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Editorials

Norman R. Eaton (1926-2019)



Dr. Nasim Khan informed me of the death of his doctoral mentor, Prof. Norman R. Eaton. Prof. Eaton was a long-time subscriber to the Yeast Newsletter. From his online obituary, I learned that he was a peaceful, gentle person, with a broad interest in the arts and a profound dedication to science. His major contributions were in the area of yeast genetics and metabolism, as Professor at Brooklyn College of the City University of New York. During his retirement in Sacramento, California, he held an adjunct professorship at the University of California at Davis. On behalf of all readers, I express our warm condolences to Dr. Khan and to Prof. Eaton's family and friends.

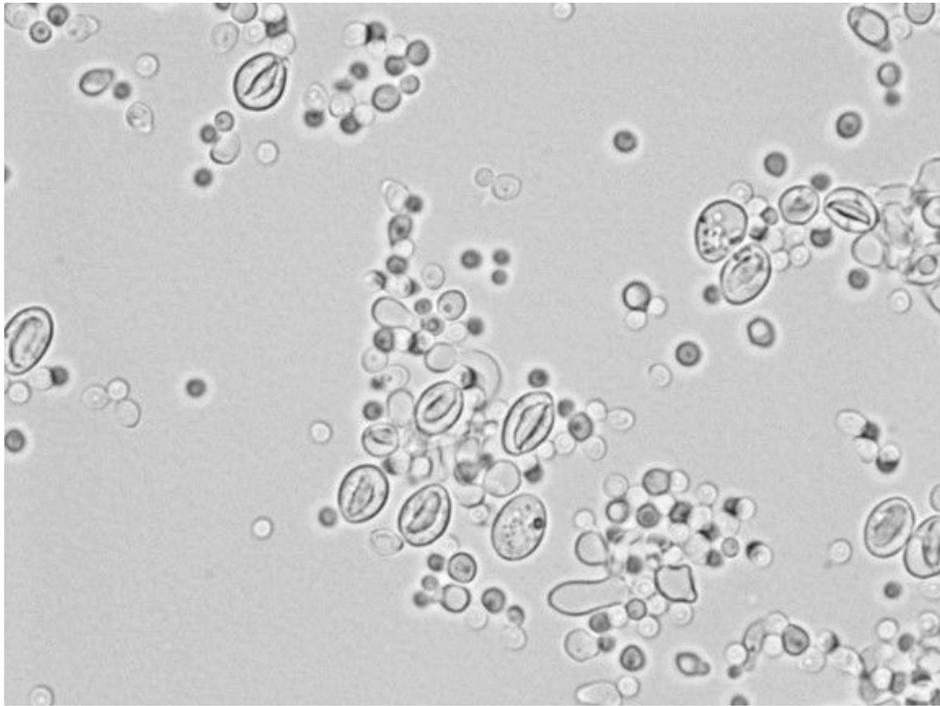
Matti Korhola (1946-2019)

I and many colleagues were saddened by the news of the death of Matti Korhola, an active member of the International Yeast Commission and a beloved colleague. My thanks to Elena Naumova as well as Richard Degré and Jean Chagnon for their tributes to Matti.

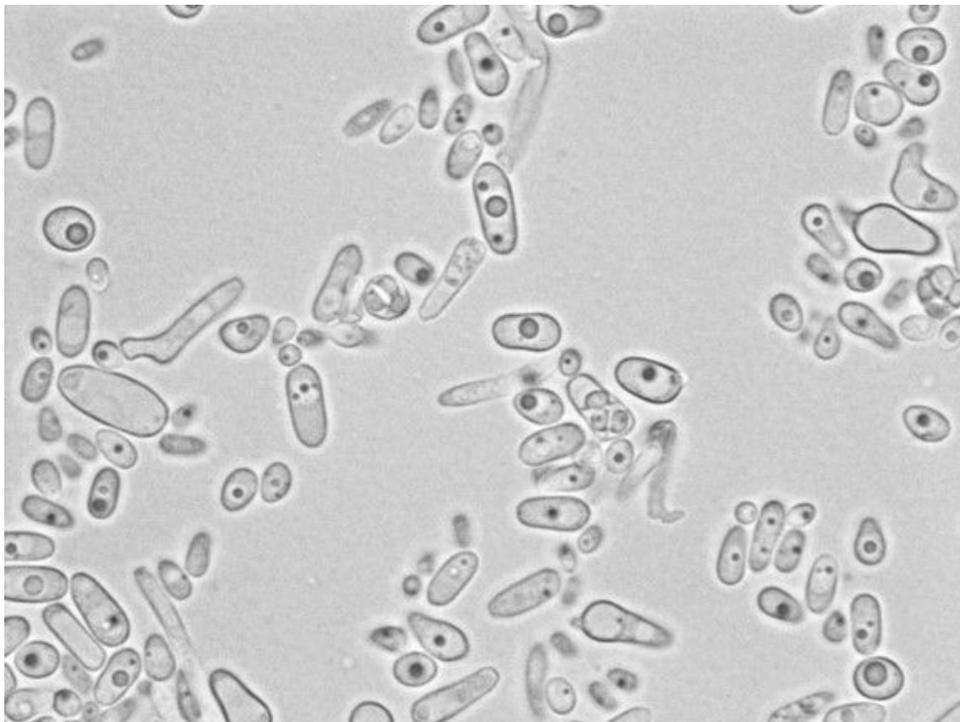
I wish all our readers and happy and scientifically prosperous New Year!

M.A. Lachance, Editor

In defense of yeast sexual life cycles: two new *formae sexuales*
Photomicrographs by Maudy Smith



Sugiyamaella sungouii



Suhomyces atakaporum

The teleomorph states were observed in strains of the following two species introduced initially as anamorphic taxa. See images in the preceding page.

1 *Sugiyamaella sungouii* Wang, James, Sylvester & Hittinger ex M. Groenew. & M.T.Sm. sp. nov.

