whole meeting. We look forward to seeing you in Nove Hrady!

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www.smyte37.eu

The 35th International Specialised Symposium on Yeasts
21 - 25 October 2019, Antalya, Turkey

The aim of ISSY35 is to bring together academic and postdoctoral researchers, industry scientists and graduate students working in the field of yeast biodiversity and biotechnology to discuss the latest developments in fundamental yeast research linked to biotechnological applications.

This is the first time ISSY is being held in Turkey. A broad international and regional scientific organizing committee is behind this important meeting. The ISSY series are very international meetings and we expect to attract around 250 delegates from all over the world. As an example, previous ISSY meeting in Cork, Ireland, attracted 285 delegates (from 37 countries), with their diversity indicating the global reach and relevance of yeast research in society. The 5 inhabited continents were well represented: Europe 219; North America 27; Asia 18; South America 15, Africa 6) and there was strong private sector participation: 46 delegates from 31 different companies. These headline numbers demonstrate both that yeast research is alive and well across the globe, and that this research has fundamental and biotechnological dimensions to it.

Prof. Dr. Huseyin ERTEN
Chair of the Organizing Committe of ISSY 35
Department of Food Engineering
Faculty of Agriculture
University of Cukurova, Turkey

ISSY35 will take place in the beautiful city of Antalya, on the South of Turkey; one of the tourism capitals of Europe. There are 2 international airports with direct flights over 50 capitals in the World and two planes per hour to and from Istanbul. Symposium Hotel is 5 Star, All-inclusive, Amara Premier Palace Hotel. There will be transfer opportunities from airports to hotel for our sponsors.

For details on registration and abstract submission, please consult

http://www.issy35.com/en/index.html

Brief News Item

PhD student positions - International PhD Program
"Biomolecular Technology of Proteins (BioToP)"
Vienna Institute of BioTechnology of BOKU, Vienna, Austria

BioToP offers an inter- and multi-disciplinary research-based doctoral education at the interface of basic and applied science in the field of protein biotechnology. BioToP offers a challenging scientific environment with state-of-the-art facilities and provides comprehensive and thorough up-to-date research training in the fields of:

- structure-function analysis, engineering and design of proteins
- protein synthesis, targeting and post-translational modifications
- expression systems and cell factories
- bioinformatics and molecular modelling

The BioToP-specific educational program comprises lectures, seminars and instructional courses that complement the research work in the participating groups. Highly qualified and motivated students of any nationality are invited to apply for the 3-year studentships. Funding will be according to the salary scheme of the Austrian Science Fund. Additionally students will receive funding for research stays abroad and for the participation at international conferences.

Further information on research projects as well as application guidelines and forms are available at:

