Yeast

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

Editorial

Gennadi Naumov (1944-2018)

With much regret I must announce the death of our colleague Gennadi Naumov, this past May. A well-known yeast geneticist, Gennadi applied genetic compatibility to the problem of taxon delineation. He made important contributions to our understanding of the evolutionary genetics of *Saccharomyces*. He was a prominent member of the yeast research community, attending most meetings of the International Commission on Yeasts, providing regular contributions to the Yeast Newsletter, and visiting most laboratories interested in yeast evolution worldwide. On behalf of all readers, I offer my sincere condolences to his wife Elena.

M.A. Lachance, Editor

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Recent publication

1 Carreté L, Ksiezopolska E, Pegueroles C, Gómez-Molero E, Saus E, Iraola-Guzmán S, Loska D, Bader O, Fairhead C, Gabaldón T. 2018. Patterns of genomic variation in the opportunistic pathogen *Candida glabrata* suggest the existence of mating and a secondary association with humans. Curr Biol 28(1): 15-27.e7. doi: 10.1016/j.cub.2017.11.027

Candida glabrata is an opportunistic fungal pathogen that ranks as the second most common cause of systemic candidiasis. Despite its genus name, this yeast is more closely related to the model yeast *Saccharomyces cerevisiae* than to other *Candida* pathogens, and hence its ability to infect humans is thought to have emerged independently. Moreover, *C. glabrata* has all the necessary genes to undergo a sexual cycle but is considered an asexual organism due to the lack of direct evidence of sexual reproduction. To reconstruct the recent evolution of this pathogen and find footprints of sexual reproduction, we assessed genomic and phenotypic variation across 33 globally distributed *C. glabrata* isolates. We catalogued extensive copy-number variation, which particularly affects genes encoding cell-wall-associated proteins, including adhesins. The observed level of genetic variation in *C. glabrata* is significantly higher than that found in *Candida albicans*. This variation is structured into seven deeply divergent clades, which show recent geographical dispersion and large within-clade genomic and phenotypic differences. We show compelling evidence of recent admixture between differentiated lineages and of purifying selection on mating genes, which provides the first evidence for the existence of an active sexual cycle in this yeast. Altogether, our data point to a recent global spread of previously genetically isolated populations and suggest that humans are only a secondary niche for this yeast.

II Bioprocess & Metabolic Engineering Lab (LEMeB), University of Campinas, Campinas, São Paulo, Brazil. Communicated by Andreas K. Gombert <gombert@unicamp.br>.

LEMeB's recent activities can be followed at https://sites.google.com/site/unicampfealemeb/

Recent publications.

1 da Costa BLV, Basso TO, Raghavendran V, Gombert AK. 2018 Anaerobiosis revisited: growth of *Saccharomyces cerevisiae* under extremely low oxygen availability. Appl Microbiol Biotechnol 102(5):2101-2116. doi: 10.1007/s00253-017-8732-4. Review. Erratum in: Appl Microbiol Biotechnol 2018 Apr 27 - PubMed PMID: 29397429.

2 Marques WL, Mans R, Henderson RK, Marella ER, Horst JT, Hulster E, Poolman B, Daran JM, Pronk JT, Gombert AK, van Maris AJA. 2017 Combined engineering of disaccharide transport and phosphorolysis for enhanced ATP yield from sucrose fermentation in *Saccharomyces cerevisiae*. Metab Eng 45:121-133. doi:10.1016/j.ymben.2017.11.012. PubMed PMID: 29196124.

3 Dias O, Basso TO, Rocha I, Ferreira EC, Gombert AK. 2017 Quantitative physiology and elemental composition of *Kluyveromyces lactis* CBS 2359 during growth on glucose at different specific growth rates. Antonie Van Leeuwenhoek 111(2):183-195. doi: 10.1007/s10482-017-0940-5. Erratum in: Antonie Van Leeuwenhoek. 2017 Oct 12;:. PubMed PMID: 28900755.

4 Raghavendran V, Basso TP, da Silva JB, Basso LC, Gombert AK. 2017 A simple scaled down system to mimic the industrial production of first generation fuel ethanol in Brazil. Antonie Van Leeuwenhoek 110(7):971-983. doi: 10.1007/s10482-017-0868-9. PubMed PMID: 28470565.

III 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 Lachance MA, Hittinger CT. 2018. Introducing 'ecoYeast': ecology and communities of yeasts. Yeast 35: 313. (call for papers)

Building on the success of the Yeast Primer series, the ecoYeast collection of invited reviews begins in this issue with an article by Irene Stefanini on the ecology of yeasts associated with insects. In keeping with the desire to feature research on a broad diversity of potential model organisms, often (and oddly) referred to as 'non conventional' yeasts, *Yeast*'s Editorial Board wishes to headline emerging knowledge of yeast ecology. ecoYeast will focus on yeast rich communities found in both natural and anthropogenic habitats. Rather than report on specific yeasts, reviews will cover aquatic or terrestrial habitats such as the sea, the soil, the plant–insect interface or methanol rich substrates, as well as domestic realms, such as the vineyard and other agricultural settings, the clinical microbiome, the cheese house, the bakery or the brewery. We are grateful for the generous reception met by our invitation to experts in yeast ecology to provide these timely summaries. Readers can expect a dozen or so such articles to appear in the next several months. The Yeast Primer series will continue to offer invited reviews that are focused on specific emerging or non conventional model yeasts, including our recent emphasis on model clades and genera.

2 Hittinger CT, Steele JL, Ryder DS. 2018. Diverse yeasts for diverse fermented beverages and foods. Curr Opin Biotechnol 49: 199-206. (review)

Yeasts play vital roles in food biotechnology, especially in fermented products. Yeasts are monoculture bioprocessing agents, are members of complex microbial communities, and are even consumed directly. Advances in genetic technologies, such as whole genome and environmental DNA sequencing, have shed light on the diverse yeasts used in both traditional and industrialized processes. The yeast *Saccharomyces cerevisiae* plays an outsized role in fermented beverage and food production, but new research has revealed a cornucopia of yeast biodiversity that includes dozens of species. These often surprising studies have shown how yeasts are related, how they interact with other microbes, and how valuable traits are encoded in their genomes. This deeper understanding illuminates current practices in food biotechnology, while foreshadowing future innovation.

3 Peris D, Pérez-Torrado R, Hittinger CT, Barrio E, Querol A. 2018. On the origins and industrial applications of *Saccharomyces cerevisiae* x *Saccharomyces kudriavzevii* hybrids. Yeast 35: 51-69. (review)

Companies based on alcoholic fermentation products, such as wine, beer, and biofuels, use yeasts to make their products. Each industrial process utilizes different media conditions, which differ in sugar content, the presence of inhibitors, and fermentation temperatures. *Saccharomyces cerevisiae* has traditionally been the main yeast responsible for most fermentation processes. However, the market is changing due to the consumer demands or external factors, such as climate change. Some processes, such as biofuel production or winemaking, require new yeasts to solve specific challenges, especially those associated with sustainability, novel flavors, and altered alcohol contents. One of the proposed solutions is the application of yeast hybrids. The lager beer market has been dominated by *S. cerevisiae* x *Saccharomyces eubayanus* hybrids. However, several less thoroughly studied hybrids have been isolated from other diverse industrial processes. Here we focus on *S. cerevisiae* x *Saccharomyces kudriavzevii* hybrids, which have been isolated from diverse industrial conditions that include wine, ale beer, cider, and dietary supplements. Emerging data suggest an extended and complex story of adaptation of these hybrids to traditional industrial conditions. *S. cerevisiae* x *S. kudriavzevii* hybrids are also being

explored for new industrial applications, such as biofuels. This review describes the past, present, and future of *S. cerevisiae* x *S. kudriavzevii* hybrids.

4 Kuang MC, Kominek J, Alexander WG, Cheng J-F, Wrobel RL, Hittinger CT. Repeated cis-regulatory tuning of a metabolic bottleneck gene during evolution. Mol Biol Evol - in press.

Repeated evolutionary events imply underlying genetic constraints that can make evolutionary mechanisms predictable. Morphological traits are thought to evolve frequently through cis-regulatory changes because these mechanisms bypass constraints in pleiotropic genes that are reused during development. In contrast, the constraints acting on metabolic traits during evolution are less well studied. Here we show how a metabolic bottleneck gene has repeatedly adopted similar cis-regulatory solutions during evolution, likely due to its pleiotropic role integrating flux from multiple metabolic pathways. Specifically, the genes encoding phosphoglucomutase activity (*PGM1*/*PGM2*), which connect *GAL*actose catabolism to glycolysis, have gained and lost direct regulation by the transcription factor Gal4 several times during yeast evolution. Through targeted mutations of predicted Gal4-binding sites in yeast genomes, we show this galactose-mediated regulation of *PGM1/2* supports vigorous growth on galactose in multiple yeast species, including *Saccharomyces uvarum* and *Lachancea kluyveri*. Furthermore, the addition of galactose-inducible *PGM1* alone is sufficient to improve the growth on galactose of multiple species that lack this regulation, including *Saccharomyces cerevisiae*. The strong association between regulation of *PGM1/2* by Gal4 even enables remarkably accurate predictions of galactose growth phenotypes between closely related species. This repeated mode of evolution suggests that this specific cis-regulatory connection is a common way that diverse yeasts can govern flux through the pathway, likely due to the constraints imposed by this pleiotropic bottleneck gene. Since metabolic pathways are highly interconnected, we argue that cis-regulatory evolution might be widespread at pleiotropic genes that control metabolic bottlenecks and intersections.

5 Krassowski T, Coughlan AY, Shen XX, Zhou X, Kominek J, Opulente DA, Riley R, Grigoriev IV, Maheshwari N, Shields DC, Kurtzman CP,Hittinger CT, Rokas A, Wolfe KH. 2018. Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. Nat Commun 9: 1887.