Five strains (CBS 14414, CBS 14420, CBS 14421, CBS 14425, CBS 14427) that resembled morphologically species of the heterothallic genus *Sugiyamaella* were identified as *Candida sungouii* by rDNA sequence analyzes. Pair-wise mating experiments among these strains as well as the type strain of *C. sungouii* (CBS 13907) resulted in some cases, after 1 week of incubation at 25°C on V8 and YM media, in the formation of asci with one hat to helmet shaped ascospore. From these results, it could be concluded that CBS 14414, CBS 14420, CBS 14421 and CBS 14425 represented the same mating type (mating type a) and strains CBS 13907 and CBS 14427 mating type alpha. Mating between CBS 14427 x CBS 14420 is illustrated in the preceding page.

Candida sungouii was placed in a clade close to the anamorph genus *Blastobotrys* by Sylvester et al. (2015). *Candida sungouii* Q.M. Wang, B. James, K. Sylvester & Hittinger (2015) was invalidly published due to Art. 40.7 of the ICBN (<https://www.iapt-taxon.org/nomen/main.php>) and therefore the following name change is proposed:

Sugiyamaella sungouii Q.M. Wang, B. James, K. Sylvester & Hittinger ex M. Groenew. & M.T. Sm., sp. nov.

Holotype: CBS 13907, preserved in a metabolically inactive state.

Cultures ex-type: CBS 13907 and NRRL Y-63726.

Mycobank No.: MB 833214

For description see Sylvester et al., FEMS Yeast Research 15 (3): 10 (2015).

Synonym: *Candida sungouii* Q.M. Wang, B. James, K. Sylvester & Hittinger, FEMS Yeast Research 15 (3): 10 (2015), nom. inval.

2 First report of a teleomorphic state in the anamorph genus *Suhomyces*: *Suhomyces atakaporum* (Suh & Blackwell) M. Blackwell & Kurtzman

Four strains (CBS 15827, CBS 15828, CBS 15829 and CBS 15841) deposited as *Suhomyces atakaporum* were found to produce the ascospore state in some pair wise mating experiments after 1 week of incubation on V8 medium 25°C. Strain CBS 15827 represented one mating type, while CBS 15828, CBS 15829 and CBS 15841 were of the opposite mating type. Pair wise mating tests of these strains with CBS 9833, the Type strain of *Suhomyces atakaporum*, showed that lytic asci with 3-4 hat shaped ascospores were obtained between CBS 9833 when crossed with CBS 15828, CBS 15829 (Fig. 2) as well as with CBS 15841. The ascospore state was not observed in the mating test between CBS 9833 and CBS 15827. Arbitrarily mating type alpha was assigned to CBS 9833 and CBS 15827 and mating type a to CBS 15828, CBS 15829 and CBS 15841.

To date, this is the first report of a teleomorph species assigned to the anamorph genus *Suhomyces* introduced by Kurtzman et al. (2016).

References

Kurtzman CP, Robnett CJ & M Blackwell. 2016. Description of *Teunomyces* gen.nov. for the *Candida kruisii* clade, *Suhomyces* gen. nov. for the *Candida tanzawaensis* clade and *Suhomyces kilbournensis* sp.nov. FEMS Yeast Research 16, 2016, fow041.

Sylvester K,Wang QM, James B, Mendez R, Hulfachor AB & Hittinger T. 2015. Temperature and host preferences drive the diversification of *Saccharomyces* and other yeasts: a survey and discovery of eight new yeast species. FEMS Yeast Research 15, 2015, fov002.

Recent publications.

- 1 Caridi A, Panebianco F, Scibetta S, Schena L 2019. Selection of yeasts for their anti-mold activity and prospective use in table olive fermentation. *Journal of Food Processing and Preservation*, 2019; 00:e14259. <https://doi.org/10.1111/jfpp.14259>.

The growth of molds represents a major problem during table olive fermentation. Molds are recognized as spoilage agents and may reduce the product safety for their ability to produce mycotoxins. Yeasts, instead, are usually found in table olive processing and are generally considered desirable microorganisms for their technological properties. In the present study, a model system to select anti mold yeasts usable as protective adjunct cultures in table olive fermentation was developed. Two hundred and ninety nine strains of yeasts, isolated from cheese, olive, vinegar, and wine, were tested in vitro for their growth characteristics, fermentative activity, salt tolerance, and antagonistic activity against 10 mold strains isolated from table olives and olive brines.

Experimental steps led to the selection of a strain of *Yarrowia lipolytica* exhibiting all the previously listed characteristics.

Practical applications - A strain of *Yarrowia lipolytica* was selected because of its high potentiality as adjunct culture in table olive fermentation to contrast mold growth and increase the product quality and safety. The experimental model system developed in this study may be easily applied to select yeasts usable as adjunct cultures in table olive fermentation in order to contrast mold growth and increase the product safety. These outcomes showed how the use of selected yeasts constitutes a promising way to control mold growth during table olive fermentation.

Recent publication.

- 1 Patricia Portero Barahona, Jesús Martín-Gil, Pablo Martín-Ramos, Ana Briones Pérez, Enrique Javier Carvajal Barriga. 2019. Assessment of the effect of nitrogen concentration on fermentation and selection of a highly competitive *Saccharomyces cerevisiae* strain for efficient ethanol production. *Energies* 12:2614; doi:10.3390/en12132614

The optimum nitrogen concentration for media supplementation and strain dominance are aspects of key importance to the industrial production of ethanol with a view to reducing costs and increasing yields. In this work, these two factors were investigated for four ethanologenic *Saccharomyces cerevisiae* strains (CLQCA-INT-001, CLQCA-INT-005, CLQCA-10-099, and UCLM 325), selected from the screening of 150 isolates, mostly from Ecuadorian yeast biodiversity. The effect of nitrogen concentration was assessed in terms of cellular growth, glucose consumption and ethanol production, and the yeast strains' dominance was evaluated in continuous

co-fermentation with cellular recycling by mitochondrial DNA analyses. Among the four selected yeast strains under study, CLQCA-INT-005 presented the highest glucose consumption at a nitrogen supplement concentration as low as 0.4 g L⁻¹, attaining an ethanol yield of up to 96.72% in 24 h. The same yeast strain was found to be highly competitive, showing a dominance of 80% after four cycles of fermentation in co-culture. Thus, CLQCA-INT-005 may be deemed as a very promising candidate to be used both at pilot-plant scale and at industrial scale cellulosic ethanol production.

