

Yeast

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Editorials

Dini Eisikowitch (1936-2022)

Yeast Newsletter readers may not be familiar with Professor Dan Eisikowitch of the Department of Botany at Tel Aviv University, Israel. Dan made an important contribution to yeast ecology when he discovered that *Metschnikowia* species, when present in the nectar of milkeeds (*Asclepias* spp.), could cause pollen abortion and consequently decrease the fertility of the plant. I had the pleasure of meeting Dan and collaborating with him. He was an endearing colleague. Dan died recently at the age of 86. He was a leading scholar in pollination ecology. An overview of his life and contributions has been published [Dafni A, Kevan PG. 2022. Beyond botany: in appreciation of the life and contributions of Dini Eisikowitch (1936 – 2022). J Pollin Ecol 32:170-173].

ISSY36 - Vancouver, British Columbia, Canada

Based on about 50% sampling since 1977, I have observed that International Specialized Symposia on Yeasts have shared the characteristic of a steady increase in overall success. ISSY36, held on the beautiful Vancouver campus of the University of British Columbia in July 2022, was no exception to that trend. Our colleague Professor Vivien Measday put together a scientific program that featured breadth at all levels, looking at yeast and yeasts from the molecular to the global. Our long days of presentations were suitably peppered with generous breaks and meals, and the social program was intelligent and tasteful. The relatively small attendance made for warm interactions, with few people left not knowing one another by the end of the conference. Student and postdoctoral fellow participation was exemplary and certainly put to rest any worry that the next generation might be wanting in talent or enthusiasm. From my own standpoint, I must single out a fascinating exposé, by Ken Wolfe, of his latest hypotheses on the relationship between killer toxins and the evolution of alternative codon usage. The conference ended with the traditional banquet held in a delightful venue with a view on the Pacific Ocean, featuring a challenging yeast trivia quiz and the enthralling sound program provided by an award-winning DJ, who created the atmosphere needed for wild action on the dance floor. After many stressful months of wondering whether ISSY36 would go ahead as an *in vivo*, and not a *virtualis* meeting, Vivien can now release a well-deserved sigh of relief and a proud sense of accomplishment. On behalf of all participants, I offer my warmest thanks and congratulations to Vivien and her team for such a success!

M.A. Lachance, Editor

I Biology Department, Saint Mary's University, Halifax, Nova Scotia, Canada. Communicated by A.L. Bunbury-Blanchette <adele.bunbury@smu.ca>.

Recent publication.

- 1 Bunbury-Blanchette A, Fan L, English M, Kernaghan G. 2022. Yeast communities before and after spontaneous fermentation of wine grapes: a case study from Nova Scotia. *Can J Microbiol* - <https://doi.org/10.1139/cjm-2022-0179>

Wine fermentations are generally completed by the domestic yeast *Saccharomyces cerevisiae*, but many indigenous vineyard yeasts also influence wine flavour and aroma. Despite the flourishing wine industry in Nova Scotia, there has yet to be any systematic evaluation of these yeasts in Atlantic Canada. The yeast communities of pressed L'Acadie blanc grapes sampled from an organic vineyard in the Annapolis Valley in 2018 and 2019 were characterized before and after spontaneous fermentation by both Illumina and PacBio sequencing, to address and compare potential platform biases. Chemical and sensory evaluations were also conducted. Basidio-

mycete yeasts including *Vishniacozyma carnescens*, *Filobasidium globisporum* and *Curvibasidium cygneicollum* dominated pre-fermentation diversity. Species of *Saccharomyces* made up ~0.04% of sequences prior to fermentation, but 85-100% after fermentation, with some replicates dominated by *S. cerevisiae* and some by *S. uvarum*. PacBio sequencing detected high proportions of *Hanseniaspora uvarum*, while Illumina sequencing did not. A better understanding of Nova Scotia vineyard yeast communities will allow local wine makers to make better use of non-traditional yeasts and spontaneous fermentations to produce high-quality wines unique to the region.

II Department of AGRARIA, "Mediterranea" University of Reggio Calabria, Via Feo di Vito, I-89122 Reggio Calabria, Italy. Communicated by Andrea Caridi <acaridi@unirc.it>.

Recent publication.

- 1 Caridi A, Panebianco F, De Bruno A, Piscopo A, Martorana A, Sidari R. 2022. New procedure to pre-select lactic acid bacteria able to control table-olive fermentation. *Acta Scientiarum Technol* 44(1):e57309,7. <https://doi.org/10.4025/actascitechnol.v44i1.57309>.

Using 35 artisanal Calabrian table-olive brines, 153 strains of lactic acid bacteria were isolated. A screening procedure was designed, involving the following steps: 1) Gram stain, cellular morphology, homolactic fermentation, acidifying activity in MRS broth; 2) growth in olive paste with NaCl 11%; 3) increase of the antioxidant activity; 4) identification of the best strains. The proposed procedure allows an

evaluation of the technological aptitude of lactic acid bacteria to ferment table olives excluding, cheaply and easily, all those strains definitely unable to act as starter. The use of olive paste as a screening medium allows the resistance of the new isolates against olive phenolic compounds to be tested. The selection of strains able to increase the antioxidant power of olive paste can improve the shelf-life of table olives.

III Russian Collection of Microorganisms (VKM), Institute for Biochemistry and Physiology of Microorganisms, Pushchino, 142290, Russia - <http://www.vkm.ru>. Communicated by WI Golubev <wig@ibpm.pushchino.ru>.

Recent publication.

- 1 Golubev WI. 2022. Sensitivity of yeasts to mycotoxins. *Probl Med Mycol* 24(2):9-11. (in Russ.)

The yeasts (members of more than 30 genera) are resistant to aflatoxin B1 and ochratoxin A. Rare strains only basidiomycetous yeasts are sensitive to zearalenone. The sensitivity to aurofusarin and toxin T-2 is a strain-specific property but on the whole the

proportion of resistant species is larger in basidiomycetous yeasts than ascomycetous ones. Rather many yeasts are resistant to all mycotoxins examined.

Papers submitted or recently published.

- 1 Crandall JG, Fisher KJ, Sato TK, Hittinger CT. An adaptive interaction between cell type and metabolism drives ploidy evolution in a wild yeast. bioRxiv submitted.

Ploidy is an evolutionarily labile trait, and its variation across the tree of life has profound impacts on evolutionary trajectories and life histories. The immediate consequences and molecular causes of ploidy variation on organismal fitness are frequently less clear, although extreme mating type skews in some fungi hint at links between cell type and adaptive traits. Here we report an unusual recurrent ploidy reduction in replicate populations of the budding yeast *Saccharomyces eubayanus* experimentally evolved for improvement of a key metabolic trait, the ability to use maltose as a carbon source. We find that haploids have a substantial, but conditional, fitness advantage in the absence of other genetic variation. Using engineered

genotypes that decouple the effects of ploidy and cell type, we show that increased fitness is primarily due to the distinct transcriptional program deployed by haploid-like cell types, with a significant but smaller contribution from absolute ploidy. The link between cell-type specification and the carbon metabolism adaptation can be traced to the noncanonical regulation of a maltose transporter by a haploid-specific gene. This study provides novel mechanistic insight into the molecular basis of an environment-cell type fitness interaction and illustrates how selection on traits unexpectedly linked to ploidy states or cell types can drive karyotypic evolution in fungi.

- 2 Schmitz JM, Wolters JF, Murray NH, Guerra RM, Bingman CA, Hittinger CT, Pagliarini DJ. Aim18p and Aim46p are CHI-domain-containing mitochondrial hemoproteins in *Saccharomyces cerevisiae*. bioRxiv submitted.

Chalcone isomerases (CHIs) have well-established roles in the biosynthesis of plant flavonoid metabolites. *Saccharomyces cerevisiae* possesses two predicted CHI-like proteins, Aim18p (encoded by YHR198C) and Aim46p (YHR199C), but it lacks other enzymes of the flavonoid pathway, suggesting that Aim18p and Aim46p employ the CHI fold for distinct purposes. Here, we demonstrate that Aim18p and Aim46p reside on the mitochondrial inner membrane and adopt CHI folds, but they lack select active site residues and possess an extra fungal-

specific loop. Consistent with these differences, Aim18p and Aim46p lack chalcone isomerase activity and also the fatty acid-binding capabilities of other CHI-like proteins, but instead bind heme. We further show that diverse fungal homologs also bind heme and that Aim18p and Aim46p possess structural homology to a bacterial hemoprotein. Collectively, our work reveals a distinct function and cellular localization for two CHI-like proteins, introduces a new variation of a hemoprotein fold, and suggests that ancestral CHI-like proteins were hemoproteins.

- 3 Nalabothu RL, Fisher KJ, LaBella AL, Meyer TA, Opulente DA, Wolters JF, Rokas, A, Hittinger CT. Codon optimization, not gene content, predicts *XYL*ose metabolism in budding yeasts. bioRxiv under revision. <https://doi.org/10.1101/2022.06.10.495693>

Xylose is the second most abundant monomeric sugar in plant biomass. Consequently, xylose catabolism is an ecologically important trait for saprotrophic organisms, as well as a fundamentally important trait for industries that hope to convert plant mass to renewable fuels and other bioproducts using microbial metabolism. Although common across fungi, xylose catabolism is rare within *Saccharomycotina*, the subphylum that contains most

industrially relevant fermentative yeast species. Several yeasts unable to consume xylose have been previously reported to possess complete predicted xylolytic metabolic pathways, suggesting the absence of a gene-trait correlation for xylose metabolism. Here, we measured growth on xylose and systematically identify *XYL* pathway orthologs across the genomes of 332 budding yeast species. We found that most yeast species possess complete predicted xylolytic

pathways, but pathway presence did not correlate with xylose catabolism. We then quantified codon usage bias of *XYL* genes and found that codon optimization was higher in species able to consume xylose. Finally, we showed that codon optimization of *XYL2*, which encodes xylitol dehydrogenase, positively correlated

with growth rates in xylose medium. We conclude that gene content cannot predict xylose metabolism; instead, codon optimization is now the best predictor of xylose metabolism from yeast genome sequence data.