The genetic code used in nuclear genes is almost universal, but here we report that it changed three times in parallel during the evolution of budding yeasts. All three changes were reassignments of the codon CUG, which is translated as serine (in 2 yeast clades), alanine (1 clade), or the 'universal' leucine (2 clades). The newly discovered Ser2 clade is in the final stages of a genetic code transition. Most species in this clade have genes for both a novel $tRNA^{Ser}$(CAG) and an ancestral $tRNA^{Leu}$(CAG) to read CUG, but only $tRNA^{Ser}$(CAG) is used in standard growth conditions. The coexistence of these alloacceptor tRNA genes indicates that the genetic code transition occurred via an ambiguous translation phase. We propose that the three parallel reassignments of CUG were not driven by natural selection in favor of their effects on the proteome, but by selection to eliminate the ancestral $tRNA^{Leu}$(CAG).

6 Gonçalves C, Wisecaver JH, Kominek J, Oom MS, Leandro MJ, Shen XX, Opulente DA, Zhou X, Peris D, Kurtzman CP, Hittinger CT, Rokas A, Gonçalves P. 2018. Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. eLife 7: e33034.

Fructophily is a rare trait that consists of the preference for fructose over other carbon sources. Here, we show that in a yeast lineage (the *Wickerhamiella*/*Starmerella*, W/S clade) comprised of fructophilic species thriving in the high-sugar floral niche, the acquisition of fructophily is concurrent with a wider remodeling of central carbon metabolism. Coupling comparative genomics with biochemical and genetic approaches, we gathered ample evidence for the loss of alcoholic fermentation in an ancestor of the W/S clade and subsequent reinstatement through either horizontal acquisition of homologous bacterial genes or modification of a pre-existing yeast gene. An enzyme required for sucrose assimilation was also acquired from bacteria, suggesting that the genetic novelties identified in the W/S clade may be related to adaptation to the high-sugar environment. This work shows how even central carbon metabolism can be remodeled by a surge of HGT events.

7 Opulente DA, Rollinson EJ, Bernick-Roehr C, Hulfachor AB, Rokas A, Kurtzman CP, Hittinger CT. 2018. Factors driving metabolic diversity in the budding yeast subphylum. BMC Biol 16: 26.

BACKGROUND: Associations between traits are prevalent in nature, occurring across a diverse range of taxa and traits. Individual traits may co-evolve with one other, and these correlations can be driven by factors intrinsic or extrinsic to an organism. However, few studies, especially in microbes, have simultaneously investigated both across a broad taxonomic range. Here we quantify pairwise associations among 48 traits across 784 diverse yeast species of the ancient budding yeast subphylum Saccharomycotina, assessing the effects of phylogenetic history, genetics, and ecology. RESULTS: We find extensive negative (traits that tend to not occur together) and positive (traits that tend to co-occur) pairwise associations among traits, as well as between traits and environments. These associations can largely be explained by the biological properties of the traits, such as overlapping biochemical pathways. The isolation environments of the yeasts explain a minor but significant component of the variance, while phylogeny (the retention of ancestral traits in descendant species) plays an even more limited role. Positive correlations are pervasive among carbon utilization traits and track with chemical structures (e.g., glucosides and sugar alcohols) and metabolic pathways, suggesting a molecular basis for the presence of suites of traits. In several cases, characterized genes from model organisms suggest that enzyme promiscuity and overlapping biochemical pathways are likely mechanisms to explain these macroevolutionary trends. Interestingly, fermentation traits are negatively correlated with the utilization of pentose sugars, which are major components of the plant biomass degraded by fungi and present major bottlenecks to the production of cellulosic biofuels. Finally, we show that mammalian pathogenic and commensal yeasts have a suite of traits that includes growth at high temperature and, surprisingly, the utilization of a narrowed panel of carbon sources. CONCLUSIONS: These results demonstrate how both intrinsic physiological factors and extrinsic ecological factors drive the distribution of traits present in diverse organisms across macroevolutionary timescales.

8 Vakirlis N, Hebert AS, Opulente DA, Achaz G, Hittinger CT, Fischer G, Coon JJ, Lafontaine I. 2018. A molecular portrait of de novo genes in yeasts. Mol Biol Evol 35: 631-645.

New genes, with novel protein functions, can evolve "from scratch" out of intergenic sequences. These *de novo* genes can integrate the cell's genetic network and drive important phenotypic innovations. Therefore, identifying de novo genes and understanding how the transition from noncoding to coding occurs are key problems in evolutionary biology. However, identifying de novo genes is a difficult task, hampered by the presence of remote homologs, fast evolving sequences and erroneously annotated protein-coding genes. To overcome these limitations, we developed a procedure that handles the usual pitfalls in de novo gene identification and predicted the emergence of 703 de novo gene candidates in 15 yeast species from 2 genera whose phylogeny spans at least 100 million years of evolution. We validated 85 candidates by proteomic data, providing new translation evidence for 25 of them through mass spectrometry experiments. We also unambiguously identified the mutations that enabled the transition from noncoding to coding for 30 *Saccharomyces de novo* genes. We established that de novo gene origination is a widespread phenomenon in yeasts, only a few being ultimately maintained by selection. We also found that de novo genes preferentially emerge next to divergent promoters in GC-rich intergenic regions where the probability of finding a fortuitous and transcribed ORF is the highest. Finally, we found a more than 3-fold enrichment of *de novo* genes at recombination hot spots, which are GC-rich and nucleosome-free regions, suggesting that meiotic recombination contributes to *de novo* gene emergence in yeasts.

9 Zhou X, Shen XX, Hittinger CT, Rokas A. 2018. Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. Mol Biol Evol 35: 486-503.

The sizes of the data matrices assembled to resolve branches of the tree of life have increased dramatically, motivating the development of programs for fast, yet accurate, inference. For example, several different fast programs have been developed in the very popular maximum likelihood framework, including RAxML/ExaML, PhyML, IQ-TREE, and Fast Tree. Although these programs are widely used, a

systematic evaluation and comparison of their performance using empirical genome-scale data matrices has so far been lacking. To address this question, we evaluated these four programs on 19 empirical phylogenomic data sets with hundreds to thousands of genes and up to 200 taxa with respect to likelihood maximization, tree topology, and computational speed. For single-gene tree inference, we found that the more exhaustive and slower strategies (ten searches per alignment) outperformed faster strategies (one tree search per alignment) using RAxML, PhyML, or IQ-TREE. Interestingly, single-gene trees inferred by the three programs yielded comparable coalescent-based species tree estimations. For concatenation-based species tree inference, IQ-TREE consistently achieved the best-observed likelihoods for all datasets, and RAxML/ExaML was a close second. In contrast, PhyML often failed to complete concatenation-based analyses, whereas FastTree was the fastest but generated lower likelihood values and more dissimilar tree topologies in both types of analyses. Finally, data matrix properties, such as the number of taxa and the strength of phylogenetic signal, sometimes substantially influenced the programs' relative performance. Our results provide real-world gene and species tree phylogenetic inference benchmarks to inform the design and execution of large-scale phylogenomic data analyses.

IV Food and Bioproduct Sciences, Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon SK S7N5A8 Canada (Retired to 1421 Saturna Drive, Parksville, B.C. V9P2Y1 Canada). Communicated by W.M. (Mike) Ingledew <mike.ingledew@usask.ca>.

The following are recent publications.

Journal Article.

1 Ingledew WM. 2015. Wallowing with the yeasts used to make alcohol. J. Am. Soc. Brew. Chem. 73(3):209-222.

Book Chapters.

2 Ingledew WM. 2017. Yeast stress and fermentation. Chapter 18. *The Alcohol Textbook 6th Edition.* Ethanol Technology Institute, Duluth Georgia. Eds. Walker G, Abbas CA, Ingledew WM and Pilgrim C. pp. 273-285.

3 Ingledew WM. 2017. Commercial yeast production for distilled beverage and fuel alcohol fermentations. Chapter 20. The Alcohol Textbook 6th Edition. Ethanol Technology Institute, Duluth Georgia. Eds. Walker G, Abbas CA, Ingledew WM and Pilgrim C. pp. 299-320.

4 Ingledew WM. 2017. Very high gravity (VHG) and associated new technologies for fuel alcohol production. Chapter 23. The Alcohol Textbook 6th Edition. Ethanol Technology Institute, Duluth Georgia. Eds. Walker G, Abbas CA, Ingledew WM and Pilgrim C. pp. 363-376.

V Department of Microbial Biotechnology, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran. Commuunicated by S. Nasr <nasr@ibrc.ir>

I am pleased to announce that my organization has been accepted as a formal member of ACM (the Asian Consortium for the Conservation and Sustainable Use of Microbial Resources) during the 14th meeting which was held on December 04 – 06, 2017 in Taipei, Taiwan. The following is an abstract presented at the meeting.