As happens not unfrequently in science, two research groups dedicated themselves to the same topic, in this case, the taken-for-granted aspect that *Saccharomyces cerevisiae* cannot grow under fully anaerobic conditions, unless appropriate growth factors are provided in the medium (an at least 70 year-old story!). These are most commonly added as ergosterol and oleic acid (as part of Tween 80) to laboratory media. One group took an approach based on chemostat cultivations, in which aerobic growing cells were switched to anaerobiosis, without these growth factors, hoping to observe wash-out. This did not occur for any of the two strains they investigated,

and the results lead us to at least rethink how far this yeast species is indeed dependent on these nutrients, to thrive without oxygen. The other researchers took a different approach, making use of an anaerobic chamber, and demonstrated that at least the provision of oleic acid is not necessary for the *S. cerevisiae* CEN.PK113-7D strain to grow under anaerobiosis. Both studies also illustrate how difficult it is to achieve full anaerobiosis in the lab and how far the history of the cells prior to examination under anaerobiosis is important. The two articles were conveniently published in the same issue of FEMS Yeast Research:

- 1 da Costa BLV, Raghavendran V, Franco LFM, Chaves Filho AB, Yoshinaga MY, Miyamoto S, Basso TO, Gombert AK. 2019. Forever panting and forever growing: physiology of *Saccharomyces cerevisiae* at extremely low oxygen availability in the absence of ergosterol and unsaturated fatty acids. FEMS Yeast Res. 19(6). pii: foz054. doi: 10.1093/femsyr/foz054. PubMed PMID: 31425576.
- 2 Dekker WJC, Wiersma SJ, Bouwknegt J, Mooiman C, Pronk JT. 2019. Anaerobic growth of *Saccharomyces cerevisiae* CEN.PK113-7D does not depend on synthesis or supplementation of unsaturated fatty acids. FEMS Yeast Res. 19(6). pii: foz060. doi: 10.1093/femsyr/foz060. PubMed PMID: 31425603; PubMed Central PMCID: PMC6750169.

Recent publications.

- 1 Stewart GG. 2019. Brewer's Yeast Research – a keynote paper. - part 1. Brewing Science, 72:31-49.
 - 2 Stewart GG. 2019. Brewer's Yeast Research – a keynote paper. - part 2. Brewing Science, 72:94-108.
 - 3 Hill A and Stewart GG. 2019. Free amino nitrogen in brewing. Fermentation 2019. MDPI AG, Basel, Switzerland. 5:1–14.
 - 4 Stewart GG. 2019. Genetic manipulation of *Saccharomyces sp.* that produce ethanol related metabolites and biomass. Food Science, Elsevier, Boston, Mass., pp. 62-84.
 - 5 Stewart GG. 2019. A History of Brewing in Canada. Brewery History, No. 181.
 - 6 Stewart GG and Ryder D.S. 2019. Sulfur metabolism during brewing. Master Brewers Association of the Americas, Technical Quarterly, 56(2)39-46.
 - 7 Stewart GG and Speers RA. 2019. Yeast nutrition and metabolism: effects on beer flavor. Master Brewers Association of the Americas, Technical Quarterly, 56(3):76-92.
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Recent publications.

- 1 Crous PW, Luangsa-ard JJ, Wingfield MJ, ... Kachalkin AV, ... Groenewald JZ. 2018. *Kwoniella endophytica* A.M. Glushakova & Kachalkin, sp. nov. – endophytic yeast species isolated from different fruit tissues. Fungal planet description sheets: 785–867 Persoonia 41:238-417.
- 2 Streletskii RA, Kachalkin AV, Glushakova AM, Yurkov AM, Demin VV. 2019. Yeasts producing zeatin. Peer J 7:e6474.

The present paper describes the first screening study of the ability of natural yeast strains to synthesize in culture the plant-related cytokine hormone zeatin, which was carried out using HPLC-MS/MS. A collection of 76 wild strains of 36 yeast species (23 genera) isolated from a variety of natural substrates was tested for the production of zeatin using HPLC-MS/MS. Zeatin was detected in more than a half (55%) of studied strains and was more frequently observed among basidiomycetous than ascomycetous species. The amount of zeatin accumulated during the experiment varied among species and strains. Highest

zeatin values were recorded for basidiomycete *Sporobolomyces roseus* and ascomycete *Taphrina* sp. that produced up to 8,850.0 ng and 5,166.4 ng of zeatin per g of dry biomass, respectively. On average, the ability to produce zeatin was more pronounced among species isolated from the arctic-alpine zone than among strains from tropical and temperate climates. Our study also demonstrated that epiphytic strains and pigmented yeast species, typically for phyllosphere, are able to more often produce a plant hormone zeatin than other yeasts.

- 3 Nikitin DA, Semenov MV, Semikolennykh AA, Maksimova IA, Kachalkin AV, Ivanova AE. 2019. Biomass of fungi and species diversity of the cultivated mycobiota of soils and substrates in Northbrook Island (Franz Josef Land. Mikologiya i Fitopatologiya (Russian) 53(4):210-222.