- 4 Peris D, Ubbelohde EJ, Kuang MC, Kominek J, Langdon QK, Adams M, Koshalek JA, Hulfactor AB, Opulente DA, Hall DJ, Hyma K, Fay JC, Leducq JB, Charron G, Landry CR, Libkind D, Gonçalves C, Gonçalves P, Sampaio JP, Wang QM, Bai FY, Wrobel RL, Hittinger CT. Macroevolutionary diversity of traits and genomes in the model yeast genus *Saccharomyces*. bioRxiv under revision. <https://doi.org/10.1101/2022.03.30.486421>

Species is the fundamental unit to quantify biodiversity. In recent years, the model yeast *Saccharomyces cerevisiae* has seen an increased number of studies related to its geographical distribution, population structure, and phenotypic diversity. However, seven additional species from the same genus have been less thoroughly studied, which has limited our understanding of the macroevolutionary events leading to the diversification of this genus over the last 20 million years. Here, we show the geographies, hosts, substrates, and phylogenetic relationships for approximately 1,800

Saccharomyces strains, covering the complete genus with unprecedented breadth and depth. We generated and analyzed complete genome sequences of 163 strains and phenotyped 128 phylogenetically diverse strains. This dataset provides insights about genetic and phenotypic diversity within and between species and populations, quantifies reticulation and incomplete lineage sorting, and demonstrates how gene flow and selection have affected traits, such as galactose metabolism. These findings elevate the genus *Saccharomyces* as a model to understand biodiversity and evolution in microbial eukaryotes.

- 5 Li Y, Liu H, Steenwyk JL, LaBella AL, Harrison MC, Groenewald M, Zhou X, Shen XX, Zhao T, Hittinger CT, Rokas A. Contrasting modes of macro and microsynteny evolution in a eukaryotic subphylum. *Curr Biol* epub: <https://doi.org/10.1016/j.cub.2022.10.025>.

Examination of the changes in order and arrangement of homologous genes is key for understanding the mechanisms of genome evolution in eukaryotes. Previous comparisons between eukaryotic genomes have revealed considerable conservation across species that diverged hundreds of millions of years ago (e.g., vertebrates, bilaterian animals, and filamentous fungi). However, understanding how genome organization evolves within and between eukaryotic major lineages remains underexplored. We analyzed high-quality genomes of 120 representative budding yeast species (subphylum Saccharomycotina) spanning ~400 million years of eukaryotic evolution to examine how their genome organization evolved and to compare it with the evolution of animal and plant genome organization. We found that the decay of both macrosynteny (the conservation of homologous chromosomes) and microsynteny (the conservation of

local gene content and order) was strongly associated with evolutionary divergence across budding yeast major clades. However, although macrosynteny decayed very fast, within ~100 million years, the microsynteny of many genes—especially genes in metabolic clusters (e.g., in the *GAL* gene cluster)—was much more deeply conserved both within major clades and across the subphylum. We further found that when genomes with similar evolutionary divergence times were compared, budding yeasts had lower macrosynteny conservation than animals and filamentous fungi but higher conservation than angiosperms. In contrast, budding yeasts had levels of microsynteny conservation on par with mammals, whereas angiosperms exhibited very low conservation. Our results provide new insight into the tempo and mode of the evolution of gene and genome organization across an entire eukaryotic subphylum.

- 6 Gabaldon T, Hittinger CT. 2022. Editorial: Genomic insights on fungal hybrids. *Front Fungal Biol* 3:1063609. <https://doi.org/10.3389/ffunb.2022.1063609>

Hybrids are chimeric organisms that result from the crossing of two genetically divergent lineages. Compared to their parents, hybrids sometimes show higher adaptive capacities towards specific niches, thereby contributing to diversification. Fungal hybrids have been neglected by formal studies for a long time due to the inherent challenges of the microbial species concept and the difficulty of identifying hybrids based on morphological characters. Although the first fungal hybrids were identified in *Saccharomyces*, thanks to careful dissection of metabolic properties and emerging genome sequencing technologies, it was the spread of these sequencing technologies that revealed the true pervasiveness of hybrids across the fungal tree of life.

Sequencing techniques, particularly genomic approaches, have not only unearthed the hybrid nature of many fungal organisms, but also serve as ideal tools for the study of hybrids. Hybrids have chimeric genomes, which usually display high instability and are subject to evolutionary pressures that are different from that of non-hybrid genomes. Understanding how hybrids are formed, how they cope with their chimeric genomes, and how they evolve and adapt to distinct environments is a matter of intensive research. This Research Topic gathers six outstanding contributions that use genomic approaches to tackle diverse questions that relate to fungal hybrids.

- 7 Krause DJ, Hittinger CT. 2022. Functional divergence in a multi-gene family is a key evolutionary innovation for anaerobic growth in *Saccharomyces cerevisiae*. *Mol Biol Evol* 39:msac202. <https://doi.org/10.1093/molbev/msac202>

The amplification and diversification of genes into large multi-gene families often mark key evolutionary innovations, but this process often creates genetic redundancy that hinders functional investigations. When the model budding yeast *Saccharomyces cerevisiae* transitions to anaerobic growth conditions, the cell massively induces the expression of seven serine/threonine-rich anaerobically-induced cell wall mannoproteins (anCWMPs): *TIP1*, *TIR1*, *TIR2*, *TIR3*, *TIR4*, *DAN1*, and *DAN4*. Here, we show that these genes likely derive evolutionarily from a single ancestral anCWMP locus, which was duplicated and translocated to new genomic contexts several times both prior to and following the budding yeast whole genome duplication (WGD) event. Based on synteny and their phylogeny, we separate the anCWMPs into four gene subfamilies. To resolve prior inconclusive genetic investigations of these genes, we constructed a

set of combinatorial deletion mutants to determine their contributions toward anaerobic growth in *S. cerevisiae*. We found that two genes, *TIR1* and *TIR3*, were together necessary and sufficient for the anCWMP contribution to anaerobic growth. Over-expressing either gene alone was insufficient for anaerobic growth, implying that they encode non-overlapping functional roles in the cell during anaerobic growth. We infer from the phylogeny of the anCWMP genes that these two important genes derive from an ancient duplication that predates the WGD event, whereas the *TIR1* subfamily experienced gene family amplification after the WGD event. Taken together, the genetic and molecular evidence suggests that one key anCWMP gene duplication event, several auxiliary gene duplication events, and functional divergence underpin the evolution of anaerobic growth in budding yeasts.

- 8 Wadler CS, Wolters JF, Fortney NW, Throckmorton KO, Zhang Y, Miller CR, Schneider RM, Wendt-Pienkowski E, Currie CR, Donohue TJ, Noguera DR, Hittinger CT, Thomas MG. 2022. Utilization of lignocellulosic biofuel conversion residue by diverse microorganisms. *Biotechnol Biofuels Bioprod* 15:70. <https://doi.org/10.1186/s13068-022-02168-0>

Lignocellulosic conversion residue (LCR) is the material remaining after deconstructed lignocellulosic biomass is subjected to microbial fermentation and treated to remove the biofuel. Technoeconomic analyses of biofuel refineries have shown that further microbial processing of this LCR into other bioproducts may help offset the costs of biofuel

generation. Identifying organisms able to metabolize LCR is an important first step for harnessing the full chemical and economic potential of this material. In this study, we investigated the aerobic LCR utilization capabilities of 71 *Streptomyces* and 163 yeast species that could be engineered to produce valuable bioproducts. The LCR utilization by these individual

microbes was compared to that of an aerobic mixed microbial consortium derived from a wastewater treatment plant as representative of a consortium with the

highest potential for degrading the LCR components and a source of genetic material for future engineering efforts.

- 9 Vanaclouig-Pedros E, Fisher KJ, Liu L, Debrauske DJ, Young MKM, Place M, Hittinger CT, Sato TK, Gasch AP. 2022. Comparative chemical genomic profiling across plant-based hydrolysate toxins reveals widespread antagonism in fitness contributions. *FEMS Yeast Res* 21:foac036. <https://doi.org/10.1093/femsyr/foac036>

The budding yeast *Saccharomyces cerevisiae* has been used extensively in fermentative industrial processes, including biofuel production from sustainable plant-based hydrolysates. Myriad toxins and stressors found in hydrolysates inhibit microbial metabolism and product formation. Overcoming these stresses requires mitigation strategies that include strain engineering. To identify shared and divergent mechanisms of toxicity and to implicate gene targets for genetic engineering, we used a chemical genomic approach to study fitness effects across a library of *S. cerevisiae* deletion mutants cultured anaerobically in dozens of individual compounds found in different

types of hydrolysates. Relationships in chemical genomic profiles identified classes of toxins that provoked similar cellular responses, spanning inhibitor relationships that were not expected from chemical classification. Our results also revealed widespread antagonistic effects across inhibitors, such that the same gene deletions were beneficial for surviving some toxins but detrimental for others. This work presents a rich dataset relating gene function to chemical compounds, which both expands our understanding of plant-based hydrolysates and provides a useful resource to identify engineering targets.