1 Mohammad Ali Amoozegar, Shaghayegh Nasr, Seyed Abolhassan Shahzadeh Fazeli. 2018. Microorganisms Bank of Iranian Biological Resource Center (IBRC) - www.ibrc.ir

According to the data available at the World Data Center for Microorganisms (WDCM) of World Federation for Culture Collection (WFCC), Iran (of I.R.) has 8 registered Culture Collections that preserve microbial strains. Microorganisms Bank was founded on 2008 under the authority of Academic Center for

Education, Culture and Research (ACECR) and housed within the Biological Resource Center (IBRC) in Iran (I.R. of) and it is one of the largest public collection of microorganisms in the country and a member of WFCC [WDCM950]. Collection has currently containing strains of archaea, bacteria, filamentous fungi, yeasts and algae that can be handled in Biosafety level 1 or 2 facilities (Risk Group 1 or 2). It has been acquired the certification of ISO 9001:2008 for its quality management system to maintain and improve the quality of its services. All biological materials accepted in the collection are subject to extensive quality control and physiological and molecular characterization. In addition, Micro-organisms Bank provides an extensive documentation and detailed diagnostic information on the biological material. At present, it holds more than 3907 microorganisms, majority of which are isolated under internal research projects while others are deposited by investigators across the country or obtained from other reputable culture collections around the world. These cultures are available for research purpose to the investigators around the world who wish to undertake large scale screening programs, with Material Transfer Agreement (MTA). Microorganisms Bank of IBRC provides various services on payment basis which are as follow: Supply of cultures; Culture deposit service, Identification services and other Services that include services like isolation and purification of microorganisms with certain biotechnological potential, isolation and purification of genomic DNA and Freeze-drying of microbial cultures or biomass. Apart from providing various research related services, IBRC is also involved in the highest quality research. The center is actively involved in research which is focused on microbial diversity, metagenomics, ecology and taxonomy using classical as well as modern molecular approaches. Expertise and publication records of bank reflect the research potential of the center. At present a total of 18 staff members including senior researcher (3), consultant (2), technicians (12) and administrative staff (1) are making their efforts to maintain the standards of the research and services at Microorganisms Bank of IBRC. IBRC offer career oriented workshops in microbiology and related areas. The organization tries to keep the balance of practical and theoretical guidance. Time table of these programs designed to provide the trainees with ample time for hand on experiences on instruments and equipment are available at our center. IBRC also accepts master and Ph.D. students across the country to carry out their research project as part of their degree in the field of microbial diversity and taxonomy. It also accept application from foreign students under exchange/bilateral programs to carry out training or research studies. In the future, IBRC will continue to provide high quality microbial resources, information and techniques to support and promote the development of bio-industry in Iran.

Recent publications.

2 Shaghayegh Nasr, Mona Mohammadimehr, Marzieh Geranpayeh Vaghei, Mohammad Ali Amoozegar, Seyed Abolhassan Shahzadeh Fazeli. 2018. *Aureobasidium mangrovei* sp. nov., an ascomycetous species recovered from Hara protected forests in the Persian Gulf, Iran. Antonie van Leeuwenhoek - https://doi.org/10.1007/s10482-018-1059-z

A new ascomycetous black yeast-like species was recovered from healthy plant (*Avicennia marina*) of Hara protected mangrove forests at Qeshm Island, Iran. Morphological, physiological analysis as well as a molecular analysis of the internal transcribed spacer (ITS) and partial large ribosomal subunit (D1/ D2 domains) confirmed the placement of this strain in the genus *Aureobasidium* and based on considerable sequence divergence, distinguishable cardinal growth temperatures and salt tolerance a new species *Aureobasidium mangrovei* sp. nov. is proposed. However, the type strain micro-morphologically is not clearly distinguishable from other members of the genus. The type strain, *Aureobasidium mangrovei* was preserved in a metabolically inactive state at the Iranian Biological Resource Centre, Tehran, Iran as IBRCM 30265T and the ex-type culture is deposited in the CBS yeast collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands as CBS 142205T. The GenBank accession numbers for the nucleotide sequences of the large subunit ribosomal DNA and ITS region are KY089084 and KY089085, respectively. The MycoBank number of the new species is MB 823444.

3 Shaghayegh Nasr, Steffen Bien, Mohammad Reza Soudi, Nayyereh Alimadadi, Seyed Abolhassan Shahzadeh Fazeli, Ulrike Damm. 2018. Novel *Collophorina* and *Coniochaeta* species from *Euphorbia polycaulis*, an endemic plant in Iran. Mycological Progress - https://doi.org/10.1007/s11557-018-1382-9

During a study on the biodiversity of yeasts and yeast-like ascomycetes from wild plants in Iran, four strains of yeast-like filamentous fungi were isolated from a healthy plant of Euphorbia polycaulis in the Qom Province, Iran (IR. of). All four strains formed small hyaline one-celled conidia from integrated conidiogenous cells directly on hyphae and sometimes on discrete phialides, as well as by microcyclic conidiation. Two strains additionally produced conidia in conidiomata that open by rupture. The internal transcribed spacer (ITS) sequences suggested the placement of these strains in the genera Collophorina (Leotiomycetes) and Coniochaeta (Sordariomycetes), respectively. Blast search results on NCBI GenBank and phylogenetic analyses of ITS, the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and the translation elongation factor 1α (EF-1α) sequences, and the nuclear large subunit ribosomal gene (LSU), partial actin (ACT), and β-tubulin (TUB) sequences, respectively, revealed the isolates to belong to three new species, that are described here as *Collophorina euphorbiae*, *Coniochaeta iranica*, and *C. euphorbiae*. All three species are characterised by morphological, physiological, and molecular data.

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

The following are papers for 2017 and 2018 or in press.

1 Shalamitskyi MYu, Naumov GI. 2017. Phylogenetic analysis of pectinases of ascomycetous yeasts. Biotekhnologiya (Moscow) 6: 28–36.

2 Naumova ES, Sadykova AZh, Martynenko NN, Naumov GI. 2017. Hybrid selection of *Saccharomyces cerevisiae* yeasts for thermotolerance and fermentation activity. Microbiology (Moscow) 87(2): 215–221.

3 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 (in press).

Five methylotrophic strains (UCDFST 71-1024^T, UCDFST 54-11.16, UCDFST 54-11.141, UCDFST 68-967.1 and UCDFST 74-1030) from the Phaff Yeast Culture Collection (University of California Davis, USA) that were originally designated as *Pichia pastoris* were found to represent a novel *Komagataella* species. Strains of *Komagataella mondaviorum* sp. nov. UCDFST 71-1024^T(type strain) = CBS 15017, UCDFST 54-11.16, UCDFST 54-11.141, UCDFST 68-967.1, and UCDFST 74-1030 were isolated in USA, respectively, from cottonwood tree *Populus deltoides* in 1971 (Davis, CA), slime flux of *Quercus* sp. in 1954 (CA), exudate of black oak *Q. kelloggii* in 1954 (Central Sierra Nevada. CA), dry frass from *Salix* sp. in 1968 (Soleduck Road, Olympic National Park, WA) and from flux of hackberry tree *Celtis* sp. in 1974 (CA). The new species was differentiated from *K. kurtzmanii*, *K. pastoris*, *K. phaffii*, *K. populi*, *K. pseudopastoris* and *K. ulmi* by divergence in gene sequences for D1/D2 LSU rRNA, ITS1-5.8S-ITS2, RNA polymerase subunit I and translation elongation factor-1α. *Komagataella mondaviorum* sp. nov. is registered in MycoBank under MB 821789.

VII National Collection of Agricultural and Industrial Microorganisms, Faculty of Food Science, Szent István University, Somlói út 14-16, H-1118 Budapest, Hungary. Communicated by Gábor Péter <Peter.Gabor@etk.szie.hu>.

Please note that our collection has been transferred from Corvinus University of Budapest to Szent István University.

The following articles have been published since our latest report.

1 Morais CG, Lara CA, Oliveira ES, Péter, G, Dlauchy D & Rosa CA. 2016. *Spencermartinsiella silvicola* sp. nov., a yeast species isolated from rotting wood. Int J Syst Evol Microbiol 66: 604-608

Three strains of a new xylanase-producing yeast species were isolated from rotting wood samples collected in the Atlantic Rain Forest of Brazil. The sequences of the internal transcribed spacer region and D1/D2 domains of the large subunit of the rRNA gene showed that this novel yeast species belongs to the genus *Spencermartinsiella*, and its closest relatives among recognized species are *Spencermartinsiella europaea* and *Spencermartinsiella ligniputridi*. A novel species, named *Spencermartinsiella silvicola* sp. nov., is proposed to accommodate these isolates. The type strain is UFMG-CM-Y274^T (=CBS 13490^T). The MycoBank number is MB 813053. In addition, *Candida cellulosicola* is reassigned to the genus *Spencermartinsiella* as a new combination.

2 James SA, Bond CJ, Stanley R, Ravella SR, Peter G, Dlauchy D, Roberts IA. 2016 *Apiotrichum terrigenum* sp. nov., a novel soil-associated yeast found in both the UK and mainland Europe. Int J Syst Evol Microbiol 66: 5046-5050

Five arthroconidium-producing yeast strains representing a novel *Trichosporon*-like species were independently isolated from the UK, Hungary and Norway. Two strains (Bio4^T and Bio21) were isolated from biogas reactors used for processing grass silage, with a third strain (S8) was isolated from soil collected at the same UK site. Two additional strains were isolated in mainland Europe, one from soil in Norway (NCAIM Y.02175) and the other from sewage in Hungary (NCAIM Y.02176). Sequence analyses of the D1/D2 domains of the LSU rRNA gene and internal transcribed spacer (ITS) region indicated that the novel species belongs to the recently reinstated genus Apiotrichum and is most closely related to Apiotrichum scarabaeorum, a beetle-associated species first found in South Africa. Despite having similar physiological characteristics, the two species can be readily distinguished from one another by ITS sequencing. The species name Apiotrichum terrigenum sp. nov. is proposed to accommodate these strains, with Bio4^T (=CBS 11373^T=NCYC 3540^T) designated as the type strain. The Mycobank deposit number is MB817431.

3 Péter G, Dlauchy D, Tóbiás A, Fülöp L, Podgorsek M, Cadez N. 2017. *Brettanomyces acidodurans* sp. nov., a new acetic acid producing yeast species from olive oil. Antonie van Leeuwenhoek 110: 657-664

Two yeast strains representing a hitherto undescribed yeast species were isolated from olive oil and spoiled olive oil originating from Spain and Israel, respectively. Both strains are strong acetic acid producers, equipped with considerable tolerance to acetic acid. The cultures are not short-lived. Cellobiose is fermented as well as several other sugars. The sequences of their large subunit (LSU) rRNA gene D1/D2 domain are very divergent from the sequences available in the GenBank. They differ from the closest hit, *Brettanomyces naardenensis* by about 27%, mainly substitutions. Sequence analyses of the concatenated dataset from genes of the small subunit (SSU) rRNA, LSU rRNA and translation elongation factor-1α (EF-1α) placed the two strains as an early diverging member of the *Brettanomyces*/*Dekkera* clade with high bootstrap support. Sexual reproduction was not observed. The name *Brettanomyces acidodurans* sp. nov. (holotype: NCAIM Y.02178^T; isotypes: CBS 14519^T = NRRL Y-63865^T = ZIM 2626T, MycoBank no.: MB 819608) is proposed for this highly divergent new yeast species.