The research of fungal biomass and species diversity of the cultivated microscopic fungi and yeast of the Northbrook Island (Franz Josef Land) was carried out. Biomass of fungi depending on type of substratum varied from 129 to 634 mkg/g of a substratum. The share of viable biomass in the majority of objects made about 60–70%, decreasing to 30–40% in algae-bacterial mats, primitive soils and the several anthropogenic biotopes. In the majority of soils and substrata of the island up to 70% of biomass it is presented by spores of the shallow sizes (up to 2.5 microns). Mycelium prevailed over spores as a part of fungal biomass (up to 82%) only on bird's nests, and in

other substrata its share made from 41 to 53%. The number of the cultivated micromycetes varied from 10^2 to 10^5 CFU/g. A species diversity of fungi was sequentially increased on relief elements from a watershed (6–7 species), downhill and was maximal in a coastal zone (15 species). An absolute dominants on abundance and occurrence was *Pseudogymnoascus pannorum* which number reached 10^5 CFU/g. As subdominants the representatives of genera *Mortierella* and *Penicillium* were marked. Among yeast in the wet biotopes with a vegetable cover, such species as *Goffeauzyma gilvescens* reaching 10^4 CFU/g.

- 4 Akhapkina IG, Glushakova AM, Antropova AB, Kachalkin AV, Bilanenko EN, Zheltikova TM. 2019. House dust microbiota: Prospect of the assessment of allergenic and pyrogenic loads // Gigiena i sanitaria (Russian). 98(4):380-387.

Aerobic and facultative anaerobic bacteria prevailed, numbers varying from 4.8×10^4 to 2.0×10^9 MPN/g of dust in hostels and from 3.0×10^4 to 1.0×10^9 of dust MPN/g in apartments. Gram-positive bacteria

were revealed in 100% of apartments and in 80% of hostels, Gram-negative, in 47% of apartments, and in 73% of hostels. 9 yeast species were isolated: *Filobasidium wieringae*, *F. magnum*, *Papiliotrema*

flavescens, *Vishniacozyma victoriae*, *Rhodotorula mucilaginosa*, *Debaryomyces hansenii*, *Candida parapsilosis*, *C. tropicalis*, *Meyerozyma guilliermondii*. *R. mucilaginosa* and *Candida* spp. were more frequent in hostels, while *Filobasidium* spp., in apartments. Yeast cell number varied from 3.5×10^3 to 1.3×10^6 CFU/g of dust in hostels, and from 2.3×10^3 to 2.5×10^6 CFU/g of dust in apartments. 56 mycelial fungi species were revealed. *Penicillium chrysogenum* (100%),

Aspergillus niger (100%), *Rhizopus stolonifer* (100%), *A. ochraceus* (80%), *Mucor plumbeus* (67%), *P. cyclopium* (60%) were the most frequent in hostels. *P. cyclopium* (60%), *P. chrysogenum* (60%) were the most frequent in apartments. Mold concentration varied from 1.8×10^5 to 7.5×10^6 CFU/g of dust in hostels and from 3.3×10^3 to 2.3×10^5 CFU/g of dust in apartments. Micromycetes complexes were similar in different hostels but differed in apartments.

- 5 Kachalkin AV, Turchetti B, Inácio J, Carvalho C, Маљнновб Т, Pontes A, Рцћл О., Glushakova AM, Akulov A, Baldrian P, Begerow D, Buzzini P, Sampaio JP, Yurkov AM. 2019. Rare and undersampled dimorphic basidiomycetes. *Mycological Progress* 18(7):945-971.

The diversity of yeasts has grown rapidly as the discovery of new species has benefited from intensified sampling and largely improved identification techniques. An environmental study typically reports the isolation of yeast species, some of which are new to science. Rare species represented by a few isolates often do not result in a taxonomic description. Nucleic acid sequences from these undescribed yeasts remain in public sequence databases, often without a proper taxonomic placement. This study presents a constrained phylogenetic analysis for many rare yeasts from unpublished but publicly available DNA sequences and from studies previously conducted by the authors of this work. We demonstrate that single isolates are an important source of taxonomic findings such as including new genera and species. Independent surveys performed during the last 20 years on a large geographic scale yielded a number of single strains, which were proved to be conspecific in the phylogenetic analyses presented here. The following new species were resolved and described: *Vustinia terrea* Kachalkin, Turchetti & Yurkov gen. nov. et sp. nov.; *Udeniomyces caspiensis* Kachalkin sp. nov.; *Udeniomyces orazovii* Kachalkin sp. nov.; *Tausonia rosea* Kachalkin sp. nov.; *Itersonilia diksonensis* Kachalkin sp. nov.; *Krasilnikovozyma fibulata*

Glushakova & Kachalkin, *Kwoniella fici* Turchetti sp. nov.; *Heterocephalacria fruticeti* f.a. Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Heterocephalacria gelida* f.a. Turchetti & Kachalkin sp. nov.; *Heterocephalacria hypogea* f.a. Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Heterocephalacria lusitanica* f.a. Inacio, Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Piskurozoma arborea* Yurkov, Kachalkin, Маљнновб & Baldrian sp. nov.; *Piskurozoma silvicultrix* Turchetti, Маљнновб, Baldrian & Yurkov sp. nov.; *Piskurozoma stramentorum* Yurkov, Маљнновб & Baldrian sp. nov.; *Naganishia nivalis* Turchetti sp. nov.; and *Yurkovia nerthusi* Yurkov & Begerow, sp. nov. In addition, two new combinations were proposed *Krasilnikovozyma curviuscula* (Babeva, Lisichkina, Reshetova & Danilevich) Yurkov, Kachalkin & Sampaio comb. nov. and *Hannaella taiwanensis* (F.L. Lee & C.H. Huang) Yurkov comb. nov. The order Cyphobasidiales T. Spribille & H. Mayrhofer is rejected in favor of the older name Erythrobasidiales R. Bauer, Begerow, J.P. Sampaio, M. Weiss & Oberwinkler. Other potential novel species identified in this paper await future description. Phylogenetic placement of yet unpublished sequences is believed to facilitate species descriptions and improve classification of yeasts from environmental sequence libraries.