- 10 Case NT, Berman J, Blehert DS, Cramer RA, Cuomo C, Currie CR, Ene IV, Fisher MC, Fritz-Laylin LK, Gerstein AC, Glass NL, Gow NAR, Gurr SJ, Hittinger CT, Hohl TM, Iliev ID, James TY, Jin H, Klein BS, Kronstad JW, Lorch JM, McGovern V, Mitchell AP, Segre JA, Shapiro RS, Sheppard DC, Sil A, Stajich JE, Stukenbrock EE, Taylor JW, Thompson D, Wright GD, Heitman J, Cowen LE. 2022. The future of fungi: threats and opportunities. *G3 (Bethesda)* 12:jkac224. <https://doi.org/10.1093/g3journal/jkac224>

The fungal kingdom represents an extraordinary diversity of organisms with profound impacts across animal, plant, and ecosystem health. Fungi simultaneously support life, by forming beneficial symbioses with plants and producing life-saving medicines, and bring death, by causing devastating diseases in humans, plants, and animals. With climate change, increased antimicrobial resistance, global trade, environmental degradation, and novel viruses altering the impact of fungi on health and disease, developing new approaches is now more crucial than ever to combat the threats posed by fungi and to harness their extraordinary potential for applications in human health, food supply, and environmental remediation. To address this aim, the Canadian Institute for Advanced Research (CIFAR) and the

Burroughs Wellcome Fund convened a workshop to unite leading experts on fungal biology from academia and industry to strategize innovative solutions to global challenges and fungal threats. This report provides recommendations to accelerate fungal research and highlights the major research advances and ideas discussed at the meeting pertaining to 5 major topics: (1) Connections between fungi and climate change and ways to avert climate catastrophe; (2) Fungal threats to humans and ways to mitigate them; (3) Fungal threats to agriculture and food security and approaches to ensure a robust global food supply; (4) Fungal threats to animals and approaches to avoid species collapse and extinction; and (5) Opportunities presented by the fungal kingdom, including novel medicines and enzymes.

Recent publications.

1 Crous PW et al. 2021. Novel yeast species described in this study – *Papiliotrema horticola* Kachalkin, A.M. Glushakova & M.A. Tomashevskaya, sp. nov. from of apples. Fungal Planet description sheets: 1284–1382. Persoonia 47:178–374. DOI: 10.3767/persoonia.2021.47.06

2 Deshevaya EA, Kachalkin AV, Maksimova IA. et al. 2022. Microbiological analysis of the cloth bundle exposed on the external surface of the international space station over 8 years // BioNanoScience. 12:142–148 - DOI: 10.1007/s12668-021-00930-6

As a part of the space experiment TEST, the cloth bundle was placed on the external surface of the International Space Station (ISS) and returned to Earth after 8 years of exposure to the open space.

Microbiological investigation of the cloth resulted in the detection of viable yeasts. Analysis of nucleotide sequences of the rDNA ITS region established that the yeasts belonged to *Rhodotorula mucilaginosa*.

3 Kachalkin AV. 2022. Phylogeny of *Rhodotorula pinalis* and its reclassification as *Fellozyma pinalis* comb. nov. Microbiology 91:417–420 - DOI: 10.1134/S0026261722100915

The type strain *Rhodotorula pinalis* VKM Y-2963 has been characterized genetically and phylogenetically. Strains from the Moscow region, *Fellozyma* sp. KBP 3851 from *Sphagnum* mosses and

Rh. pinalis VKM Y-2963 from dead conifer needles, were found to be conspecific. The results of phylogenetic analysis suggested that the species *Rh. pinalis* should be reassigned to the genus *Fellozyma*.

4 Glushakova AM, Kachalkin AV, Umarova AB, Ivanova AE, Prokof'eva TV. 2022. Changes in urban soil yeast communities after a reduction in household waste during the COVID-19 pandemic. Pedobiologia 93-94:150822 - DOI: 10.1016/j.pedobi.2022.150822

The soils of streets, urban parks and suburban areas were examined for yeasts in the summer of 2020 on the territory of the southern cities of Russia and the Republic of Crimea: Krasnodar, Maykop, Sochi and Simferopol. The results of this study are compared with the results of a previous study carried out in these cities in 2019. This study was conducted three months after the lockdown due to the COVID-19 pandemic, which led to a sustained decline in household waste deposition in these areas. The number of tourists visiting these southern cities decreased significantly, and the number of walkers and visitors to urban parks fell sharply. In 2020, after the decline of household waste loads, the yeast abundance was slightly but reliably higher than in 2019. A total of 30 yeast

species were observed - 11 ascomycetes and 19 basidiomycetes. This was more than in 2019 and was caused by twice as many autochthonous basidiomycetous yeast species (natural core community), which were found in urban soils only after the reduction in household waste in the environment - *Apiotrichum dulcitum*, *A. laibachii*, *Saitozyma podzolica* *Solicoccozyma terricola*. And at the same time, the proportion of clinically significant (opportunistic) yeasts, *Candida sake* and *Meyerozyma guilliermondii*, was much lower in 2020 than in 2019. Thus, the observed changes in yeast communities in urban soils could be a short-time response of the microbial community to a reduction in household waste.

5 Kachalkin A, Glushakova A, Streletskii R. 2022. Diversity of endophytic yeasts from agricultural fruits positive for phytohormone IAA production. BioTech 11(3):38 - DOI: 10.3390/biotech11030038

This study reports the diversity of cultivable endophytic yeasts from agricultural fruits that respond positively to the plant-promoting property of indole-3-

acetic acid (IAA) production. The IAA synthesis by the strains was quantified with an Agilent 1100 series liquid chromatography system. IAA was present in the

culture liquid of 72% of all 97 strains examined after three days of cultivation. The most active endophytic yeast strains in this study belonged to the species *Aureobasidium pullulans*, *Candida zeylanoides*, *Hanseniaspora uvarum*, *Metschnikowia pulcherrima*, *Meyerozyma caribbica*, *Rhodotorula mucilaginosa*, and *Yarrowia galli*. The highest IAA production was observed in the endophytic strain of *A. pullulans*

(9109.19 ± 146.02 µg/g). No significant differences were found between IAA production in strains from agricultural products of different countries. However, the level of IAA production was strictly strain-specific. Our results suggest that the internal tissues of fruits may be a promising source for the isolation of plant-beneficial yeasts that can be used to promote plant growth.

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<miloshev@bio21.bas.bg> <gmlab@chromatinepigenetics.com>.

The following are abstracts of recently published papers and attended conferences from the lab members.

- 1 Vasileva B, Staneva D, Grozdanova T, Petkov H, Trusheva B, Alipieva K, Popova M, Miloshev G, Bankova V, Georgieva M. 2022. Natural deep eutectic extracts of propolis, *Sideritis scardica* and *Plantago major* reveal potential antiageing activity during yeast chronological lifespan. *Oxidative Med Cellul Longevity* 2022:8368717 - <https://doi.org/10.1155/2022/8368717>

Nowadays, the environmentally friendly approach to everyday life routines including body supplementation with pharma-, nutraceuticals and dietary supplements gains popularity. This trend is implemented in pharmaceutical as well as cosmetic and antiageing industries by adopting a newly developed green chemistry approach. Following this trend, a new type of solvents has been created, called Natural Deep Eutectic Solvents (NADES), which are produced by plant primary metabolites. These solvents are becoming a much better alternative to the already established organic solvents like ethanol and ionic liquids by being nontoxic, biodegradable, and easy to make. An interesting fact about NADES is that they enhance the biological activities of the extracted biological compounds. Here, we present our results that investigate the potential antiageing effect of CiAPD14 as a NADES solvent and three plant extracts with it. The tested NADES extracts are from propolis

and two well-known medicinal plants—*Sideritis scardica* and *Plantago major*. Together with the solvent, their antiageing properties have been tested during the chronological lifespan of four *Saccharomyces cerevisiae* yeast strains—a wild type and three chromatin mutants. The chromatin mutants have been previously proven to exhibit characteristics of premature ageing. Our results demonstrate the potential antiageing activity of these NADES extracts, which was exhibited through their ability to confer the premature ageing phenotypes in the mutant cells by ameliorating their cellular growth and cell cycle, as well as by influencing the activity of some stress-responsive genes. Moreover, we have classified their antiageing activity concerning the strength of the observed bioactivities.

Acknowledgment: This research was funded by the Bulgarian National Science Fund (grant number DN-19/4).

- 2 Mateusz M, Stepień K, Kielar P, Vasileva B, Lozanska B, Staneva D, Ivanov P, Kula-Maximenko M, Molestak E, Tchórzewski M, Miloshev G, Georgieva M. 2022. Actin-related protein 4 and linker histone sustain yeast replicative ageing. *Cells* 11:2754. <https://doi.org/10.3390/cells11172754>

Ageing is accompanied by dramatic changes in chromatin structure organization and genome function. Two essential components of chromatin, the linker histone Hho1p and actin-related protein 4 (Arp4p), have been shown to physically interact in *Saccharomyces cerevisiae* cells, thus maintaining chromatin dynamics and function, as well as genome stability and cellular morphology. Disrupting this interaction has

been proven to influence the stability of the yeast genome and the way cells respond to stress during chronological ageing. It has also been proven that the abrogated interaction between these two chromatin proteins elicited premature ageing phenotypes. Alterations in chromatin compaction have also been associated with replicative ageing, though the main players are not well recognized. Based on this

knowledge, here, we examine how the interaction between Hho1p and Arp4p impacts the ageing of mitotically active yeast cells. For this purpose, two sets of strains were used - haploids (WT(n), *arp4*, *hho1Δ* and *arp4 hho1Δ*) and their heterozygous diploid counterparts (WT(2n), *ARP4/arp4*, *HHO1/hho1Δ* and *ARP4 HHO1/arp4 hho1Δ*) - for the performance of extensive morphological and physiological analyses during replicative ageing. These analyses included a comparative examination of the yeast cells' chromatin structure, proliferative and reproductive potential, and resilience to stress, as well as polysome profiles and chemical composition. The results demonstrated that

the haploid chromatin mutants *arp4* and *arp4 hho1Δ* demonstrated a significant reduction in replicative and total lifespan. These findings lead to the conclusion that the importance of a healthy interaction between Arp4p and Hho1p in replicative ageing is significant. This is proof of the concomitant importance of Hho1p and Arp4p in chronological and replicative ageing.