4 Yurkov AM, Dlauchy D, Péter, G. 2017. *Meyerozyma amylolytica* sp. nov. from temperate deciduous trees and the transfer of five *Candida* species to the genus *Meyerozyma*. Int J Syst Evol Microbiol 67: 3977-3981; doi: 10.1099/ijsem.0.002232

In the course of two independent studies three yeasts have been isolated from temperate deciduous trees in Hungary and Germany. Analyses of nucleotide sequences of D1/D2 domains of the 26S rRNA gene (LSU) suggested that these strains belong to the *Meyerozyma* clade in Debaryomycetaceae (Saccharomycetales). The phylogenetic analysis of a concatenated alignment of the ITS region and LSU gene sequences confirmed the placement of the three strains in the *Meyerozyma* clade close to *Candida elateridarum*. If mixed in proper combinations, the strains formed one to two hat shaped ascospores in deliquescent asci. In addition to the ascospore formation, the three studied strains differed from *Candida elateridarum* and other members of the *Meyerozyma* clade in terms of ribosomal gene sequence and some physiological properties. To accommodate the above-noted strains, we describe the new species as *Meyerozyma amylolytica* sp. nov. (holotype: DSM 27310^{T}; ex-type cultures: NCAIM $Y.02140^{T}$=MUCL 56454^{T}, allotype: NCAIM $Y.01955^{A}$; ex-allotype culture: DSM 27468), MB 821663. Additionally, we propose the transfer of five non-ascosporic members of the *Meyerozyma* clade to the genus *Meyerozyma* as the following new taxonomic combinations *Meyerozyma athensensis* f.a., comb. nov. (MB 821664), *Meyerozyma carpophila* f.a., comb. nov. (MB 821665), *Meyerozyma elateridarum* f.a., comb. nov. (MB 821666), *Meyerozyma neustonensis* f.a., comb. nov. (MB 821667), and *Meyerozyma smithsonii* f.a., comb. nov. (MB 821668).

5 Čadež N, Dlauchy D, Tóbiás A, Péter G. 2017. *Kuraishia mediterranea* sp. nov., a methanol-assimilating yeast species from olive oil and its sediment. Int J Syst Evol Microbiol 67: 4846-4850; doi: 10.1099/ijsem.0.002392

Six yeast strains isolated from olive oil sediments and spoiled olive oils originating from Slovenia and Portugal, respectively, proved to represent an undescribed yeast species based on DNA sequence comparisons. The analysis of gene sequences for internal transcribed spacer regions and the large subunit rRNA gene D1/D2 domain placed the novel species in the genus *Kuraishia* in a subclade containing *Kuraishia capsulata*, the type species of the genus. Although the novel species is well separated genetically from the recognized species of the genus, only a minor phenotypic difference differentiating it from *Kuraishia capsulata* and *K. molischiana* was observed. Relevant to its isolation source, no lipolytic activity was detected in the strains of the novel species. To accommodate the above-noted strains, *Kuraishia mediterranea* sp. nov. (holotype: ZIM 2473T; isotype: CBS 15107T; MycoBank no.: MB 822817) is proposed.

6 Péter G, Takashima M, Čadež N. 2017. Yeast habitats: different but global. In: Buzzini P, Lachance MA, Yurkov A (eds) Yeasts in Natural Ecosystems: Ecology. Springer pp 39-71.

Yeasts, a taxonomically heterogenic group of unicellular fungi, populate many different habitats on our planet. They occur in aquatic and terrestrial environments and also in the atmosphere; however, they are not evenly distributed. While some species are ubiquitous generalists occurring in wide geographic range and dwelling in different habitats, others may have more restricted distribution either geographically or by habitats. Some are known from very few isolates, and about one third of the known yeast species are represented by only one strain. In these cases their ecology remains to be elucidated. As nonmotile organisms their dispersal depends on the vectors carrying them. Insects are of outstanding importance among yeast vectors. Several exciting questions can be raised about the habitat-yeasts-vector associations. For example, which yeasts are there? Why are they only there? How did they get there? What are they doing there? The last two decades witnessed the widespread application of DNA sequencing, providing quicker and more reliable yeast identification than earlier phenotype-based methods. Nowadays, the culture-independent methods are gaining ground in the study of biodiversity and ecology of yeasts. In this chapter some new achievements from the field of habitat-yeasts-vector system are introduced and are embedded in a broader context.

VIII International Centre for Brewing and Distilling, Heriot Watt University, Edinburgh, Scotland EH14 4AS. and GGStewart Associates, 13 Heol Nant Castan, Rhiwbina, Cardiff, Wales, CF14 6RP. Communicated by Graham G. Stewart
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Recent publications.

1 Walker GM and Stewart GG. 2016. *Saccharomyces cerevisiae* in the production of fermented beverages. Beverages 2016, Pub. by MDPI AG, Basel, Switzerland 2: 30.

2 Stewart GG. 2016. *Saccharomyces* species in the production of beer. Beverages 2016, Pub. by MDPI AG, Basel, Switzerland 2: 34.

3 Stewart GG. 2017. Brewer's yeast propagation – the basic principles. Master Brewers Association of the Americas, Technical Quarterly 54: 125-131.

4 Stewart GG. 2017. The production of secondary metabolites with flavor potential during brewing and distilling wort fermentations. Fermentation Pub. by MDPI AG, Basel, Switzerland, 3: 63.

5 Stewart GG. 2017. Brewing and Distilling Yeasts. Pub. by Springer, Berlin ISBN 978-3-319-69126-8.

6 Stewart GG, Anstruther AM and Russell I (eds.) 2018, Handbook of Brewing, 3rd Ed., Pub. by Taylor & Francis, Boca Raton, Fl. ISBN 13-978-1-4987-5191.

7 Stewart GG. 2018. Yeast flocculation – sedimentation and flotation. Fermentation, Pub. by MDPI AG, Basel, Switzerland, 4: 28.

8 Stewart GG. 2018. Management of yeast species and strains in a multiproduct brewery. In Proc. 35th Convention of the Institute of Brewing and Distilling, Asia Pacific Section.

IX VTT Technical Research Centre of Finland Ltd, Solutions for Natural Resources and Environment, Tietotie 2, Espoo, FI-02044 VTT, Finland. Communicated by Brian Gibson <brian.gibson@vtt.fi > - www.vttresearch.com.

Recent publications.

1 Kristoffer Krogerus, Sami Holmström, Brian Gibson (2018) Enhanced wort fermentation with de novo lager hybrids adapted to high-ethanol environment. Appl Environ Microbiol. 84:e02302-17. doi: 10.1128/AEM.02302-17

Interspecific hybridization is a valuable tool for developing and improving brewing yeast in a number of industry-relevant aspects. However, the genomes of newly formed hybrids can be unstable. Here, we exploited this trait by adapting four brewing yeast strains, three of which were de novo interspecific lager hybrids with different ploidy levels, to high ethanol concentrations in an attempt to generate variant strains with improved fermentation performance in high-gravity wort. Through a batch fermentation-based adaptation process and selection based on a two-step screening process, we obtained eight variant strains which we compared to the wild-type strains in 2-liter-scale wort fermentations replicating industrial conditions. The results revealed that the adapted variants outperformed the strains from which they were derived, and the majority also possessed several desirable brewing-relevant traits, such as increased ester formation and ethanol tolerance, as well as decreased diacetyl formation. The variants obtained from the polyploid hybrids appeared to show greater improvements in fermentation performance than those derived from diploid strains. Interestingly, it was not only the hybrid strains, but also the *Saccharomyces cerevisiae* parent strain, that appeared to adapt and showed considerable changes in genome size. Genome sequencing and ploidy analysis revealed that changes had occurred at both the chromosome and single nucleotide levels in all variants. Our study demonstrates the possibility of improving de novo lager yeast hybrids through adaptive evolution by generating stable and superior variants that possess traits relevant to industrial lager beer fermentation.

2 Joosu Kuivanen, Sami Holmström, Birgitta Lehtinen, Merja Penttilä, Jussi Jäntti. 2018. A High throughput workflow for CRISPR/Cas9 mediated combinatorial promoter replacements and phenotype characterization in yeast. Biotechnology Journal, in press.

Due to the rapidly increasing sequence information on gene variants generated by evolution and our improved abilities to engineer novel biological activities, microbial cells can be evolved for the production of a growing spectrum of compounds. For high productivity, efficient carbon channeling towards the end product is a key element. In large scale production systems the genetic modifications that ensure optimal performance cannot be dependent on plasmid based regulators, but need to be engineered stably into the host genome. Here we describe a CRISPR/Cas9 mediated high throughput workflow for combinatorial and multiplexed replacement of native promoters with synthetic promoters and the following high throughput phenotype characterization in the yeast *Saccharomyces cerevisiae*. The workflow is demonstrated with three central metabolic genes, *ZWF1*, *PGI1* and *TKL1* encoding a glucose 6 phosphate dehydrogenase, phosphoglucose isomerase and transketolase, respectively. The synthetic promoter donor DNA libraries were generated by PCR and transformed to yeast cells. A 50% efficiency was achieved for simultaneous replacement at three individual loci using short 60 bp flanking homology sequences in the donor promoters. Phenotypic strain characterization was validated and demonstrated using liquid handling automation and 150 µl cultivation volume in 96 well plate format. The established workflow offers a robust platform for automated engineering and improvement of yeast strains.