- 6 Yakushev AV, Matyshak GV, Tarhov MO, Kachalkin AV, Sefilyan AR, Petrov DG. 2019. Microbiological characteristics of bare peat circles on flat-topped peat mounds in the north of Western Siberia. *Eurasian Soil Science* 52(9):1081-1090.

A destructive peat horizon Tmd of bare peat circles on flat-topped peat mounds in the north of Western Siberia differs from peat horizons (T) of typical peat soils in its higher density, water content, and comminution of peat residues; lower microbial biomass; low mineralization and hydrolase activities; low physiological diversity of hydrolytic bacteria; and specific composition of the fungal complex with an

uncharacteristically high proportion and quantity of psychrophilic yeasts *Leucosporidium drummii*. Specific respiration rate and hydrolase activity in the Tmd and T horizons are relatively close, which indicates that, in general, the metabolic activity of microorganisms decomposing the organic matter of peat and increasing the degree of peat decomposition remains unchanged in the soils of bare peat circles.

- 7 Crous PW, Carnegie AJ, Wingfield MJ, ... Kachalkin AV, ... Groenewald JZ. 2019. *Nakazawaea ambrosiae* Kachalkin, M.A. Tomashevskaya, T.A. Kuznetsova & M.V. Vecherskii, sp. nov. associated with ambrosia beetles (*Ips typographus*), the galleries and the larvae of which served as the source of the strains. Fungal Planet description sheets 868–950 Persoonia 42:291-473.
- 8 Dmitrieva AS, Ivnitsky SB, Maksimova IA, Panchenko PL, Kachalkin AV, Markov AV. 2019. Yeasts affect tolerance of *Drosophila melanogaster* to food substrate with high NaCl concentration. PLoS ONE 14(11):e0224811.

The ability of model animal species, such as *Drosophila melanogaster*, to adapt quickly to various adverse conditions has been shown in many experimental evolution studies. It is usually assumed by default that such adaptation is due to changes in the gene pool of the studied population of macroorganisms. At the same time, it is known that microbiome can influence biological processes in macroorganisms. In order to assess the possible impact of microbiome on adaptation, we performed an evolutionary experiment in which some *D. melanogaster* lines were reared on a food substrate with high NaCl concentration while the others were reared on the standard (favourable) substrate. We evaluated the reproductive efficiency of experimental lines on the high salt substrate three years after the experiment started. Our tests confirmed that the lines reared on the salty substrate became more tolerant to high NaCl concentration. Moreover, we found that pre-inoculation of the high salt medium with

homogenized salt-tolerant flies tended to improve reproductive efficiency of native flies on this medium (compared to pre-inoculation with homogenized control flies). The analysis of yeast microbiome in fly homogenates revealed significant differences in number and species richness of yeasts between salt-tolerant and control lines. We also found that some individual yeast lines extracted from the salt-tolerant flies improved reproductive efficiency of native flies on salty substrate (compared to baker's yeast and no yeast controls), whereas the effect of the yeast lines extracted from the control flies tended to be smaller. The yeast *Starmerella bacillaris* extracted from the salt-tolerant flies showed the strongest positive effect. This yeast is abundant in all salt-tolerant lines, and very rare or absent in all control lines. The results are consistent with the hypothesis that some components of the yeast microbiome of *D. melanogaster* contribute to flies' tolerance to food substrate with high NaCl concentration.

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

The following articles have been published since our last report:

- 1 Morais CG, Lara CA, Oliveira ES, Péter G, Dlačny D. & Rosa, C.A. 2016. *Spencermartinsiella silvicola* sp. nov., a yeast species isolated from rotting wood. International Journal of Systematic and Evolutionary Microbiology 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 cellulocola* is reassigned to the genus *Spencermartinsiella* as a new combination.

- 2 James SA, Bond CJ, Stanley R, Ravella SR, Peter G, Dlačny D, Roberts IA. 2016. *Apiotrichum terrigenum* sp. nov., a novel soil-associated yeast found in both the UK and mainland Europe. International Journal of Systematic and Evolutionary Microbiology 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, Dlačhy 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-1 α (EF-1 α) 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 2626^T, MycoBank no.: MB 819608) is proposed for this highly divergent new yeast species.

- 4 Yurkov AM, Dlačhy D, Péter G. 2017. *Meyerozyma amylolytica* sp. nov. from temperate deciduous trees and the transfer of five *Candida* species to the genus *Meyerozyma*. *International Journal of Systematic and Evolutionary Microbiology* 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, Dlačny D, Tóbiás A, Péter G. 2017. *Kuraishia mediterranea* sp. nov., a methanol-assimilating yeast species from olive oil and its sediment. *International Journal of Systematic and Evolutionary Microbiology* 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 2473^T; isotype: CBS 15107^T; 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, Cham. 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.

- 7 Brysch-Herzberg, M, Tobias A, Seidel M, Wittmann R, Wohlmann E, Fischer R, Dlačny D, Peter G. 2019. *Schizosaccharomyces osmophilus* sp. nov., an osmophilic fission yeast occurring in bee bread of different solitary bee species, *FEMS Yeast Research*, doi: 10.1093/femsyr/foz038

Eight yeast strains that asexually reproduce by cell fission were isolated from bee bread of different solitary bees in Germany. DNA sequence analysis revealed that the strains shared the same sequence in the D1/D2 domain of the nuclear large subunit (LSU) rRNA gene with a strain that was previously isolated from a fig snack from Spain. The closest related type strain was that of *Schizosaccharomyces octosporus*, which showed 98.2% sequence similarity (11 substitutions) with the new strains. By clone sequence analysis of the internal transcribed spacer (ITS) region (ITS1, 5.8S rDNA, and ITS2) a total of nine different

copy types were identified. The new strains differed from *S. octosporus* by approximately 31% in the ITS region. Sequence analysis of the RNase P gene further supported the description of a new species. The strains isolated during this study show some phenotypic characteristics that separate them from the closest related species, *S. octosporus* and *S. cryophilus*. Since all strains showed true osmophily the name of the new species is *S. osmophilus* (holotype: CBS 15793^T; isotype: CLIB 3267^T = NCAIM Y.02225^T, MycoBank no.: MB829586).