Acknowledgments: This research was funded by the Bulgarian National Research Fund with a grant number DN 11/15 and partially by a grant from the National Science Centre in Poland (UMO-2018/29/B/NZ1/01728) to MT.

3 Bela Vasileva. Exploring the role of the linker histone Hho1p and the actin-related protein Arp4p in yeast *Saccharomyces cerevisiae*'s ageing. PhD thesis.

Saccharomyces cerevisiae is a type of organism that allows the distinction between replicatively and chronologically ageing cells, providing a perfect opportunity to study the relationship between these two ageing models. Therefore, we aimed to investigate the different molecular mechanisms during the chronological ageing process in yeast cells with mutations in chromatin structure. More specifically, the role of the yeast linker histone Hho1p and the actin-like protein Arp4p in this process. The results showed that altered chromatin dynamics during the chronological life span led to significant changes in growth and cell cycle and in the expression profiles of stress-responsive genes. This opens up new horizons for developments to slow down the ageing process by influencing chromatin organization and gene expression.

Proving that aberrant chromatin organization has severe consequences for ageing and showing that preventing the interaction between the yeast linker histone Hho1p and Arp4p led to premature ageing phenotypes in mutant cells, we tested the prospect of

using Natural Deep Eutectic Solvents (NADES)-derived biological compounds in antiaging therapies. NADES are connected to the green chemistry branch by being non-toxic, biodegradable, and eco-friendly compared to well-known solvents like ethanol and ionic liquids. They also can increase the biological properties of their extracts. Therefore, we tested the potential antiaging action of NADES extracts of two well-known Bulgarian medicinal plants - *Sideritis scardica* Griseb and *Plantago major* L., as well as propolis. Our results confirmed that yeast chromatin mutants are a suitable model organism for testing substances with antiaging effects. Furthermore, we have proven that our NADES solvent exhibited an antiaging effect. However, the strength of this effect was different when combined with extracts of propolis, *S. scardica* and *P. major*, with the propolis extract exhibiting the most substantial antiaging properties.

Acknowledgments: This research was partially supported by the Bulgarian National Research Fund by Grants number DN 11/15 and DN 19/4.

4 Ivanov P, Staneva D, Georgieva M, Fleming A, Miloshev G. 2022. Comparison of the impacts of linker histone and an HMG protein on the chromatin loop organization in yeast. Jubilee scientific conference "100th anniversary of the birth of Acad. Roumen Tsanev", 5th - 7th October 2022, Sofia, Bulgaria

Over the years our understanding of the importance of chromatin have grown substantially. A large part of our knowledge about the chromatin structure and dynamics has come from extensive research conducted in yeast. Yeast contain only a single linker histone which has profound effects on higher-order chromatin organization and also have impact on cellular ageing and viability under different stress factors like calorie restriction. Hmo1 is a non-

histone chromatin protein in yeast, member of the HMG protein family and homologue of human HMGB1. It is involved in reorganization of chromatin structure in response to nutrient deficiency and DNA damage. Because two proteins have similar localizations in chromatin, binding sites with the nucleosome and in addition, interact with other chromatin proteins and enzymatic complexes a hypothesis appeared that they have inter-replaceable

functions in the chromatin. In this study we have checked the rationality of the above hypothesis.

In order to make a comparison between these two proteins we first assessed cellular viability of yeast deletion mutant strains - *Δhho1* and *Δhmo1*. Then, by the help of Yeast Chromatin Comet Assay (YChCA) – a method for studying chromatin loop organization we have compared the chromatin organization. Our findings showed that both proteins perform important roles in chromatin loop organization and cellular

viability. However, according to our results, Hho1p and Hmo1p possess bold differences in the loop organization. Therefore, although similar by place and contacts in the chromatin Hho1p and Hmo1p have distinctly different roles in its higher levels of organization.

Acknowledgments: This work is partially sponsored by Grant Number DN 11-15 and Grant Number KP-06-N31/15 at the Bulgarian Science Fund.

- 5 Staneva D, Vasileva B, Podlesniy P, Miloshev G, Georgieva M. 2022. mtDNA copy number and mitochondrial membrane potential during CLS of yeast chromatin mutants. Jubilee scientific conference “100th anniversary of the birth of Acad. Roumen Tsanev“, 5th - 7th October 2022, Sofia, Bulgaria

Mitochondria, the powerhouse of the eukaryotic cell, are multifunctional, highly dynamic organelles. In the process of ATP synthesis, reactive metabolic intermediates and reactive oxygen species are generated that can serve as fine-tuning regulators of cell signalling pathways and cellular metabolism. Mounting evidence has shown the importance of mitochondria in the stress response, cell longevity, ageing and death. Although the mitochondrion possesses its own genome, nuclear encoded proteins are essential in the regulation of mitochondria biogenesis, morphology, dynamics and function.

The structure of chromatin and the epigenetic mechanisms govern the accessibility to DNA and control gene transcription and thus, can indirectly influence the nucleo-mitochondrial communications. Chromatin components, such as the linker histone Hho1p and the actin-related protein Arp4/Act3, a subunit of several chromatin remodelling complexes, were found to be crucial for the maintenance of proper chromatin structure. *Saccharomyces cerevisiae hho1Δ*, *arp4* and *arp4hho1Δ* mutant cells showed impaired chromatin organization, accompanied by changes in

cell morphology, gene expression, stress resistance and ageing. In this article we present our studies on the mitochondrial functionality in *S. cerevisiae arp4*, *hho1Δ*, and *arp4hho1Δ* mutant cells in comparison with the wild type. We assessed the ability of mutants to utilize non-fermentative carbon sources, petit colonies formation, mitochondrial DNA integrity and copy number, the mitochondrial membrane potential and the expression of two nuclear genes, *ATG18* and *CDC28*, involved in the regulation of mitochondria biogenesis and turnover. Follow-up of the last three parameters over the course of the chronological lifespan showed that the three chromatin mutants acquired strain-specific changes compared to the WT strain. The most pronounced were the alterations found in the *arp4hho1Δ* strain, which was the only petit colony-forming mutant, unable to grow on respiratory substrates and with partial or complete depletion of the mitochondrial genome.

Acknowledgments: This work is partially sponsored by Grant Number DN 11-15 and Grant Number KP-06-N31/15 at the Bulgarian Science Fund.

- 6 Vasileva B, Staneva D, Grozdanova T, Petkov H, Trusheva B, Alipieva K, Popova M, Miloshev G, Bankova V and Georgieva M. 2022. Natural deep eutectic solvents as antiageing compounds. Jubilee scientific conference “100th anniversary of the birth of Acad. Roumen Tsanev“, 5th - 7th October 2022, Sofia, Bulgaria

The green chemistry approach has gained a vast popularity among the pharmaceutical, cosmetic and antiageing industries. Following this trend, a new type of solvents has been created, called Natural Deep Eutectic Solvents (NADES), which are produced by plant primary metabolites. NADES are becoming a superior alternative to the already established organic solvents like ethanol and ionic liquids by being non-toxic, biodegradable, and easy to make. In addition to

all its beneficial properties, these types of solvents have been found to enhance the biological activities of the extracted biological compounds. Our results examine the potential antiageing effect of a newly developed NADES solvent - CiAPD14 together with its three extracts from propolis and two well-known medicinal plants – *Sideritis scardica* and *Plantago major*. Together with the solvent, their antiageing properties have been tested during the chronological

lifespan of four *Saccharomyces cerevisiae* yeast strains – a wild type and three chromatin mutants, which have been previously proven to exhibit characteristics of premature ageing. Our results demonstrate the potential antiageing activity of the NADES solvent and its extracts, as they have influenced the premature ageing phenotypes in the mutant cells by mitigating their cellular growth and cell cycle, as well as by

influencing the activity of some stress-responsive genes. The antiageing activity of the compounds has been classified according to the strength of the observed bioactivities.

Acknowledgments: This work is partially sponsored by Grant Number DN 11-15 and Grant Number KP-06-N31/15 at the Bulgarian Science Fund.

VII State Scientific-Research Institute for Genetics and Selection of Industrial Microorganisms (GosNIIGenetika), NRC “Kurchatov Institute”, I-Dorozhnyi 1, Moscow 117545, Russia. Communicated by E.S. Naumova <[lena_naumova@yahoo.com](mailto:lenua_naumova@yahoo.com)>.

The following are papers for 2022 or in press.

- 1 Lyutova LV, Naumov GI, Shnyreva AV, Naumova ES. 2022. Intraspecific polymorphism of the yeast *Kluyveromyces lactis*: genetic populations. *Microbiology (Moscow)* 91 (4): 421–431.
- 2 Borovkova AN, Shalamitskiy MYu, Naumova ES. 2023. Pectinolytic yeast *Saccharomyces paradoxus* is a new gene pool for winemaking. *Microbiology (Moscow)* 92 (2) (in press).

A large-scale screening of pectinolytic activity in the yeast *Saccharomyces paradoxus* isolated from various natural sources in Europe, Asia, North America and the Hawaiian Islands was carried out. Of the 98 studied strains, pectinolytic activity was absent only in five Hawaiian and two European strains. Most strains were able to secrete active endo-polygalacturonase. North American strains UCDFST 52-225, UCDFST 61-359, UCDFST 61-220, 95-3, and UCDFST 62-186 have very high pectinolytic activity, comparable or even higher than that of the experimentally obtained tetraploid strain *S. cerevisiae* VKPM Y-718. A comparative analysis of the nucleotide and

amino acid sequences of pectinase genes showed that the North American and Far Eastern populations of *S. paradoxus* are more genetically diverse than the European and Hawaiian ones. Phylogenetic analysis confirmed the species specificity of the *PGU* genes of *Saccharomyces* yeasts. Of the eight *Saccharomyces* species, high pectinolytic activity is characteristic of *S. bayanus* and *S. paradoxus*. Five North American strains with the highest pectinolytic activity are of interest for further molecular genetic studies and breeding work with wine yeasts. The ecological role of endo-polygalacturonase is discussed.