3 Virve Vidgren, John Londesborough. 2018. Transporters in laboratory and lager yeasts: localization and competition with endogenous transporters. Yeast, in press.

Plain and fluorescently tagged versions of *Agt1*, *Mtt1* and *Malx1* maltose transporters were over-expressed in two laboratory yeasts and one lager yeast. The plain and tagged versions of each transporter supported similar transport activities, indicating that they are similarly trafficked and have similar catalytic activities. When they were expressed under the control of the strong constitutive PGK1 promoter only minor proportions of the fluorescent transporters were associated with the plasma membrane, the rest being found in intracellular structures. Transport activity of each tagged transporter in each host was roughly proportional to the plasma membrane-associated fluorescence. All three transporters were subject to glucose-triggered inactivation when the medium glucose concentration was abruptly raised. Results also suggest competition between endogenous and over-expressed transporters for access to the plasma membrane.

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 Spirin, V., Malysheva, V., Yurkov, A., Miettinen, O., Larsson, K. H. 2018. Studies in the *Phaeotremella foliacea* group (Tremellomycetes, Basidiomycota). Mycological Progress 17: 451-466.

The taxonomy of the *Phaeotremella foliacea* group is revised based on morphological, ecological, geographic and DNA data. The name *P. foliacea* is retained for the gymnosperm-dwelling species associated with *Stereum sanguinolentum* in Eurasia and North America. *Tremella neofoliacea* and *Cryptococcus skinneri* are considered synonyms of *P. foliacea* s. str. Three other species in the complex inhabit deciduous trees. Of them, *Phaeotremella fimbriata*, comb. nov., is associated with *Stereum rugosum*; this species possesses blackening basidiocarps and small basidiospores, and it occurs in Europe. Its close relative is the East Asian *Phaeotremella eugeniae*, sp. nov., inhabiting *Quercus mongolica* and having larger basidiospores. The third species, *Phaeotremella frondosa*, comb. nov., produces the largest basidiospores in the genus and is associated either with *S. rugosum* (mainly in North Europe) or with other *Stereum* species (temperate Eurasia and North America). Additionally, *Tremella nigrescens* is typified and placed in the synonyms of *P. frondosa*, and two species, *T. fuscosuccinea* and *T. roseotincta*, are combined to *Phaeotremella*.

2 Mašínová T, Yurkov A, Baldrian P. 2018. Forest soil yeasts: Decomposition potential and the utilization of carbon sources. Fungal Ecology 34: 10-19.

Fungi that inhabit forest topsoil can be distinguished into two morphological guilds: filamentous, multicellular fungi and predominantly unicellular yeasts. The nutritional mode of these two groups is expected to differ due to the dependence of yeasts on locally present nutrients. Here we explored the decomposition potential and carbon utilization profiles of dominant yeasts from the temperate forest topsoil. The results indicated that despite taxonomic heterogeneity, yeasts represent a fungal group with a specific nutritional strategy that is dissimilar from other tested fungi. While the efficient decomposition of hemicellulose, cellulose or chitin appeared to be restricted to only a few yeast taxa, carbon source utilization assays indicated that most yeasts could efficiently act as opportunists, utilizing the decomposition products generated by other microbes. Importantly, a large fraction of enzyme activity was associated with yeast cell surfaces indicating their adaptation to generate decomposition products so that they are readily available for intake.

3 Yurkov A. 2018. Yeasts of the soil - obscure but precious. Yeast 35 (5): 369-378.

Pioneering studies performed in the nineteenth century demonstrated that yeasts are present in below ground sources. Soils were regarded more as a reservoir for yeasts that reside in habitats above it. Later studies showed that yeast communities in soils are taxonomically diverse and different from those above ground. Soil yeasts possess extraordinary adaptations that allow them to survive in a wide range of environmental conditions. A few species are promising sources of yeast oils and have been used in agriculture as potential antagonists of soil borne plant pathogens or as plant growth promoters. Yeasts have been studied mainly in managed soils such as vineyards, orchards and agricultural fields, and to a lesser extent under forests and grasslands. Our knowledge of soil yeasts is further biased towards temperate and boreal forests, whereas data from Africa, the Americas and Asia are scarce. Although soil yeast communities are often species poor in a single sample, they are more diverse on the biotope level. Soil yeasts display pronounced endemism along with a surprisingly high proportion of currently unidentified species. However, like other soil inhabitants, yeasts are threatened by habitat alterations owing to anthropogenic activities such as agriculture, deforestation and urbanization. In view of the rapid decline of many natural habitats, the study of soil yeasts in undisturbed or low managed biotopes is extremely valuable. The purpose of this review is to encourage researchers, both biologists and soil scientists, to include soil yeasts in future studies.

4 Buzzini P, Turchetti B, Yurkov A. 2018. Extremophilic yeasts: the toughest yeasts around? Yeast: online first.

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: anthropo-centric, microbial centric, or zymo centric. Micro-organisms 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 organ-isms that are not frequently considered the toughest microorganisms in comparison to prokaryotes. Nevertheless extremophilic or extremotolerant species are present also within this group. Here a brief description of the main extreme habitats and the metabolic and physiological modifications adopted by yeasts to face depending on one's adverse conditions is reviewed. Additionally the main extremophilic and extremotolerant yeast species associated to a few extreme habitats are listed.

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

1 Lachance MA 2018 Personal Reflections on Cletus P. Kurtman. Antonie van Leeuwenhoek 111:1-4. https://www.ncbi.nlm.nih.gov/pubmed/29247403

2 Varize CS, Cadete RM. Lopes LD, Christofoleti-Furlan RM, Lachance MA, Rosa CA, Basso LC 2018 *Spathaspora piracicabensis* f. a., sp. nov., a D-xylose-fermenting yeast species isolated from rotting wood in Brazil. Antonie van Leeuwenhoek 111:525–531

Two strains of a novel yeast species were isolated from rotting wood of an ornamental tree (purple quaresmeira, *Tibouchina granulosa*, Melastomataceae) in an Atlantic Rainforest area in Brazil. Analysis of the sequences of the internal transcribed spacer (ITS-5.8S) region and the D1/D2 domains of the large subunit rRNA gene showed that this species belongs to the *Spathaspora* clade, and is phylogenetically related to *Spathaspora brasiliensis*, *Candida materiae* and *Sp. girioi*. The novel species ferments D-xylose, producing ethanol, with amounts between 3.37 and 3.48 g L−1 ethanol from 2% d-xylose. Ascospores were not observed from this new species. The name *Spathaspora piracicabensis* f. a., sp. nov. is proposed to accommodate these isolates. The type strain is UFMG-CM-Y5867^T (= CBS 15054^T = ESALQ-I54^T). The MycoBank number is MB 822320.

3 Thanh VN, Hien DD, Yaguchi T, Sampaio JP, Lachance MA 2018 *Moniliella sojae* sp. nov., a species of black yeasts isolated from Vietnamese soy paste (tuong), and reassignment of *Moniliella suaveolens* strains to *Moniliella pyrgileucina* sp. nov., *Moniliella casei* sp. nov., and *Moniliella macrospora* emend. comb. nov. Int J Syst Evol Microbiol 68:1806-1814.

The presence of yeasts at different steps of Vietnamese soy paste production was studied. Yeast growth occurred during primary soybean fermentation, with the cell density reaching 4.106 c.f.u. ml−1, and terminated during brine fermentation. The dominant species were *Pichia kudriavzevii* and *Millerozyma farinosa*. Over the span of 14 years, nine strains of *Moniliella* were isolated. The strains had identical PCR fingerprints generated with primer (GAC)5 and identical D1/D2 and internal transcribed spacer (ITS) sequences. A D1/D2-based phylogeny indicated that the strains were closest to a group of four previously assigned as *Moniliella suaveolens* strains. Together they form a new lineage that is well separated from all known species, including *M. suaveolens* (over 12.7 % divergence). ITS sequences indicated the presence of four species differing from each other by 9–57 nt. The name *Moniliella* sojae sp. nov. is proposed to accommodate the strains isolated from Vietnamese soy paste, *Moniliella pyrgileucina* sp. nov. is proposed for PYCC 6800 and *Moniliella casei* sp. nov. is proposed for CBS 157.58. An emended combination *Moniliella macrospora* is proposed for CBS 221.32 and CBS 223.32. The type strains and MycoBank numbers are: *M. sojae* sp. nov., SS 4.2^T=CBS 126448^T=NRRL Y-48680^T and MB 822871; *M. pyrgileucina* sp. nov., PYCC 6800^T=CBS 15203^T and MB 823030; *M. casei* sp. nov., CBS 157.58^T=IFM 60348^T and MB 822872; *M. macrospora* emend. comb. nov., CBS 221.32^T (=MUCL 11527^T) and MB 822874.

4 Santos AR, Leon M, Barros K, Freitas L, Hughes A, Morais PB, Lachance MA, Rosa CA 2018 Description of *Starmerella camargoi* f.a., sp. nov., *Starmerella ilheusensis* f.a., sp. nov., *Starmerella litoralis* f.a., sp., *Starmerella opuntiae* f.a.,sp. nov., *Starmerella roubikii* f.a., sp. nov., *Starmerella vitae* f.a., sp. nov. isolated from flowers and bees, and transfer of related *Candida* species to the genus *Starmerella* as new combinations. Int J Syst Evol Microbiol 68:1333-1343.