- 8 Péter G, Mounier J, Garnier L, Soós D, Dlačny, D. 2019. *Cutaneotrichosporon suis* sp. nov., a lipolytic yeast species from food and food-related environment. *International Journal of Systematic and Evolutionary Microbiology* - doi: 10.1099/ijsem.0.003485

Two conspecific yeast strains, which based on DNA sequence comparisons represented an undescribed species in the order Trichosporonales were isolated during two independent studies in Hungary and France. One of them (NCAIM Y.02224) was recovered from minced pork in Hungary while the other one (UBOCC-A-218003) was isolated from the air of a dairy plant in France. The two strains shared identical nucleotide sequences in the D1/D2 domain of the nuclear large subunit (LSU) rRNA gene and in the internal transcribed spacer (ITS) region. Analysis of the concatenated DNA sequences for the ITS region and D1/D2 domain of the LSU rRNA gene indicated

- 9 Péter G, Nagy ES, Dlačny D. 2019. Systematics, Diversity and Ecology of the Genus *Yarrowia* and the Methanol-Assimilating Yeasts. In: Sibirny A. (eds) Non-conventional Yeasts: from Basic Research to Application. Springer, Cham. pp: 297-339.

Yeasts have been exploited by humankind for millennia. Currently, numerous yeast species beyond *Saccharomyces cerevisiae* are utilised by the bioindustry, the so-called non-conventional yeasts. Among the non-conventional yeasts, *Yarrowia lipolytica* and some methanol-utilising yeast species occupy an important position. During the past one and half decade, *Yarrowia* has expanded from a monotypic genus including only *Y. lipolytica* to a genus containing 14 species. Similarly, the number of known methanol-utilising yeasts has increased dynamically. Currently, their number exceeds 90, and the majority

that the novel species belongs to the recently erected genus *Cutaneotrichosporon*. According to sequence comparisons and phylogenetic analysis, the novel species is most closely related to *Cutaneotrichosporon curvatum* (formerly *Cryptococcus curvatus*), which is often associated with humans and warm-blooded animals. The physiological characteristics of this novel species are also very similar to that of *Cutaneotrichosporon curvatum*. The only clear-cut difference is that, unlike *C. curvatum*, the novel species does not utilize imidazole as a nitrogen-source. The species name *Cutaneotrichosporon suis* sp. nov. is proposed to accommodate the above-noted two strains.

of them are assigned to the genera *Komagataella*, *Kuraishia*, *Ogataea*, and some of them yet to *Candida*. Methanol-assimilating *Candida* species are related to the genus *Ogataea*. The most important changes in the systematics of these important yeasts are summarised, and some aspects of their ecology and diversity are discussed as well. Diversity of these yeasts in a few habitats, including a newly recognised one, is briefly introduced. Selective enrichment-based isolation methods for recovering strains of these two exciting yeast groups are discussed as well.

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In December 2019, I will begin my tenure as Postdoctoral Researcher in the Department of Biosciences, University of Oslo, Norway under the supervision of Dr. Inger Skrede.

New papers.

- 1 Perea-Sanz L, Peris D, Belloch C, Flores M. 2019. *Debaryomyces hansenii* metabolism of sulfur amino acids as precursors of volatile compounds of interest in meat products. *Journal of Agricultural and Food Chemistry* 67(33):9335-9343.

The ability of *Debaryomyces hansenii* to produce volatile sulfur compounds from sulfur amino acids and the metabolic pathway involved have been studied in seven strains from different food origins. Our results proved that L-methionine is the main precursor for sulfur compound generation. Crucial differences in the sulfur compound profile and amino acid consumption among *D. hansenii* strains isolated from different food sources were observed. Strains isolated from dry pork sausages displayed the most complex sulfur compound profiles. Sulfur compound production, such as that of

methional, could result from chemical reactions or yeast metabolism, while according to this study, thioester methyl thioacetate appeared to be generated by yeast metabolism. No relationship between sulfur compounds production by *D. hansenii* strains and the expression of genes involved in sulfur amino acid metabolism was found, except for the *ATF2* gene in the L1 strain for production of methyl thioacetate. Our results suggest a complex scenario during sulfur compound production by *D. hansenii*.

- Langdon QK, Peris D, Baker ECP, Opulente DA, Nguyen HV, Bond U, Gonçalves P, Sampaio JP, Libkind D, Hittinger CT. 2019. Fermentation innovation through complex hybridization of wild and domesticated yeasts. *Nature Ecology and Evolution* 3:1576-1586

The most common fermented beverage, lager beer, is produced by interspecies hybrids of the brewing yeast *Saccharomyces cerevisiae* and its wild relative *S. eubayanus*. Lager-brewing yeasts are not the only example of hybrid vigour or heterosis in yeasts, but the full breadth of interspecies hybrids associated with human fermentations has received less attention. Here we present a comprehensive genomic analysis of 122 *Saccharomyces* hybrids and introgressed strains. These strains arose from hybridization events between two to four species. Hybrids with *S. cerevisiae* contributions originated from three lineages of domesticated *S. cerevisiae*, including the major wine-making lineage and two distinct brewing lineages. In contrast, the undomesticated parents of these interspecies hybrids

were all from wild Holarctic or European lineages. Most hybrids have inherited a mitochondrial genome from a parent other than *S. cerevisiae*, which recent functional studies suggest could confer adaptation to colder temperatures. A subset of hybrids associated with crisp flavour profiles, including both lineages of lager-brewing yeasts, have inherited inactivated *S. cerevisiae* alleles of critical phenolic off-flavour genes and/or lost functional copies from the wild parent through multiple genetic mechanisms. These complex hybrids shed light on the convergent and divergent evolutionary trajectories of interspecies hybrids and their impact on innovation in lager brewing and other diverse fermentation industries.