- 3 Borovkova AN, Naumov GI, Shnyreva AV, Naumova ES. 2023. Genetically isolated population of *Saccharomyces bayanus* in New Zealand and Australia. *Russian J Genet.* 59(4) (in press).

The genetic relatedness of yeasts in the *Saccharomyces bayanus* complex has been studied using the methods of molecular and classical genetics. A divergent population of *S. bayanus* has been found in New Zealand and Australia. The *S. bayanus* complex includes four genetic populations: *S. bayanus* var. *bayanus*, *S. bayanus* var. *uvarum*, *S. eubayanus* and New Zealand population. The strains of the New Zealand population differ significantly in the nucleotide sequences of nuclear (*FSY1*, *HIS3*, *MET2*) and mitochondrial (*FUN14*, *COX2*) genes and form

semi-sterile hybrids with other populations: viability of ascospores is 6.2–23.3%. There is no complete interspecific postzygotic isolation between *S. bayanus* var. *bayanus*, *S. bayanus* var. *uvarum*, *S. eubayanus*, and New Zealand populations: all hybrids showed regular meiotic segregation of control auxotrophic markers. According to the results obtained, four genetic populations belong to the same biological species with genomic divergence at the level of taxonomic varieties.

VIII University of Helsinki, Faculty of Biological and Environmental Sciences, Organismal and Evolutionary Biology Research Programme, and the Viikki Plant Science Centre, PL 65, Viikinkaari 1, 00014 Helsinki Finland. Communicated by Kirk Overmyer <kirk.overmyer@helsinki.fi>.

Recent publication.

- 1 Wang K, Auzane A, Overmyer K. 2022. The immunity priming effect of the *Arabidopsis* phyllosphere resident yeast *Protomyces arabidopsidicola* strain C29. *Frontiers in Microbiology* 13: 956018. doi: 10.3389/fmicb.2022.956018.

The phyllosphere is a complex habitat for diverse microbial communities. Under natural conditions, multiple interactions occur between host plants and phyllosphere resident microbes, such as bacteria, oomycetes, and fungi. Our understanding of plant-associated yeasts and yeast-like fungi lags behind other classes of plant-associated microbes, largely due to a lack of yeasts associated with the model plant *Arabidopsis*, which could be used in experimental model systems. The yeast-like fungal species *Protomyces arabidopsidicola* was previously isolated from the phyllosphere of healthy wild-growing *Arabidopsis*, identified, and characterized. Here we explore the interaction of *P. arabidopsidicola* with *Arabidopsis* and found *P. arabidopsidicola* strain C29 was not pathogenic on *Arabidopsis*, but was able to survive in its phyllosphere environment both in

controlled environment chambers in the lab and under natural field conditions. Most importantly, *P. arabidopsidicola* exhibited an immune priming effect on *Arabidopsis*, which showed enhanced disease resistance when subsequently infected with the fungal pathogen *Botrytis cinerea*. Activation of the mitogen-activated protein kinases (MAPK), camalexin, salicylic acid, and jasmonic acid signaling pathways, but not the auxin-signaling pathway, was associated with this priming effect, as evidenced by MAPK3/MAPK6 activation and defense marker expression. These findings demonstrate *Arabidopsis* immune defense priming by the naturally occurring phyllosphere resident yeast species, *P. arabidopsidicola*, and contribute to establishing a new interaction system for probing the genetics of *Arabidopsis* immunity induced by resident yeast-like fungi.

IX Laboratory of Yeast Systematics, Tokyo NODAI Research Institute (TNRI), Tokyo University of Agriculture, 1-1-1 Sakuragaoka, Setagaya, Tokyo 156-8502 Japan. Communicated by M. Takashima <mt207623@nodai.ac.jp>.

The following paper was recently accepted.

- 1 Takashima M, Sugita T. 2022. Taxonomy of pathogenic yeasts *Candida*, *Cryptococcus*, *Malassezia*, and *Trichosporon*: current status, future perspectives, and proposal for transfer of six *Candida* species to the genus *Nakaseomyces*. *Med Mycol J* 63:119-132.

This review describes the changes in yeast species names in the previous decade. Several yeast species have been reclassified to accommodate the “One fungus = One name”(1F=1N) principle of the Code. As the names of medically important yeasts have also been reviewed and revised, details of the genera *Candida*, *Cryptococcus*, *Malassezia*, and *Trichosporon* are described in Section 3, along with the history of name changes. Since the phylogenetic positions of

Candida species in several clades have not been clarified, revision of this species has not been completed. Among the species that remain unrevised despite their importance in the medical field, we propose the transfer of six *Candida* species to be reclassified in the *Nakaseomyces* clade, including *Nakaseomyces glabratus* and *Nakaseomyces nivalensis*.

X Dept. of Molecular & Cell Biology, University of California, Berkeley, 142 Weill Hall #3200 Berkeley, CA 94720-3200. Communicated by Jeremy Thorner <jthorner@berkeley.edu>.

On Tuesday, 27 September 2022, Distinguished Professor Emeritus Jeremy Thorner delivered (remotely) the Sir Frederick Gowland Hopkins Memorial Lecture at the 5th European Workshop on AMPK and AMPK-related Protein Kinases in Glasgow, Scotland, as part of his receipt of the 2022 Centenary Award of The (UK) Biochemical Society.

[see: <https://www.biochemistry.org/grants-and-awards/awards/the-centenary-award/>]. Much of the content of the talk can be found in the following publication.

- 1 Thorner J (2022) TOR complex 2 is a master regulator of plasma membrane homeostasis. *Biochem J.* 479:1917-1940 (doi: 10.1042/BCJ202203888).

XI International Centre of Brewing and Distilling, Heriot-Watt University, Edinburgh, Scotland and Canadian Institute of Fermentation Technolog, Department of Process Engineering and Applied Science, Dalhousie University, PO Box 15000, Halifax, Nova Scotia, Canada B3H 4R2. Communicated by <Alex.Speers@Gmail.com>.

Recent publication.

- 1 Speers RA. 2022. A review of pasteurization literature for alcohol and non-alcohol beers. *MBAA Technical Quarterly*, In Press.

Presentation.

- 2 Speers RA. 2022. Keeping your beer young. Invited Presentation. Nov 15, 2022. Quebec City, PQ. MBAA Eastern Canada Section/ Congrès AMBQ 2022.

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

Recently published papers.

- 1 He MQ, Zhao RL, Liu DM, Denchev TT, Begerow D, Yurkov A *et al.* 2022. Species diversity in Basidiomycota. *Fungal Diversity* 114(1): 281-325.

Fungi are eukaryotes that play essential roles in ecosystems. Among fungi, Basidiomycota is one of the major phyla with more than 40,000 described species. We review species diversity of Basidiomycota from five groups with different lifestyles or habitats: saprobic in grass/forest litter, wood-decaying, yeast-like, ectomycorrhizal, and plant parasitic. Case studies of *Agaricus*, *Cantharellus*, *Ganoderma*, *Gyroporus*, *Russula*, *Tricholoma*, and groups of lichenicolous yeast-like fungi, rust fungi, and smut fungi are used to determine trends in discovery of biodiversity. In each case study, the number of new species published during 2009–2020 is analysed to determine the rate of discovery. Publication rates differ between taxa and reflect different states of progress for species discovery in different genera. The results showed that

lichenicolous yeast-like taxa had the highest publication rate for new species in the past two decades, and it is likely this trend will continue in the next decade. The species discovery rate of plant parasitic basidiomycetes was low in the past ten years, and remained constant in the past 50 years. We also found that the establishment of comprehensive and robust taxonomic systems based on a joint global initiative by mycologists could promote and standardize the recognition of taxa. We estimated that more than 54,000 species of Basidiomycota will be discovered by 2030, and estimate a total of 1.4–4.2 million species of Basidiomycota globally. These numbers illustrate a huge gap between the described and yet unknown diversity in Basidiomycota.

- 2 Mozzachiodi S, Bai FY, Baldrian P, Bell G, Boundy-Mills K, Buzzini, P *et al.* 2020. Yeasts from temperate forests. *Yeast* 39(1-2):4-24.
- 3 Boekhout, T, Amend, A.S, El Baidouri, F, Gabaldón, T, Geml, J, Mittelbach, M, et al. 2020. Trends in yeast diversity discovery. *Fungal Diversity* 114 (1): 491-537.
- 4 da Silva M, Desmeth P, Venter SN, Shouche Y, Yurkov A. 2022. Trends in Microbiology. In press. DOI: 10.1016/j.tim.2022.10.010

Restrictions placed on the distribution of biological material by the legislation of countries such as India, South Africa, or Brazil exclude strains that could serve as type material for the validation or valid

publication of prokaryotic species names. This problem goes beyond prokaryotic taxonomy and is also relevant for other areas of biological research.

Community paper providing an outline of the classification of the kingdom *Fungi*.

- 5 Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena, RK *et al.* 2020. Outline of Fungi and fungus-like taxa - 2021. *Mycosphere* 13(1):53-453.

The ‘Outline of Fungi and fungus-like taxa’ (Wijayawardene et al. 2020a) was the first attempt at compiling a classification of all taxa (from genera to higher levels) in the Kingdom Fungi, with the contribution and agreement of 155 authors. The Outline listed higher-level taxa (phyla, classes, orders, families and genera) in the higher fungi (i.e, Ascomycota, Basidiomycota), early-diverging lineages of fungi, fossil fungi and fungus-like taxa. Moreover, the estimated number of species based on the available data, for each genus, was included. During preparation of the manuscript, the authors recognized the necessity to continuously update such an important database, and thus www.outlineoffungi.org was developed (Wijayawardene et al. 2020b). One of the important features of the Outline of Fungi is providing a

platform for different opinions on different taxa, mainly at higher ranks. As an example, Wijayawardene et al.(2020a) included two different classifications for Leotiomycetes and Glomeromycota. The aim of including these differing opinions was to make these aware to taxonomists and mycologists since it is vital to discuss divergent views broadly, rather than ignoring or excluding them without rational arguments. It is widely accepted that only ca. 150,000 (5-10%) species of fungi (Species Fungorum 2021) are currently recognized, thus classification conclusions will be subjective. Nevertheless, publishing such controversial opinions in a single peer reviewed article is challenging; hence, the series of Outline of Fungi and its web page (<https://www.outlineoffungi.org/>) aim to provide an opportunity for this.