Six novel yeast species, *Starmerella camargoi* f.a., sp. nov., *Starmerella ilheusensis* f.a., sp. nov., *Starmerella litoralis* f.a., *Starmerella opuntiae* f.a., sp. nov., sp. nov., *Starmerella roubikii* f.a., sp. nov. and *Starmerella vitae* f.a, sp. nov. are proposed to accommodate 19 isolates recovered from ephemeral flowers or bees in Brazil, Costa Rica and Belize. Sequence analysis of the ITS-5.8S region (when available) and the D1/D2 domains of the large subunit of the rRNA gene showed that the six novel yeasts are

phylogenetically related to several species of the *Starmerella* clade. The type strains are *Starmerella camargoi* f.a., sp. nov. UFMG-CM-Y595T (=CBS 14130T; Mycobank number MB 822640), *Starmerella ilheusensis* f.a., sp. nov. UFMG-CM-Y596T (=CBS CBS14131T; MB 822641), *Starmerella litoralis* f.a., sp. nov. UFMG-CM-Y603^T (=CBS14104^T; MB 822642), *Starmerella opuntiae* f.a., sp. nov. UFMG-CM-Y286^T (=CBS 13466^T; MB 822643), *Starmerella roubikii* f.a., sp. nov. UWOPS 01–191.1^T (=CBS 15148^T; MB 822645) and *Starmerella vitae* f.a., sp. nov. UWOPS 00–107.2 (=CBS 15147^T; MB 822646). In addition, 25 species currently assigned to the genus *Candida* are reassigned formally to the genus *Starmerella*.

5 de Vega C, Albaladejo RG, Lachance MA 2018 *Metschnikowia maroccana* fa, sp. nov., a new yeast species associated with floral nectar from Morocco Int J Syst Evol Microbiol (accepted April 2018).

Wild flowers, and in particular, nectar of flowers, have been shown to be a rich reservoir of yeast biodiversity. In a taxonomic study of yeasts recovered from floral nectar in Morocco, nine strains were found to represent a novel species. Morphological and physiological characteristics and sequence analyses of the D1/D2 region of the large subunit rRNA gene as well as the internal transcribed spacer region showed that the novel species belonged to the genus *Metschnikowia*. The name *Metschnikowia maroccana* f.a., sp. nov. (EBDCdVMor24-1^T=CBS 15053^T=NRRL Y-63972^T) is proposed to accommodate this new species. *Metschnikowia maroccana* was isolated from floral nectar of *Teucrium pseudochamaepitys*, *Teucrium polium* and *Gladiolus italicus*. The ascosporic state of the novel species was not found. *Metschnikowia maroccana* was phylogenetically distinct from any currently recognized species and forms a well-supported subclade (bootstrap value 81 %) containing species associated with flowers and flower-visiting insects, including *Metschnikowia gruessii*, *Metschnikowia lachancei* and *Metschnikowia vanudenii*. The close genealogical relationship of *M. maroccana* with the *M. gruessii* clade is also consistent with the striking similarity of their 'aeroplane' cells morphologies and the lack of utilization of the α-glucoside trehalose. The ecology of these novel species and its probable endemicity are discussed.

6 Lee, DK, Hsiang T, Lachance MA 2018 *Metschnikowia* mating genomics. Antonie van Leeuwenhoek (accepted April 2018).

Genes involved in mating type determination and recognition were examined in *Metschnikowia* and related species, to gather insights on factors affecting mating compatibility patterns among haplontic, heterothallic yeast species of the genus. We confirmed the universality of the special mating locus organisation found in *Clavispora lusitaniae* across and exclusive to the family Metschnikowiaceae (i.e., *Metschnikowia* and *Clavispora*). Timing of the divergence between idiomorphs was confirmed to coincide with the origin of the larger (CUG-ser) clade comprising the Debaryomycetaceae and the Metschnikowiaceae, exclusive of *Cephaloascus fragrans*. The sequence of the a mating pheromone is highly conserved within the large-spored Metschnikowia species, including *Metschnikowia orientalis* and *Metschnikowia hawaiiana*, but not *Metschnikowia drosophilae* or *Metschnikowia torresii*, which have a pattern of their own, as do other clades in the genus. In contrast, variation in α pheromones shows a more continuous, although imperfect correlation with phylogenetic distance as well as with in vivo mating compatibility.

7 Lopes MR, Bastista TM, Franco GR, Ribeiro LR, Santos ARO, Furtado C, Moreira RG, Goes-Neto A, Vital MJS, Rosa LH, Lachance MA, Rosa CA. 2018. Phylogenomic description of *Scheffersomyces stambukii* f.a., sp. nov., a D-xylose-fermenting species isolated from rotting-wood. Int J Syst Evol Microbiol (accepted May 2018).

Two isolates representing a new species of *Scheffersomyces* were isolated from rotting wood samples collected in an Amazonian forest ecosystem in Brazil. Analysis of the sequences of the D1/D2 domains showed that this new species is phylogenetically related to *Scheffersomyces* NYMU 15730, a species without a formal description, and the two are in an early emerging position with respect to the xylose-fermenting subclade containing *Scheffersomyces titanus* and *Scheffersomyces stipitis*.

Phylogenomic analyses using 474 orthologous genes placed the new species in an intermediary position between *Scheffersomyces* species and the larger genus *Spathaspora* and the *Candida albicans/Lodderomyces* clade. The novel species, *Scheffersomyces stambukii* f.a., sp. nov., is proposed to accommodate these isolates. The type strain of *Scheffersomyces stambukii* sp. nov. is UFMG-CM-Y427T (=CBS 14217T). The MycoBank number is MB 824093. In addition, we studied the xylose metabolism of this new species.

8 Lachance MA, Hittinger CT. 2018. Introducing 'ecoYeast': ecology and communities of yeasts. Yeast 35: 313. (call for papers).

Please see Dr. Hittinger's contribution for additional details.

Obituary

Gennadi Ivanovich Naumov (July 8 1944 - May 6 2018)

On May 6 2018, renowned Russian microbiologist Prof. Gennadi Naumov passed away at 74 years old. His scientific career was devoted to the study of the biology of ascomycetous yeasts. He started working with yeasts at the Biology Faculty of Lomonosov Moscow State University (MSU). His PhD thesis (completed in 1970) was dedicated to the variability of biochemical markers used in yeast systematics. This work laid down the focus of his future research on heterogeneity, both biochemical and genetic, in natural yeast populations. Most of these studies were performed at the State Research Institute of Genetics and Selection of Industrial Microorganisms (Moscow, Russia), where he worked for almost 50 years. Naumov studied the genetics of industrial yeasts, including the *MAL*, *MEL*, *LAC* and *GAL* genes and the mating gene (*MAT*) locus. He also discovered protein toxins or killer double-stranded RNA (k2) in natural and industrial strains of *Saccharomyces cerevisiae*. Naumov completed his dissertation in 1978 on the subject "Comparative genetics for yeast taxonomy".

To collect material for his work, Naumov participated in field trips and sampled yeasts worldwide. Later he and his co-workers studied in detail the yeast genera *Arthroascus*, *Galactomyces*, *Eremothecium*, *Hansenula* (*Wickerhamomyces*), *Kazachstania*, *Kluyveromyces*, *Komagataella*, *Lachancea*, *Metschnikowia*, *Ogataea*, *Pichia*, *Saccharomyces*, *Saccharomycopsis*, *Schizosaccharomyces*, *Williopsis* (*Cyberlindnera*), *Yarrowia*, and *Zygowilliopsis* (*Barnettozyma*). A fruitful collaboration during 30 years with the laboratory of Dr. Babjeva at the Soil Science Faculty of Lomonosov Moscow State University (MSU) resulted in long-term research on diversity, genetic heterogeneity and systematics of soil-related ascomycetous yeasts.

A particular focus of his studies was the development and application of the biological species concept to yeasts. Using advanced molecular-biological techniques in combination with data from mating experiments, he investigated the population structure and reproductive isolation of yeasts and described the biological species *Saccharomyces cariocanus*, Sac*charomyces kudriavzevii* and *Saccharomyces mikatae*. Working in collaboration with leading national and foreign collections and researchers, he described several new species in the genera *Arthroascus*, *Barnettozyma*, *Cyberlindnera*, *Kluyveromyces*, *Komagataella*, and *Saccharomycopsis*. In recognition of his contribution to yeast systematics, the yeast genus *Naumovozyma* was named after him.

Gennadi Naumov published over 350 research articles. He served as a member of the Editorial Board of *FEMS Yeast Research* and was a commissioner representing Russia in the ICY. A total of 17 PhD students and numerous trainees passed through his lab making it one of most influential research schools for yeast genetics in the USSR and later in Russia. He will be remembered as a talented researcher, a colleague, a teacher, and a dear friend.

Mikhail Vustin and Andrey Yurkov

Remembering Clete Kurtzman

- Obituaries for our colleague, mentor, and friend have appeared in two yeast journals:
  https://academic.oup.com/femsyr/pages/cletus_kurtzman_obituary_
  https://link.springer.com/article/10.1007%2Fs10482-017-0999-z
- A posthumous article first-authored by Clete and describing some *Metschnikowia* species has just appeared. http://www.readcube.com/articles/10.1007/s10482-018-1095-8
- A special workshop honoring Clete is in preparation for the 34th ISSY to be held in Bariloche, Argentina. https://www.issy34-bariloche.com/product/clete-kurtzman-workshop-on-taxonomy-and-systematics-of-yeasts/
- A special issue of FEMS Yeast Research dedicated to his memory is also in preparation.

The following photos will help us remember him.