- Langdon QK, Peris D, Eizaguirre JI, Opulente DA, Buh KV, Sylvester K, Jarzyna M, Rodríguez ME, Lopes CA, Libkind D, Hittinger CT. Genomic diversity and global distribution of *Saccharomyces eubayanus*, the wild ancestor of hybrid lager-brewing yeasts. *BioRxiv* - Preprint

S. eubayanus, the wild, cold-tolerant parent of hybrid lager-brewing yeasts, has a complex and understudied natural history. The exploration of this diversity can be used both to develop new brewing applications and to enlighten our understanding of the dynamics of yeast evolution in the wild. Here, we integrate whole genome sequence and phenotypic data of 200 *S. eubayanus* strains, the largest collection to date. *S. eubayanus* has a multilayered population structure, consisting of two major populations that are further structured into six subpopulations. Four of these subpopulations are found exclusively in the Patagonian region of South America; one is found predominantly in Patagonia and sparsely in Oceania and North America; and one is specific to the Holarctic ecozone. *S. eubayanus* is most abundant and genetically diverse in Patagonia, where some locations harbor more genetic diversity than is found outside of

South America. All but one subpopulation shows isolation-by-distance, and gene flow between subpopulations is low. However, there are strong signals of ancient and recent outcrossing, including two admixed lineages, one that is sympatric with and one that is mostly isolated from its parental populations. Despite *S. eubayanus*' extensive genetic diversity, it has relatively little phenotypic diversity, and all subpopulations performed similarly under most conditions tested. Using our extensive biogeographical data, we constructed a robust model that predicted all known and a handful of additional regions of the globe that are climatically suitable for *S. eubayanus*, including Europe. We conclude that this industrially relevant species has rich wild diversity with many factors contributing to its complex distribution and biology.

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Some recently published papers.

- Black K, Barnett A, Tziboula-Clarke A, White P, Iannetta P and Walker GM. 2018. Faba bean as a novel brewing adjunct: consumer evaluation. *Journal of the Institute of Brewing*. DOI 10.1002/jib.568
- Walker GM and Walker RSK. 2018. Enhancing yeast alcoholic fermentations. *Advances in Applied Microbiology* 105:87-129 - Edited by G Gadd & S Sariaslani ISSN 0065-2164 - <https://doi.org/10.1016/bs.aambs.2018.05.003>

- 3 Black K, Walker G, White P, Squire G and Iannetta P. 2018. Intercropped barley for brewing & distilling. In: *Distilled Spirits: Local Roots; Global Reach*. Eds. F Jack, D Dabrowska, S Davies, M Garden, D Maskell and D Murray Context Products Ltd, Packington, UK. ISBN9781899043781. Chapter 9, pp45-48
- 4 Lachance MA and Walker GM. 2018. Yeasts. In: *eLS: Citable Reviews in the Life Science*.
- 5 Maccarrone M, Clarke A, Zheng Y, Tickle C, Kehrer-Sawatzki H, Cooper DN, Delves P, Candi E, Perkel DJ, Hetherington AM, Bynum WF, Valpuesta JM. & Harper D (eds.) JohnWiley & Sons Inc. DOI: 10.1002/9780470015902.a0000380.pub3
- 6 Leinhardt T, Black K, Saget S, Porto Costa M, Chadwick D, Rees RM, Williams M, Spillane C, Iannetta PPM, Walker G, Styles D. 2019. Just the tonic! Legume biorefining for alcohol has the potential to reduce Europe's protein deficit and mitigate climate change. *Environment International*, 130, 104870 <https://authors.elsevier.com/sd/article/S0160412019308773>
- 7 Walker GM, Lappe-Oliveras P, Moreno-Terrazas R, Kirchmayr M, Arellano-Plaza M and Gschaedler-Mathis A. 2019. Yeasts associated with the production of distilled beverages. In: *Yeasts in the Production of Wine* Eds P Romano, M Cianni and GH Fleet. Springer Nature, New York. pp477-512. ISBN 978-1-4939-9780-0. <https://doi.org/10.1007/978-1-4939-9782-4>
- 8 Basso TO, Walker RSK, Basso LC and Walker GM. 2019. The future of bioethanol. In: *Ethanol as a Green Alternative Fuel: Insight and Perspectives*. Edited by Helen Treichel, Sérgio Luiz Alves Jr, Gislaine Fongaro and Caroline Müller. Nova Science Publishers, Inc. Hauppauge, NY, USA, (in press) - <https://novapublishers.com/shop/ethanol-as-a-green-alternative-fuel-insight-and-perspectives/>
- 9 Nasidi M, Agu R, Walker GM & Deeni YY. 2019. Sweet sorghum: agronomic practice for food, animal feed and fuel production in Sub-Saharan Africa. In: *Sweet sorghum: agronomic practice for food, animal feed and fuel production in Sub-Saharan Africa*, in *Sweet Sorghum: Characteristics, Cultivation and Uses*. Nova Science Publishers, Inc., ISBN: 978-1-53615-386-6
- 10 Walker GM and Basso TO. 2019. Mitigating stress in industrial yeasts. *Fungal Biology*, in press

X Canadian Institute of Fermentation Technology, Dalhousie University, Halifax, NS B3J 2X4, Canada and International Centre of Brewing and Distilling, Heriot-Watt University, Edinburgh, Scotland. Alex Speers <Alex.Speers@Dal.Ca>.

Workshop.

- 1 Chair, Fermentations New and Old, MBAA Annual Conference, Calgary, AB 2019

Papers.