Book chapter.

- 6 Reimer LC, Yurkov A. 2022. Data management in culture collections. In: Kurtböke I. (ed.) Importance Of Microbiology Teaching And Microbial Resource Management For Sustainable Futures. Academic Press, pp. 135-155.

Culture collections preserve the living material and the associated information alike. The physical culture and its properties are both important for users. Strain characteristics can be inferred from a detailed description of environmental parameters and results of ex situ experiments. Some of these results will be published in the literature but others remain unpublished, such as strain tests performed by collection staff. Culture collections that did not restrict their holdings to a particular taxonomic or functional group of microorganisms consequently employed a large diversity of tests. In order to handle that

heterogeneous information on a large scale, data management in culture collections is rapidly gaining importance. Data management includes several mobilisation and harmonisation steps. This chapter provides examples of data types routinely accumulated by culture collections, and how this information is unified, analysed and shared. Databases that accumulate and display records from collections worldwide become a window into modern big data research. In this chapter, we review different strategies for building up strain-related databases, point to important difficulties and name possible solutions.

The following papers have been submitted for publication or presented at conferences.

- 1 Vu HTL, Yukphan P, Tanasupawat S, Mikata K, Yamada Y. The revision of Schizosaccharomycetaceae. Jxiv - <https://doi.org/10.51094/jxiv.188>

Although the genus *Hasegawaea* was introduced along with the recognition of the genus *Octosporomyces* in the classification of fission yeasts, the two additional genera were neither accepted nor recognized. However, the genus *Schizosaccharomyces* sensu Kurtzman et Robnett was taxonomically heterogeneous-natured and corresponded to a higher-ranked taxon, i.e., a monotypic family. Thus, the following three genera were confirmed in the family Schizosaccharomycetaceae. The genus *Schizosaccharomyces* sensu stricto was comprised of *Schizosaccharomyces pombe*, the genus *Octosporomyces* was of the three species, *Schizosaccharomyces octosporus*,

Schizosaccharomyces osmophilus, and *Schizosaccharomyces cryophilus* as *Octosporomyces octosporus*, *Octosporomyces osmophilus*, and *Octosporomyces cryophilus*, and the genus *Hasegawaea* was of *Schizosaccharomyces japonicus* as *Hasegawaea japonica*. In conclusion, the precise classification of microorganisms will not be able to be expected in the generic designation without the presence of taxonomic homogeneous-natured taxa. The phylogenetic distances have to be absolutely considered. Namely, the longer the distances are, the more taxonomic heterogeneous natures will be increased in the resulting genus.

- 2 Yamada Y, Vu HTL Yukphan P, Tanasupawat S. The revision of Lipomycetaceae. Jxiv - <https://doi.org/10.51094/jxiv.189>

In the family Lipomycetaceae, the seven genera *Waltomyces*, *Zygozoma*, *Babjevia*, *Smithiozoma*, *Kawasakia*, *Limtongia*, and *Kockiozoma* were introduced. However, all of them were neither accepted nor recognized. This paper described the historical surveys in the systematics of the

Lipomycetaceous yeasts and confirmed the total of ten genera within the family, i.e., the genus *Lipomyces* sensu stricto (the type genus), the above mentioned seven genera, the monotypic genus *Dipodascopsis*, and the new genus *Neeoaidaea* from the phylogenetic and the phenotypic points of view.

- 3 Vu HTL,1 Yukphan P, Tanasupawat S, Yamada Y. The generic circumscription of *Kockiozoma* (Lipomycetaceae). Jxiv - <https://doi.org/10.51094/jxiv.221>

The genus *Kockiozoma* was introduced as the ninth and the monotypic genus in the family Lipomycetaceae. On the other hand, a number of anamorphic species were reported as *Myxozoma*. This paper deals with the phylogenetic relationships between the teleomorphic species, *Kockiozoma suomiensis* and the anamorphic species. To constitute a taxonomic homogeneous-natured genus, 1) the several species 42 concerned have to be tightly coupled with one another phylogenetically. 2) To

make the several species tightly coupled, the branch lengths have to be short or the calculated sequence similarities have to be 98% or more in the 18S rRNA gene sequences among the species. Thus, the following seven *Myxozoma* species were accommodated to the genus *Kockiozoma* as *Kockiozoma geophila* f.a., *Kockiozoma sirexii* f.a., *Kockiozoma neotropica* f.a., *Kockiozoma vanderwaltii* f.a., *Kockiozoma mucilagina* f.a., *Kockiozoma neglecta* f.a. and *Kockiozoma melibiosi* f.a.

Recent publications.

- 1 de Vega C, Álvarez-Pérez S, Albaladejo R, Steenhuisen SL, Lachance MA, Johnson S, Herrera C. 2021. The role of plant-pollinator interactions in structuring nectar microbial communities. *J Ecol* 109:3379–3395.

1. Floral nectar harbours a diverse microbiome of yeasts and bacteria that depend predominantly on animal visitors for their dispersal. Since pollinators visit specific sets of flowers and carry their own unique microbiota, we hypothesize that plant species visited by the same set of pollinators may support non-random nectar microbial communities linked together by the type of pollinator.

2. Here we explore the importance of plant–pollinator interactions in the assembly of nectar microbiome and study the role of plant geographic location as a determinant of microbial community composition. We intensively sampled the nectar of 282 flowers of 48 plant species with beetles, birds, long-tongued and short-tongued insects as pollinators in wild populations in South Africa, one of the world's biodiversity hotspots, and using molecular techniques we identified nectar yeast and bacteria taxa. The analyses provided new insights into the richness, geographic structure and phylogenetic characterization of nectar microbiome, and compared patterns of composition of bacteria and yeast communities in relation to plant and pollinator guild.

3. Our results showed that plant–pollinator interactions played a crucial role in shaping nectar

microbial communities. Plants visited by different pollinator guilds supported significantly different yeast and bacterial communities. The pollinator guild also contributed to the maintenance of beta diversity and phylogenetic microbial segregation. The results revealed different patterns for yeast and bacteria; whereas plants visited by beetles supported the highest richness and phylogenetic diversity of yeasts, bacteria communities were significantly more diverse in plants visited by other insect groups. We found no clear microbial spatial segregation at different geographical scales for bacteria, and only the phylogenetic similarity of yeast composition was correlated significantly with geography.

4. Synthesis. Interactions of animal vector, plant host traits and microbe physiology contribute to microbial community assemblages in nectar. Our results suggest that plants visited by the same pollinator guild have a characteristic nectar microbiota signature that may transcend the geographic region they are in. Contrasted patterns for yeast and bacteria stress the need for future work aimed at better understanding the causes and consequences of the importance of plants and pollinators in shaping nectar microbial communities in nature.

The following article appeared in the section “Yeast Extracts” of the journal.

- 2 Lachance MA. 2022. Phylogenies in yeast species descriptions: in defense of neighbor-joining. *Yeast* 39:513-520.

The neighbor-joining (NJ) method of tree inference is examined, with special attention to its use in yeast species descriptions. How the often-vilified method works is often misunderstood. More importantly, given the right kind of data, its output is a phylogram that illustrates a hypothetical phylogeny that is just as credible as that obtained by any other method. And as with any other method, the result is greatly affected by sampling intensity, particularly the number of aligned positions used for analysis. I

address various allegations, including the claim that the method is phenetic, and, therefore, not phylogenetic. I argue that NJ is the most suitable tree inference method to use in yeast species descriptions, primarily because it is best at visually preserving the extent of sequence divergence between close relatives, which continues to be the primary criterion for yeast species delineation. The relevance of bootstraps in the application of the phylogenetic species concept is discussed.

3 Cochrane RR et al. 2022. Superior conjugative plasmids delivered by bacteria to diverse fungi. *BioDesign Research*. 2022:9802168.

Fungi are nature's recyclers, allowing for ecological nutrient cycling and, in turn, the continuation of life on Earth. Some fungi inhabit the human microbiome where they can provide health benefits, while others are opportunistic pathogens that can cause disease. Yeasts, members of the fungal kingdom, have been domesticated by humans for the production of beer, bread, and, recently, medicine and chemicals. Still, the great untapped potential exists within the diverse fungal kingdom. However, many yeasts are intractable, preventing their use in biotechnology or in the development of novel treatments for pathogenic fungi. Therefore, as a first step for the domestication of new fungi, an efficient DNA delivery method needs to be developed. Here, we report the creation of superior conjugative plasmids and demonstrate their transfer via conjugation from bacteria to 7 diverse yeast

Symposium lecture.

4 Lachance MA. Forty years of yeast biogeography. 36th International Specialized Symposium on Yeasts, Vancouver, British Columbia, Canada.