Recent meetings

International Commission on Yeasts (ICY)
Mycology and Eukaryote Microbiology (MEM) Division
International Union of Microbiological Societies (IUMS)

ICY Commissioners Meeting, Thursday, May 17, 2018
The International Conference on Non-conventional Yeasts (2018 NCY)
Hilton Garden Inn Hotel, Rzeszów, Poland

Minutes of Meeting

Present (23): Hiroshi Takagi (ICY Chair; Japan), Charles Abbas (ICY Vice-Chair; U.S.A.), Andriy Sibirny (2018 NCY Chair; Ukraine), Tiina Alamae (Estonia), Grzegorz Bartosz (Not registered at the meeting; Poland), Neža Čadež (Slovenia), Rimantas Daugelavicius (Candidate for nomination; Lithuania), Hüseyin Erten (Turkey), Patrick Fickers (Belgium), Angelica Ganga (Chile), Mykhailo Gonchar (Ukraine), Hyun Ah Kang (South Korea), Akihiko Kondo (Japan), Diethard Mattanovich (Austria), Volkmar Passoth (Sweden), Gabor Peter (Hungary), Valentyn Pidhorskyi (Ukraine), Alexander Rapoport (Latvia), Doris Rauhut (Germany), Nitnipa Soontorngun (Thailand), Johan Thevelein (Belgium), Kenneth Wolfe (Ireland), Teresa Zoladek (Poland).

Meeting Agenda

Chair's Opening Remarks: Dr. Hiroshi Takagi welcomed the delegates to the meeting. He thanked Dr. Andriy Sibirny and the Organizing Committees for the excellent job regarding 2018 NCY and presented the agenda. He also reported on ICY14 held in Japan, 2016. ICY14 donated the surplus funds to the forthcoming ISSY33-35 (2017-2019), ICY15 (2020) and Non-conventional Yeasts (2018).

Tribute to Dr. Cletus P. Kurtzman and Dr. Gennadi Ivanovich Naumov: Dr. Takagi informed Commissioners of the sad news that our honorable Commissioners, Dr. Cletus P. Kurtzman from the U.S.A. and Dr. Gennadi Ivanovich Naumov from Russia passed away six months ago (November 27, 2017) and just two weeks ago (May 6, 2018), respectively. Both were very active members of ICY and solid and reliable persons as excellent yeast scientists, particularly in the field of yeast taxonomy. Commissioners mourned their death by holding a one-minute of silence tribute. After discussion, as sincerest condolences, Commissioners will dedicate a memorial address to honor their contributions to the community at ISSY34 organized by Dr. Diego Libkind. Some memorial talks/messages will be included in the program of ISSY34.

New Commissioners to ICY: Dr. Takagi introduced three candidates for ICY membership. Dr. Masako Takashima is Unit Leader of the Resource Advancement Unit, Microbe Division/Japan Collection of Microorganisms, RIKEN BioResource Center, Tsukuba, Japan, and is an expert on the taxonomy, ecology and biodiversity, and evolutionary genomics of yeasts, nominated by Prof. Hiroshi Takagi. Dr. Vivien Measday is Associate Professor of Wine Research Centre, the University of British Columbia, Vancouver, Canada, an expert on yeast genetics, physiology and applications to vinification, including the ecology of yeasts involved in wine production, nominated by Prof. Philip Hieter. Dr. Chen Ee Sin is Assistant Professor of Department of Biochemistry, the Medical School of National University of Singapore, and is an expert on epigenetic regulation, cell cycle research, studies on chemotherapeutic drug response using yeast systems and synthetic biology, nominated by Prof. Hiroshi Takagi. Each candidate provided his/her CV with list of publications and two Letters of Recommendation from relevant National or International Society and current members of ICY. These documents were spread electronically among Commissioners, who could express their attitude towards the candidates. All proposed candidates got full support from 56 Commissioners. Commissioners unanimously elected Drs. Takashima, Measday and Sin as new ICY members.

Updates for Future ISSY/ICY Meetings: Each organizer provided a progress report on meeting preparation. Firstly, Dr. Hüseyin Erten presented the update for ISSY35 that will be held in Turkey (October 6-10, 2019). Secondly, Dr. Diethard Mattanovich presented the update for ICY15 that will be held in Austria (August 23-27, 2020).

Suggestions for Future ISSYs: At the last meeting, Dr. Takagi proposed that the candidate venue for ISSY36 in 2021 be North America, as many recent ISSY meetings had been held in Europe - Slovakia (2013), Slovenia (2014), Italy (2015) and Ireland (2017). Dr. Charles Abbas also outlined the plan and concept for ISSY36 to be held in North America, possibly Vancouver (Canada). Dr. Vivien Measday, who has just approved as a new Canadian Commissioner, is willing to organize ISSY36. Dr. Takagi will ask Dr. Measday to officially introduce and propose ISSY36 at the ICY Commissioners meeting held in Argentina whether Commissioners endorse her proposal to host ISSY36 in Vancouver. Regarding ISSY37 (2022), Dr. Vladimir Jiranek and Dr. Sakkie Pretorius are interested in hosting, and will prepare a draft proposal for ISSY37 to be held in Australia, whichlast hosted ISY9, 1996, organized by Dr. Graham Fleet. Dr. Takagi will ask Dr. Jiranek and Dr. Pretorius to officially introduce and propose ISSY37 at the ICY Commissioners meeting held in Argentina in the hope that Commissioners will endorse their proposal to host ISSY37 in Australia.

Boot of ICY Website: To share the information or to follow past and upcoming ICY meetings, Dr. Takagi has just started the ICY website with the aid of Dr. Rob Samson, the secretary-general of IUMS, who is kindly assisting without any charges. The link to the website in the IUMS webpage is as follows: https://www.iums.org/index.php/87-icy/138-international-commission-on-yeasts

Dr. Takagi is asking the past/future Chair of ISSY/ICY to collect some available "documents, programs, PowerPoint presentations, resources, data and literature" to upload. Also, regarding "Yeast Newsletter" managed by Dr. Marc André Lachance, Dr. Takagi asked him to link its website that includes the back numbers to the ICY website. Dr. Takagi also rectified by adding some words, terms and sentences to the current statutes of ICY and asked the former Chairs, Dr. Andriy Sibirny and Dr. Charles Abbas to confirm.

Chair Closing Remarks: On behalf of ICY, Dr. Hiroshi Takagi expressed gratitude once again to Dr. Andriy Sibirny and his staff for the excellent meeting, well balanced and organized scientific and cultural program. The ICY meeting was closed.

Minutes presented by:

Dr. Hiroshi Takagi
ICY Chair

Dr. Charles Abbas
ICY Vice-Chair

Forthcoming Meeting

ISSY34 - Bariloche, Patagonia, Argentina
October 1-4 2018

The 34th International Specialized Symposium on Yeasts will take place this year in Bariloche, Patagonia, Argentina. An exciting meeting in an incredible place is being organized by a large group of latinoamerican scientists. We invite you to participate in this unique experience which will take place October 1-4 and will be followed by the first International Workshop on Brewing Yeasts (5th-6th), gathering experts all over the world. The deadline for abstract

submission and early bird registration was June 1. Please check our website for updates and more information: www.issy34-bariloche.com

Pre-ISSY34 event:

Cletus Kurtzman Workshop on Taxonomy and Systematics of Yeasts

Organized by Teun Boekhout and Marizeth Groenewald and dedicated to the memory of the great yeast taxonomist Cletus Kurtzman, this workshop is free of charge and will provide an update of the current impact of genomics into the field. It will take place in the morning of October 1st, just before sightseeing tours and the opening ceremony of ISSY34. Confirmed speakers include: Cathy Aime, Neza Cadez, Andrey Yurkov, Diego Libkind, Masako Takashima, Heide-Marie Daniel, among others. Main talk: Antonis Rokas (USA): A phylogenomic roadmap for the budding yeast subphylum.

ISSY34 Keynote lectures confirmed:

Luis Larrondo: (Chile) Optogenetic control of gene expression: putting some LOV and red-light action into yeast biotechnology

Kevin Vestrepen: (Belgium) Looking at yesterday's yeasts to brew tomorrow's beer.

Rosane Schwan: (Brazil) Recent advances in cocoa fermentation conducted with starter cultures. "Graham Fleet Memorial Lecture"

ISSY34 Main session speakers:

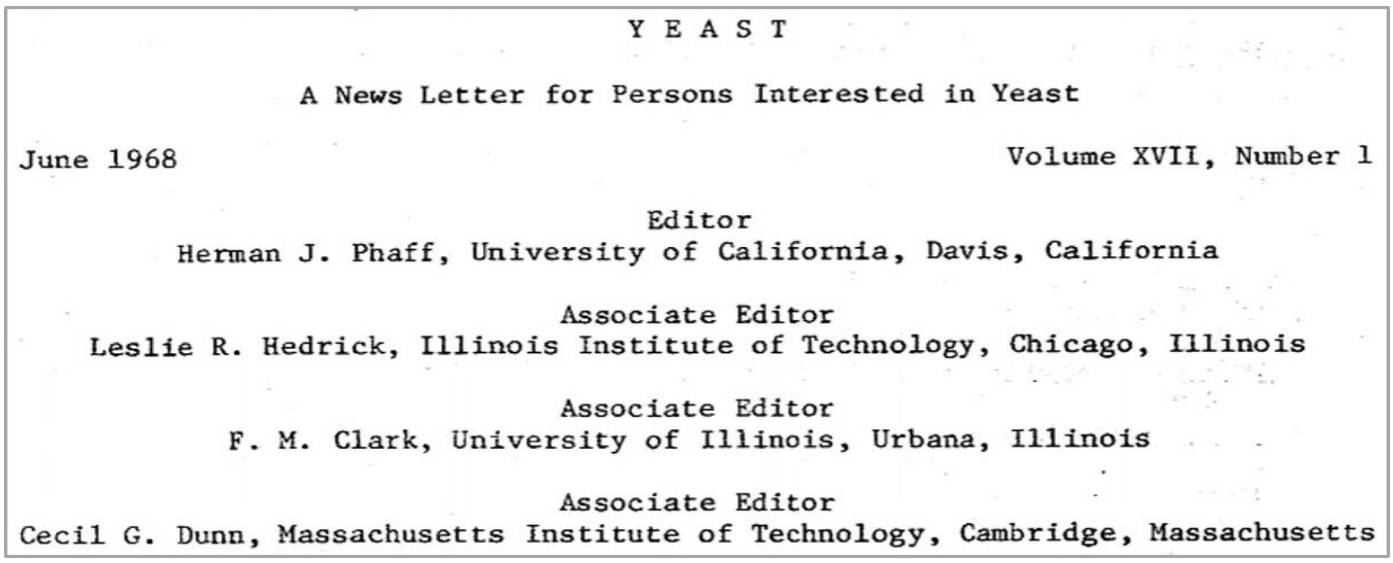
Jose Paulo Sampaio: (Portugal) A population genomics perspective of the multiple domestication paths in Saccharomyces cerevisiae. Chris Hittinger: (USA) The genomic making of yeast biodiversity. Hiroshi Takagi: (Japan) New metabolic regulations and physiological functions of amino acids found in yeast and their applications to breeding. Lene Jespersen: (Finland) Improvement of the quality of traditional fermented foods – hidden identities, small talk and gut feeling. Nina Gunden-cimerman: (Slovenia) Greenland black bloom fungi. Andre Lachance: (Canada) *Metschnikowia* mating habits. Carole Camarasa: (France) Quantitative analysis of nitrogen and aroma metabolisms of *S. cerevisiae* during wine fermentation. Francisco Girio: (Portugal) Engineering and evaluation the performance of industrial C5/C6 yeast-fermenting strains on lignocellulosic hydrolysates – a solved issue? John Morrisey: (Ireland) Contributions of genomic and genetic diversity to phenotypic variability in *Kluyveromyces marxianus*.