http://biotop.boku.ac.at

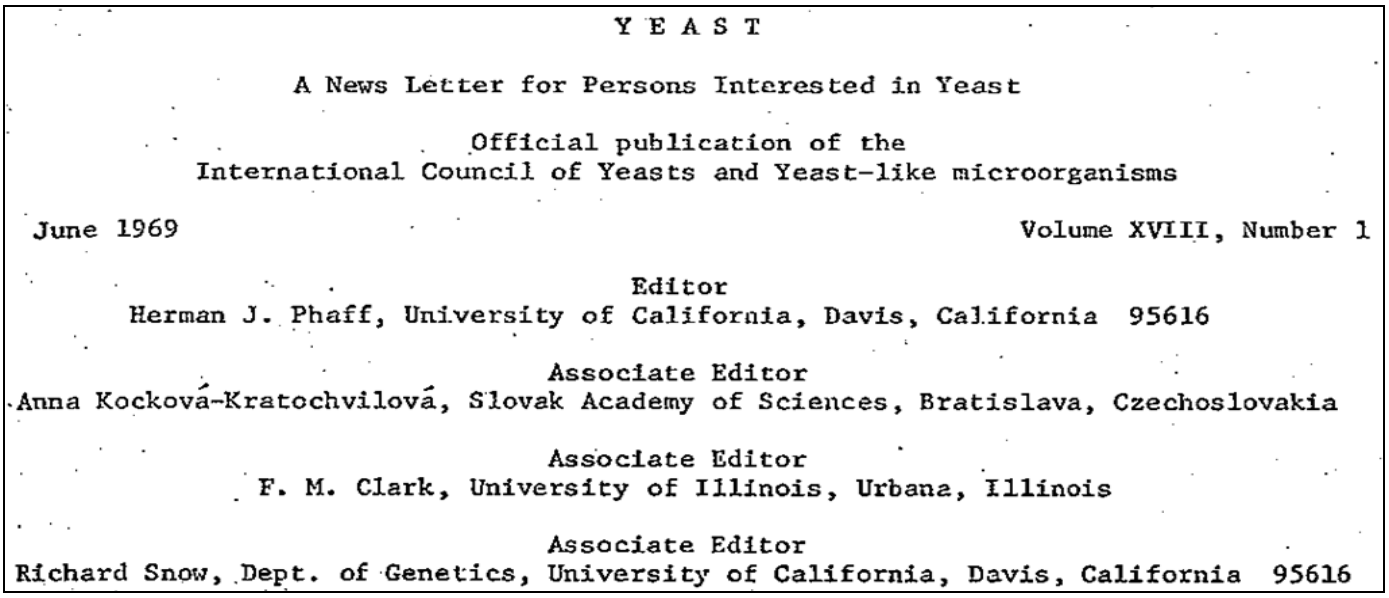
Application deadline: July 3rd, 2019

Research Projects:

Most of the offered projects in this call are collaborative research projects. These projects are highly interdisciplinary, i.e. at least two faculty members of different research areas will significantly contribute with their complementary expertise. Applicants can choose up to three projects of interest:

- Advanced analytical strategies for investigation of alternative methanol assimilation in methylotrophic yeasts
- Enzymatic properties and evolutionary origin of the cancer-associated protease cathepsin O
- Impact of cellular redox state on protein production and secretion in yeast
- Mechanistic synergism between bacterial pyranose oxidase and peroxidase in lignin depolymerization
- Microarrays of natural and remodelled glycans
- O-glycan engineering of N. benthamiana for structure-function characterization of human IgA1
- Resolving dynamic protein conformations in multidomain enzymes with SAXS
- Structure and Function of Hexosaminidases
- The cancer immunotherapy antigen CD19 and its molecular interaction network

Fifty Years Ago



Y E A S T

A News Letter for Persons Interested in Yeast

Official publication of the
International Council of Yeasts and Yeast-like microorganisms

June 1969 Volume XVIII, Number 1

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Dr. M. C. Pignal of the Université De Lyon submitted work for publication. They described three species of *Pichia,* two of *Torulopsis* and two of *Candida*. They examined the use of enzymology for systematics, specifically expression of α-glucosidase, β-galactosidase and β-glucosidase to distinguish *Kluyveromyces wikenii* and *Kl. aestuarii*. Work in progress included base composition (% G + C) in species of *Pichia* and *Kluyveromyces*.

Dr. H. Saëz of the Muséum National D'Histoire Naturelle in Paris listed published or ongoing studies of isolation of yeasts from birds, and mammals with omnivorous, piscivorous, carnivorous or herbivorous diets. [Note: these isolates include type strains of several yeast species, such as *Galactomyces pseudocandidus, Cystofilobasidium ferigula,* and *Debaryomyces coudertii*.] The species *Geotrichum gracile* and *G. pseudocandidum* were described.

Dr. E. Minarík of the Research Institute for Viticulture and Enology, Bratizlava, Czechoslovakia re-examined 32 yeast strains isolated from grapes and found that five fit the description of new species *Saccharomyces inconspicuous* van der Walt.

Prof. S. Windisch of the Universitat Berlin published research on environmental microorganisms, principles of yeast ecology, flocculation of brewing yeasts, osmotolerant yeasts, conjugation of *Saccharomyces*, and a description of *Candida friedrichii*.

Dr. James B. Siinclair of the University of Illinois, Urbana shared abstracts of two papers regarding virulence of *Geotrichum candidum* to chicken eggs, citrus fruits, and turtles.

Drs. F. Schlank and G. Svihla of Argonne National Laboratory in Illinois, USA published a manuscript in the J. Biol. Photographic Association about use of ultraviolet micrography for microbiology. They continue studying the interaction of small proteins with the yeast cell membrane.

Dr. Harlyn O. Halvorson of the University of Wisconsin in Madison, WI, USA published a paper on the redundancy of ribosomal and transfer RNA genes in *Saccharomyces cerevisiae*, and regulation of ribosomal RNA synthesis in yeast. When they compared haploid and polyploid strains, they found that the ratio of RNA to DNA was a function of the growth rate. Using ribosomal RNA-DNA hybridization

experiments, they found that a consistent percentage of the genome (2.4%) was homologous to ribosomal RNA. They also found that ribosomal genes were non-randomly distributed over the chromosomes. They listed three publications on sporulation. They requested information on antifungal agents or antibiotics that are active against yeast, in hopes of finding compounds that could inhibit RNA and protein synthesis to aid their research.

Dr. J. R. Johnston of the University of Strathclyde, Glasgow announced that P. V. Patel completed requirements for the Ph.D., and accepted a fellowship at McMaster University in Ontario. A summary of his thesis on "Genetic studies on resistance to nystatin and amphotericin B in yeast" was presented.