"Alles is overal: maar het milieu selecteert". Did Lourens Bass Becking intend his famous maxim to immunize microbial ecology against Alfred Wallace's recognition that geography is a major driver of the evolutionary process? Although the earth's microbiota is sometimes seen as a global soup in a state of constant homogenization, the view suggested by my early mentors, Herman Phaff and Tom Starmer, was different. They taught me that when yeast diversity exploration is conducted with a modicum of sampling design and intensity, the emerging patterns are anything but random. Over the course of four decades as a yeast hunter, I have attempted to show how biogeographic processes such as limited dispersal or vicariance can play a major role in the diversification of yeast species. I have succeeded in documenting instances of spatial structuring at many scales, from global to continental, regional, or local. This required identifying habitats where a small number of yeast species can be repeatedly and dependably isolated with no recourse to enrichment procedures. In the simplest instances, all that was needed is a well-designed, thorough sampling of different components of a habitat followed by identification of the yeast species, as for example the demonstration that a single prickly pear cactus plant can host two highly distinct yeast communities, one in the fruit, and another in the necrotic pads. In other cases, it was necessary to

species including the emerging pathogen *Candida auris*. To create our superior plasmids, derivatives of the 57 kb conjugative plasmid pTA-Mob 2.0 were built using designed gene deletions and insertions, as well as some unintentional mutations. Specifically, a cluster mutation in the promoter of the conjugative gene *traJ* had the most significant effect on improving conjugation to yeasts. In addition, we created Golden Gate assembly-compatible plasmid derivatives that allow for the generation of custom plasmids to enable the rapid insertion of designer genetic cassettes. Finally, we demonstrated that designer conjugative plasmids harboring engineered restriction endonucleases can be used as a novel antifungal agent, with important applications for the development of next-generation antifungal therapeutics.

secure means of unambiguously distinguishing isolates below the species level. An early success was the recovery of the cactophilic yeast *Clavispora opuntiae* from numerous sites in the Caribbean Sea, the Sonoran Desert, Hawaii, Northern Argentina, Central Brazil, and Australia. Fingerprinting of genetic individuals by restriction mapping of the ribosomal RNA gene cluster showed instances of regional partitioning, host specialization, and even founder effects, albeit anthropogenic. In 1987, the discovery of the first two of 45 floricolous insect-associated haplontic *Metschnikowia* species, in parallel with the adoption of DNA sequence-based PCR markers, gave rise to data used in demonstrating phylogeographic patterns at every possible scale. In these species, differentiation can occur for communities at the centimetre scale and populations at the kilometre scale, even leading to speciation over as little as 100 kilometres. This is due to a strong association between the yeasts and their host insects, primarily nitidulid beetles, although the nature of the association is not known. Now that it is established that "alles is NIET overal", the next challenge will be to apply the powerful tools of phylogenomics to determine what drives host specificity (het milieu selecteert) and to what extent specificity, as opposed to historical contingency, drives the process of differentiation.

International Commission on Yeasts

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ISSY36, Wednesday July 13, 2022

Restaurant Seasons in the Park, Vancouver, Canada

1. Opening Remarks from the Chair

The chair (D. Mattanovich) opened the meeting, welcomed participants and outlined the agenda. He noted that there were twenty eight ICY commissioners plus three nominees to the commission in attendance and a further twenty nine sent apologies. He thanked Vivien Measday for organising the commissioner's meeting and for the very successful organisation and hosting of ISSY36.

D. Mattanovich reported on the success of ICY15, held online (from Vienna) in August 2021. The meeting generated a substantial surplus and the organisers generously proposed allocating this surplus to future meetings as follows:

- €15k to ICY16 (to be held in South Africa in 2024)
- €10k to ICYGMB who were co-organisers in ICY15 for the 2023 meeting
- €5k each to forthcoming ISSY meetings, 36 in Vancouver in 2022, and 37 in Adelaide, Australia in 2023.

2. Minutes of 2021 ICY meeting

The minutes of the last ICY Commissioner's meeting (held online on the occasion of ICY15 24/08/2021, chaired by the previous ICY president, Hiroshi Takagi, have previously been circulated and it was noted by H. Takagi that there were only minor typographical amendments proposed. Accordingly, the minutes were accepted.

3. Past commissioners who passed away in recent times were remembered

- Milan Certik (Commissioner from Slovakia) paid a tribute to former Commissioner Prof. Ivan Hapala from the Slovak Academy of Sciences.
- The former Danish Commissioner Jørgen Stenderup who passed away on July 4, 2022, was also remembered.
- A minute's silence was observed in memory of our deceased colleagues.

4. Election of New Commissioners:

The chair reported positively on the nomination of nine new commissioners. The three nominated new commissioners who were in attendance were asked to leave the chamber for this portion of the meeting.

Details of all nominated commissioners had been circulated and current commissioners had been given the opportunity to comment in advance to the ICY President. D. Mattanovich noted that the response to all had been overwhelming positive and asked that the Commission proceed with the formal business of electing these commissioners. A motion that the entire slate be elected was proposed by Tom Jeffries and seconded by André Lachance. There was no opposition and the following commissioners were accordingly deemed to be elected.

- Andreas Gombert (Brazil)
- Olga Heidingsfeld (Czech Republic)
- Ivana Marova (Czech Republic)
- Jan-Petri Lahtvee (Estonia)
- Ildar Nisamedtinov (Estonia)
- Masaki Mizunuma (Japan)
- Paula Goncalves (Portugal)
- Paula Ludovico (Portugal)
- Verena Siewers (Sweden)

The new commissioners in attendance were invited back into the chamber and congratulated. The Chair undertook to notify the other new commissioners of their election.

5. Retired Commissioners (see appendix)

The chair reported the retirement of the six commissioners listed below. Their contribution to the yeast community and the commission was acknowledged.

- Mike Ingledew (Canada)
- Mogens Jakobsen (Denmark)
- Tiina Alamäe (Estonia)
- Akihiko Kondo (Japan)
- Teun Boekhout (Netherlands)

- Grzegorz Bartosz (Poland)

6. Status of the current ISSY36 (Vivien Measday)

Vivien Measday gave an update on the status of ISSY36 (ongoing). The final number of delegates in attendance was 150-155 which was considered good given all the uncertainty surrounding COVID. The ongoing challenges were noted and this resulted in a small number of late withdrawals due to COVID infections, travel disruption and visa difficulties. About 30% of the attendees were from North America, with major representation from Europe and a good distribution from around the globe. So far, ISSY36 is proceeding very well and there have been no on-site issues. The chair and commission again complimented V. Measday on the excellent meeting organisation.

7. Updates for Future ISSY/ICY Meetings

- ISSY37 (Adelaide, Australia) 28 Nov - 01 Dec 2023: Vladimir Jiranek outlined details of the meeting and the aspiration to attract 250 delegates to ISSY37, with the theme Yeast Biotech 2.0: New Yeast, Knowledge and Applications. He urged commissioners to support and attend the meeting.
- ICY16 (Cape Town, South Africa) in 2024: Florian Bauer outlined progress in the organisation of this meeting. Everything is in hand but the final date needs to be decided. The venue in Cape Town is held for several dates at present.

8. ISSY38 (2025) and beyond:

The idea of holding ISSY38 in Denmark in 2025 was discussed. This possibility had already been raised at previous ICY meetings but a decision had not been reached. The Danish commissioner present (Lene Jespersen) outlined again the challenges and expense of having the meeting in Denmark and indicated that it would only be possible by securing substantial sponsorship and the support from some key researchers from other disciplines like industrial biotechnology (e.g. from DTU). Jens Nielsen had made links to the relevant Danish research community, and a meeting was scheduled for August this year. Lene Jespersen suggested to

revert to the Commission Chair until September this year with a decision on whether or not the meeting could take place in Denmark in 2025.

Decision making process: At the commissioners meeting there was not another proposal for a meeting in 2025 on the table so the decision of the Commission was to support a meeting in Denmark if the Danish commissioner(s) agree to host it. This will need to be decided before the end of 2022 and given that the next meeting of the full commission will not be until November 2023 in Adelaide, it is likely that formal decisions on ISSY38 (2025) will need to be taken by email or virtual meeting in autumn 2022 or early in 2023.

Two further locations and organisers for future ISSY meetings were briefly discussed without any decisions taken:

- Poland – Ada Skoneczna reported that the Polish yeast community is interested in organising a future ISSY meeting, but location and timing still needed to be explored. It was discussed whether this could be an option for 2025 if Denmark would not be able to organize the meeting then. The Polish commissioners were encouraged to explore the opportunities and report back to the Chair.
- Uruguay – The commissioner for Uruguay (Francisco Carrau) expressed an interest in hosting a future ISSY meeting and was encouraged to develop a proposal for future consideration.
- The possibility and interest in holding an ISSY meeting in Asia was also mentioned, and appreciated by the commission.

9. Miscellaneous information

- “*theyeasts.org*” project by Teun Boekhout *et al.*, the online resource on yeast taxonomy is proceeding well, and it is accessible here: <https://theyeasts.org/>
- ICYGMB 31 Florence 2023, organized by Duccio Cavaliere: planned for August 2023
- 47th Annual Conference on Yeasts (ACY) 2023, Smolenice Castle, Slovakia (organized by Milan Certik, commissioner of Slovakia): May 16-19, 2023
<https://yeastconference.sk/home/>

- PYFF8 – Physiology of Yeast and Filamentous Fungi 8 will take place in Cork, Ireland, June 5th – 8th June 2023
<http://www.efbiotechnology.org/PYFF>. This conference is part of the European Federation of Biotechnology (EFB) conferences and is organized by John Morrissey (Ireland commissioner).
- 22nd International Mycological Congress, 2024, Maastricht, Netherlands (Teun Boekhout)

10. Any other business

Commissioners were encouraged to send any news items for the yeast newsletter to André Lachance

11. Closing Remarks from Chair

The chair thanked commissioners for their contributions and Vivien Measday for organising and hosting the meeting and commissioners' dinner. He wished everybody the best for the rest of the meeting.