ISSY34 Sponsored Talks:

Dawn Thompson: (Gingko Bioworks, USA) Leveraging the synergy of rational design in combination with natural genetic variation in a high throughput biological foundry for industrial strain improvement. Jessica Noble: (Lallemand, CANADA) From grape must to wine: towards a better knowledge of yeasts achievements.

Diego Libkind <diego.libkind@gmail.com>

Fifty Years Ago



Y E A S T

A News Letter for Persons Interested in Yeast

June 1968 Volume XVII, Number 1

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Dr. D. Yarrow of CBS, the Netherlands, reported that type strains of eleven new yeast species were deposited in the collection: *Candida bombi, C. obtusa* var. *arabinosa, C. oleophila, C. santamariae, C. santamariae* var. *membranaefaciens, C. edax, C. suecica, Pichia angophorae, Saccharomyces carmosousae, Zygolipomyces lactosus* and *Z. tetrasporus.*

Dr. Melle M. C. Pignal of Université de Lyon, France published descriptions of new species *Candida bombi,* and new varieties *C. santamariae* var. *membranaefaciens* and *C. obtuse* var. *arabinosa.* Montracher et al. compared the morphological and physiological properties of 41 species of *Candida.*

Dr. Anna Kocková-Kratochvílová published three papers on fermentation type II species of *Candida*, continuous cultivation of *Candida albicans*, and ploidy and reproduction in yeast. A new catalogue of microorganisms of the Tsechoslovakian Collections will be published in Brno in July 1968. She presented a lecture on the use of taxonomy of *Saccharomyces* for the baking industry at the International Symposium of Fermentation Industry in Leipsig (DDR) in May 1968. Three dissertations were completed, on glycoproteins from horse and beef serum, Slovak hop quality, and cell wall polysaccharides of *C. guilliermondii.*

Dr. T. Nakase of Ajinomoto Co., Kawasaki, Japan shared the abstract of a paper that would be presented at the International Conference on Culture Collections in Tokyo, October 7-12, 1968 titled, "Taxonomic Significance of Base Composition of Yeast DNA". The mole % GC content of 140 species of yeasts and yeast-like fungi were listed in the Yeast Newsletter. Species with high urease activity had high GC content with no exceptions. GC content of *Candida* species ranged from 28% to 60%. [Editor's note: the highest GC content *Candida* species are now classified as basidiomycetes, such as *Candida humicola* (now called *Vanrija humicola*) and *Candida curvata* (now called *Cutaneotrichosporon curvatus*).]

Dr. Herman J. Phaff of the University of California Davis and **Ahmed T. H. Abd-El-Al** published a paper titled, "Exo-b-glucanases in Yeast". Sally Meyer completed requirements for the M. A. degree. A summary of her thesis, titled, "Isolation and Base Composition of DNA from Yeasts" was published in the Yeast Newsletter. The % GC of 15 yeast species were listed. Examples of the taxonomic significance of base composition in yeast were detailed [many of which presaged subsequent taxonomic reclassifications]. (1)

Two strains of the same species had the same GC content. (2) A proposed sexual/asexual species pair had the same GC content. (3) The GC content of *Debaryomyces globosus* was closer to that of *Saccharomyces rosei* than to *Debaryomyces hansenii*. [Editor's note: *D. globosus* and *S. rosei* are both now classified in genus *Torulaspora*; the GC content data foretold numerous reclassifications.] (4) The GC content of *Candida* species showed a large range. [Editor's note: many former *Candida* species with high GC content have since been reclassified into Basidiomycete genera.] (5) Examination of multiple strains for taxonomic evaluation was recommended.

Dr. Edward J. Buecher, Jr. completed his doctoral dissertation, "Physiology, Dimorphism and Cell Wall Biochemistry of *Saccharomycopsis* Schiönning" under the guidance of **Herman J. Phaff**. The abstract was published in the Yeast Newsletter.

Dr. J. B. Sinclair, Louisiana State University, shared the abstract of a publication in press and the abstract of a Ph. D. dissertation regarding pathogenicity of *Geotrichum candidum.*

Dr. Michael S. Esposito and **Dr. Rochelle E. Esposito** described recent publications on the genetic control of meiosis and sporulation in *Saccharomyces*. They use UV light to generate temperature-sensitive sporulation mutants in a diploid homothallic strain.

Professor Harlyn O. Halvorson of the University of Wisconsin, Madison listed five recent publications and summarized the lab's research on yeast polyribosomes, ribonucleases, mapping of histidine genes, and time of gene expression correlated to centromere distance. DNA hybridization studies with purified nuclear and mitochondrial DNA and RNA indicated that there are 340 cistrons for 18s RNA, 340 for 26S RNA and 320 to 400 for transfer RNA. Mitochondrial RNA only hydridized to mitochondrial DNA. Doubling of DNA in sporulating *Saccharomyces* was observed starting 5 hours after introduction into sporulation medium.

Dr. T. Brock of Indiana University provided the summary of the Ph. D. dissertation of **Dr. M. A. Crandall** titled, "Genetic and Biochemical Studies of Sexual Agglutination in the Yeast *Hansenula wingei."* They studied factors that inhibit agglutination between *H. wingei* cells of opposite mating type.

Dr. J. J. Miller of McMaster University, Hamilton, Canada described work on the proteolytic activity of *S. cerevisiae* during sporulation. They compared the sporogenic capacity of 250 strains, with a goal of "putting the well-known ruggedness of the yeast spore to practical use", such as industrial inocula. This method would not be suitable for polypolids, and meiotic recombination would alter the genetic properties.

Dr. J. O. Lampen of Rutgers, The State University, New Jersey provided summaries of their work published over the last year on yeast enzymes invertase and phosphomannanase.

Dr. Sven Darling of the Royal Dental College, Århus, Denmark and Statens Seruminstitut, Copenhagen, Denmark presented work titled, "Kinetic and morphologic observations on *Saccharomcyes cerevisiae* during spheroplast formation" at the annual meeting of the Scandinavian Society for Electron Microscopy in Stockholm.

Dr. Norval A. Sinclair of the Hopkins Marine Station, Pacific Grove, California studied glucose metabolism in the obligate psychrophile *Candida gelida.* Supplementation of the growth medium with valine, leucine and isoleucine resulted in production of branched chain fatty acids.

Dr. H. Klaushofer described a method to produce monospecific anti-*Saccharomyces carlsbergensis* serum for biological quality control. They used the methods of numerical taxonomy for selecting a representative industrial strain as proposed by Dr. Anna Kocková-Kratochvílová at the International Symposium on Yeasts (Smolenice 1964).

Dr. Heikki Suomalainen of the State Alcohol Monopoly, Helsinki, Finland characterized keto-acids formed in baker's yeast during anaerobic fermentation and aerobic growth.

Dr. Morio Akaki of the University of Mie, Japan compared the properties of sake brewed using a pure culture of yeast (Kyokai No. 7) to the ordinary process using Sokujomoto.

Dr. B. C. Rankine of the Australian Wine Research Institute in Glen Osmond, South Australia compared ethanol content and higher alcohol composition of wine fermented with various *Saccharomyces* as well as other genera of yeasts: *Kloeckera, Hansenula, Schizosaccharomyces* and *Saccharomycodes.*

Dr. E. Minárik of the Technical University of Agriculture, Lednice, Czechoslovakia described the dissertation of V. Švejcar titled, "Contribution to the classification of the yeast flora of vineyards of the School Farm of the Technical University of Agriculture in Lednice (Moravia)."

Dr. N. van Uden of the Gulbenkian Institute of Science, Oeiras, Portugal listed four recent publications including several new *Candida* species, and maintenance analysis in the chemostat. He shared that **Miss Manuela Vidal Leiria** returned to Portugal after completing her M. A. in microbiology at the University of California Davis, working with **H. J. Phaff**.

Dr. C. C. Lindegren listed three publications on crossover and linkage relations in *Saccharomyces.*

Drs. Richard I. Mateles and **Steven R. Tabbenbaum** edited a book titled, "Single-Cell Protein". The book is a compilation of papers presented at a 2-day conference at the Massachusetts Institute of Technology exploring the nutritional, technological, economic, sociological and political obstacles in developing SCP into a food source.

Drs. M. W. Miller and **H. J. Phaff** planned to collect yeasts from natural habitats along the west coast of North America from Anchorage, Alaska to Davis, California. [Editor's note: Over 300 of these yeast strains are still available in the public catalog of the Phaff Yeast Culture Collection, University of California Davis.]

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

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