Dr. Yasuji Oshima of Suntory Limited, The Central Research Institute in Osaka, Japan summarized their recent discoveries on genetic control of homothallism versus heterothallism in *Saccharomyces*, which is controlled by genes *HO* and *HM*.

Dr. F. K. Zimmermann of Forstbotanisches Institute in Germany described studies of gene conversion using *S. cerevisiae* diploids heterozygous for the marker gene threonine dehydratase. Intragenic and interallelic complementation were observed among mutants of the is_1 locus, indicating this protein is active as a multi-subunit complex. Difference in pH dependence and substrate affinity in various heterozygous diploids led to conclusions regarding dominance relations and gene dosage effects.

Dr. Miguel Flores da Cunha of the Southwest Center for Advances Studies in Dallas, Texas, USA shared a summary of his doctoral dissertation on parasexuality in *Schizosaccharomyces pombe*.

H. de Robichon-Szulmajster of the Centre National de la Recherche Scientifique, Laboratoire d'Enzymologie, Gif-Sur-Yvette, France published a paper in the European J. Biochem. Titled "Regulation of Isoleucine-Valine Biosynthesis in *Saccharomyces cerevisiae.*"

Prof. Heikki Suomalainen of the Research Laboratoies of the State Alcohol Monopoly (Alko), Helsinki, Finland shared abstracts of publications on the respiratory enzyme activities of anaerobically and aerobically grown baker's and brewer's yeast, fatty acid composition of baker's and brewer's yeast, a review on production and composition of heavy liquors and distilled potable spirits, respiratory enzymes of yeast grown under anaerobic and aerobic conditions, methods for determination of carbonyl compounds in alcoholic solutions, and standardization of methods for determining alcohol content of beverages.

Dr. John G. Kleyn of the University of Puget Sound, Tacoma, Washington, USA described ongoing research topics including yeast flora present in Puget Sound, use of Ethylene Diamine Tetra Acitic [sic] Acid as a new preservative for beer, use of brewer's yeast as an indicator for tracking the flow of a sewage field in Puget Sound, and the effect of sea water on yeast viability and reproduction.

Dr. M. Hilmi Pamir of University of Ankara, Turkey plans to publish recent work on utilization of Turkish sulphite waste liquors for the production of fodder and food yeasts *Torulopsis utilis* and *Candida tropicalis*. The former species had a higher digestibility coefficient of its protein (86.19%)

Prof. T. O. Wikén successfully organized the Third International Symposium on Yeast in Delft and the Hague, June 2 to 6, 1969 with five plenary lectures the first day followed by three simultaneous sessions in subsequent days. The 391 participants were from 30 countries. This was a sharp increase from the previous meetings in Smolenice (60) and Bratislava (145). The participants passed a resolution in favour of organizing specialized Symposia in addition to general Symposia and approved a proposal by the Council for International Cooperation in Yeast Science for the following specialized symposia:

- 1971 (Smolenice, Czechoslovakia): Characterization of yeast by genetics, cytology, ecology and biochemistry
- 1972 (Japan): In connection with the Fourth International Fermentation Symposium, on technological, medical and ecological aspects
- 1973 (Helsinki, Finland): Metabolism and regulation of cellular processes

The location of the next General Symposium on Yeasts in 1974 was proposed to be in either Austria, the USA, the USSR, or elsewhere.

It was decided that in succeeding years, the chairman and secretary of the organizing committee of the general symposium shall remain in office until the next general symposium.

It was decided that the Yeast News Letter edited by Professor Dr. H. J. Phaff, Davis, California be adopted as the official medium of communication between the Council and workers in yeast science.

Dr. D. G. Ahearn invited readers to a meeting on "Recent Trends in Yeast Research" on August 15 and 16 in Plattsburgh, New York. Speakers included Cletus Kurtzman, Donald Ahearn, Sally Meyer, Lynferd Wickerham, Herman Phaff, Martin Miller, Jack Fell, and others.

The first volume of "The Yeasts", edited by **A. H. Rose and J. S. Harrison**, was to be published in April 1969. A detailed list of all chapters in all three volumes to be published in 1969 and 1970 was given.

The editor [Herman Phaff] thanked retiring associate editors of the Yeast News Letter Leslie R. Hedrick and Cecil G. Dunn for their service. He also acknowledged the contributions of Dr. E. M. Mrak, first editor of the Yeast News Letter and retiring chancellor of the University of California Davis.

Communicated by Kyria Boundy-Mills, Phaff Yeast Culture Collection, University of California Davis

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