Diethard Mattanovich

Chair of the International Commission on Yeasts

Appendix 1

Participant list

Charles Abbas, United States; Florian F. Bauer, South Africa; Kyria Boundy-Mills, United States; Neža Cadež, Slovenia; Francisco Carrau, Uruguay; Milan Certík, Slovakia; Daniela Delneri, United Kingdom; Andreas Gombert, Brazil; Paula Gonçalves, Portugal; Anne Gschaedler, Mexico; Chris Todd Hittinger, United States; Thomas Jeffries, United States; Lene Jespersen, Denmark; Vladimir Jiranek, Australia; André Lachance, Canada; Diethard Mattanovich, Austria; Vivien Measday, Canada; John Morrissey, Ireland; José Paulo Sampaio, Portugal; Evodia Setati, South Africa; Andrei Sibirny, Ukraine; Verena Siewers, Sweden; Adrianna Skoneczna, Poland; Hana Sychrová, Czech Republic; Hiroshi Takagi, Japan; Masako Takashima, Japan; Johan Thevelein, Belgium; Graeme Walker, Scotland.



Yeast Commissioners on top of Queen Elisabeth Park, Vancouver

Forthcoming Meeting

37th International Specialized Symposium on Yeasts - ISSY37 Adelaide, Australia 27 Nov–1 Dec 2023.

We are excited to announce that the 37th International Specialised Symposium on Yeasts (ISSY37) will be held in Adelaide, South Australia, 27 Nov–1 Dec 2023.

Co-chaired by Professors Vladimir Jiranek (University of Adelaide) and Sakkie Pretorius (Macquarie University), the theme for ISSY37 is *Yeast Biotech 2.0: New Yeast, Knowledge and Applications*. The meeting will bring together leading researchers, biotech executives, suppliers, government and early career researchers, whose activities span the spectrum of fundamental to applied investigations of yeast. Planned themes will likely include: Biodiversity and new yeast • Yeast-derived food and beverages • Yeast cell factories • Yeast in plant-based foods and meat/dairy alternatives • Synthetic genomes, organelles and communities • Designer yeast • Bioenergy • Biomedicine • Biosafety, amongst others.

Australia and New Zealand have vibrant yeast research communities, brought to together by the Australasian Yeast Group, and one which is well networked with researchers and businesses across

For more information: <https://issy2023.com.au/>

Vladimir Jiranek
Sakkie Pretorius



the globe. ISSY37 provides an opportunity for the world's yeast communities to get together in the iconic travel destination that is Australia. Adelaide, capital of South Australia, is at the heart of the majority of Australia's wine production and supporting research activities.

ISSY37 will be held at the National Wine Centre in the downtown area. Adelaide is a vibrant, safe, attractive and affordable destination in close proximity to pristine beaches, world-renowned wine regions, natural beauty and unique flora and fauna. Adelaide's central location places is less than 4 hrs flight from other major attractions in Australia.

Brief News Items

Changes in employment - David Peris Navarro

I am pleased to announce that I am now Group Leader in the Department of Biosciences, University of Oslo, Norway, where I previously was a Postdoctoral Researcher.

In Valencia, Spain, I have been appointed Distinguished Researcher at the Institute of Agrochemistry and Food Technology.

David Peris Navarro <david.perisnavarro@gmail.com>

theyeasts.org needs your help!



Dear colleagues:

As you know the last printed edition of *The Yeasts, a Taxonomic Study* was published in 2011. Since that time, we (Shuhui Tan, Marizeth Groenewald, Heide-Marie Daniel, Andrey Yurkov, Feng-Yan Bai, Vincent Robert and I) have been working on the digital format, *theyeasts.org*. Until recently, this was regularly updated with species descriptions from the many publications on yeast diversity and taxonomy that followed 2011.

The system is now ready for your help on the various taxa, especially genera and species of the respective genera to be updated by members of the yeast diversity and taxonomy communities.

We are looking for long term commitments of e.g. several years, and also by junior and senior researchers from all over the globe to make this a truly international project, very much like *The Yeasts, a Taxonomic Study* has been.

Senior scientists, please forward this to any young and motivated students/scientists that you know.

Early in 2023 we plan on having a number of presentations on where we are presently with *theyeasts.org*, and likely this will be two timeslots in order to make it possible for people from

various time zones to participate. Next to a number of presentations on the project, we would like to have a discussion with you on how best one can participate.

We also would like to update the introductory chapters on various aspects of yeast biology. If you are not a yeast taxonomist, but rather an expert on some aspect of yeast biology [e.g. ecology, food, biotech, medical, etc.] and wish to contribute to this online resource, you are most welcome.

If you are interested in contributing to the biodiversity and taxonomy part or the introductory topics, please send an email to t.boekhout@wi.knaw.nl, with a cc to m.groenewald@wi.knaw.nl, with subject line *theyeasts.org* and your preferred genus or topic. We hope to get many emails! These will be most helpful in organizing the 2023 online meetings.

You will then receive an invitation for the online meeting by Zoom or another platform, to be held early 2023. Note that we will also invite all authors that contributed to the 5th edition and that are still actively involved in yeast research.

Let us make *theyeast.org* a successful project!

Teun Boekhout
Marizeth Groenewald

WikiProject Fungi

You are invited to contribute to the *WikiProject Fungi*, an initiative aimed at increasing the visibility of fungi on Wikipedia. For further details, please visit the following links:

<https://blogs.biomedcentral.com/on-biology/2022/09/14/most-fungi-are-invisible-even-on-wikipedia/>
https://en.m.wikipedia.org/wiki/Wikipedia:WikiProject_Fungi

Corrado Nai <corrado.nai@gmail.com>

Fifty Years Ago

Y E A S T

A News Letter for Persons Interested in Yeast

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

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Biotechnologie, Seestr. 13, 1 Berlin 65 (West), Germany. Communicated by
S. Windisch.

I. Neumann: Biotaxonomische und systematische Untersuchungen an einigen Hefen der Gattung *Saccharomyces*. (Thesis, Technical University Berlin). Beihefte zur NOVA HEDWIGIA Nr. 40, I-V, 1-79. 1972.

151 yeast strains of different origin, belonging to 19 species and 2 varieties of the genus *Saccharomyces* were studied; 42 of these strains did not sporulate and could not be subjected to genetical control.

Determination of yeasts on the basis of critical evaluation of morphological characteristics and results of genetical studies, showed that 130 strains were related to *S. carlsbergensis* and *S. cerevisiae*. The remaining 21 yeasts, with a small number of strains, could be divided into 8 other species. Their properties are not clearly defined. The question of maintaining these species is discussed.

It is proposed that the strains studied be regarded as populations of one species, which on the basis of priority should be named *S. cerevisiae* HANSEN. Whether the "biological species concept" as described by MAYR (1967) may be used in the case of yeasts is also discussed.

XX. Laboratory of Microbiology, Gulbenkian Institute of Science, Oeiras, Portugal. Communicated by N. van Uden.

Van Uden, N. (1971) Kinetics and energetics of yeast growth, in A. H. Rose and J. S. Harrison (eds), *The Yeasts, Vol. 2, Physiology and Biochemistry of Yeasts*, Academic Press, London and New York.

XXII. The Research Laboratories of Kirin Brewery Co., Ltd., Takasaki, Gumma Pref., Japan. Communicated by Yasushi Yamamoto.

Mr. Kumpei Kitamura, Mr. Tatsuhiko Kaneko and I have engaged in research of yeast cell wall lytic enzymes produced by a strain of Arthrobacter luteus for several years, and have published or presented the following papers.

- T. Kaneko, K. Kitamura and Y. Yamamoto. Arthrobacter luteus nov. sp. Isolated from Brewery Sewage. J. Gen. Appl. Microbiol. 15, 317 (1969)
- K. Kitamura, T. Kaneko and Y. Yamamoto. Lysis of Viable Yeast Cells by Enzymes of Arthrobacter luteus. Arch. Biochem. Biophys. 145, 402 (1971)
- K. Kitamura, T. Kaneko and Y. Yamamoto. Lysis of Viable Yeast Cells by Enzymes of Arthrobacter luteus. I. Isolation of Lytic Strain and Studies on its Lytic Activity. J. Gen. Appl. Microbiol. 18, 57 (1972)
- K. Kitamura, T. Kaneko and Y. Yamamoto. Lysis of Viable Yeast Cells by an Enzyme "Zymolyase" of Arthrobacter luteus. IVth Intern. Ferm. Symp., 1972, Kyoto, Japan.
- K. Kitamura and Y. Yamamoto. Purification and Properties of an Enzyme, Zymolyase, Which Lyses Viable Yeast Cells. Arch. Biochem. Biophys. in press.

XXVI. Department of Bacteriology and Immunology, University of Western Ontario, London, Canada. Communicated by Carl Robinow.

Mitosis in three heterobasidiomycetous "yeasts", the former Candida scottii, Rhodotorula glutinis and Sporobolomyces salmonicolor has been studied by E. Kathleen McCully and C. F. Robinow.

Nuclear division in these yeasts involves migration of all of the chromatinic portion of the nucleus into the bud, dissolution of the nucleolus in the cytoplasm of the mother cell, partial breakdown of the envelope around that portion of the nucleus that enters the bud, contraction of the chromatin (chromosomes) and the development of a mitotic spindle apparatus. One of the two daughter nuclei produced by this process of "mitosis in the bud" returns to the mother cell.

We believe that our observations are of interest not only to students of mitosis but also to Yeast taxonomists. The differences between mitosis in ascomycetous yeasts and heterobasidiomycetous yeasts are so striking that future studies of mitosis in asporogenous yeasts should reveal their taxonomic affinities to either ascomycetes or basidiomycetes.

Editor's note:

Putting together this "50 Years Ago" entry reminded me that it has been 50 years since I sent my first communication to the Yeast Newsletter, the January 1973 issue, as a recent Microbiology graduate, reporting on my first conference presentation, which dealt with the recycling of waste pasta with the amylolytic yeast *Endomycopsis* (now *Saccharomycopsis*) *fibuligera*.

This is a good opportunity to remind our readers that all back issues of the Yeast Newsletter are available at <https://www.uwo.ca/biology/YeastNewsletter/BackIssues.html>.