- 2 Speers RA, Haponiuk B and Derma F. 2019. ABV Calculator. <<https://www.omnicalculator.com/food/alcohol-by-volume>>, Posted Oct 23, 2019.
- 3 Reid SJ, Speers RA, Lumsden WB, and Maskell DL. 2019. The influence of *Lactobacillus plantarum* on organic acid production and new-make spirit quality. Submitted to Food hem.
- 4 Stewart GG and Speers RA. 2019. Yeast Nutrition and Metabolism - Effects on Beer Flavor. *MBAA Technical Quarterly*, 52:76-92.
- 5 Maskell D, Maskell P, Walker G, and Speers RA. 2019. Letter to US Treasury Secretary Mnuchin: Comment on the proposed TTB rule "Modernization of the Labeling and Advertising Regulations for Wine, Distilled Spirits, and Malt Beverages," Regulation§ 7.65(c). Tracking number 1k3-9aad-udly. <<https://www.regulations.gov/document?D=TTB-2018-0007-0148>>.

- Rudolph A, MacIntosh AJ, Speers RA. St. Mary C. 2019. Modeling yeast in suspension during laboratory and commercial fermentations to detect aberrant fermentation processes. Accepted by the J. ASBC.

Presentations.

- Reid S, Maskell D, Lumsden B and Speers RA. 2019. Modelling Scotch Whisky Fermentations. Accepted for the MBAA Conf. Calgary, AB. Oct. 31-Nov. 2.
- Roy KR, Budge SM, Paulson AT and Speers RA. 2019. The effect of germination conditions on growth of *Fusarium graminearum* and secretion of deoxynivalenol during floor-malting of barley. Accepted for the MBAA Conf. Calgary, AB. Oct. 31-Nov. 2.
- Killfoil GA, Kishnani P and Speers RA. 2019. Effects of floor malting versus pneumatic malting on malt and beer quality. Accepted for the MBAA Conf. Calgary, AB. Oct. 31-Nov. 2.
- Kishnani P, Killfoil GA, Taylor J, Forney C, Jordan M and Speers RA. 2019. Preliminary studies of beers made from floor and pneumatic malt: sensory aspects. Accepted for the the MBAA Conf. Calgary, AB. Oct. 31-Nov. 2.
- AM Al Taweel, F Azizi, S Arora, W Friesen, T Dabros, A Speers, H Hamza. 2019. Using inline coagulation/flocculation to intensify multiphase separation operations. Accepted for the Can. Chem. Eng. Conference Halifax, NS, AB. Oct. 20-23.
- Huismann M, Gormley F, Zait D, Speers RA, Maskell DL. 2019. Identifying and diagnosing the source of unfilterable beer haze. Accepted for ASBC Conf. New Orleans, LA. June 24-26.
- Huismann M, Gormley F, Zait D, Speers RA, Maskell DL. 2019. Understanding aromatic stability in dry-hopped beer. Presented at the European Brewing Convention, Antwerp, BEL. June 2-6.
- Speers RA. 2019. Wort & yeast nutrition: effects on flavour. Invited Presentation. MBAA Ontario Section. Guelph, ON. Jan. 31-Feb. 1.
- Huismann M, Gormley F, Zait D, Speers RA, Maskell DL. 2018. The identification and classification of unfilterable beer haze. Young Scientists Symposium on Malting, Brewing and Distilling. September 12-14. Bitberg/Trier, DEU.
- Reid S, Speers RA, Lumsden W and Maskell DL. 2018. Organic acid development during Scotch Whisky fermentations. Young Scientists Symposium on Malting, Brewing and Distilling. Bitberg/Trier, DEU. September 12-14.

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Recent publications.

- Gibson B, Dahabieh M, Jouhten P, Krogerus K, Magalhães F, Siewers V & Vidgren V. 2020. Directed evolution of ale and lager yeast for improved brewing efficiency and beer quality. Annual Review of Food Science and Technology 11: in press.

Yeasts involved in brewing have a specific suite of traits that contribute to the character of classic beer styles. These traits resulted from a domestication process that may have spanned several millennia. During this time multiple brewing yeast properties developed incrementally, through a combination of

natural and artificial selection, to allow the production of beers that were clear, had positive flavor notes, minimal off-flavor, and could be prepared with recycled yeast due to the strains' tolerance to brewery-related stresses. The present-day beer market is, however, characterized by a demand for novel beer

properties and brewers are increasingly looking for new ways to differentiate their beers. As yeast has a significant impact on beer character, selecting or developing new yeast strains has potential to introduce diversity and functionality to beers. Reviewed here are the different approaches that have been considered thus far. These include strain screening, bioprospecting, hybridization, targeted gene modification/gene editing/synthetic biology. Particular

emphasis is placed on adaptive laboratory evolution (ALE), which represents an extension of the domestication process for generating new and useful production strains. ALE can be used to accentuate the positive traits of brewing yeast as well as remove some of the traits that are less desirable from a modern brewer's perspective. This method has the added advantage of being non-GM, and therefore suitable for food and beverage production.

- 2 Mojzita D, Rantasalo A, Jäntti J. 2019. Gene expression engineering in fungi. *Curr Opin Biotechnol* 59:141-149. doi: 10.1016/j.copbio.2019.04.007

Fungi are a highly diverse group of microbial species that possess a plethora of biotechnologically useful metabolic and physiological properties. Important enablers for fungal biology studies and their biotechnological use are well-performing gene expression tools. Different types of gene expression tools exist; however, typically they are at best only functional in one or a few closely related species. This has hampered research and development of

industrially relevant production systems. Here, we review operational principles and concepts of fungal gene expression tools. We present an overview on tools that utilize endogenous fungal promoters and modified hybrid expression systems composed of engineered promoters and transcription factors. Finally, we review synthetic expression tools that are functional across a broad range of fungal species.

- 3 Cubillos FA, Gibson B, Grijalva-Vallejos N, Krogerus K & Nikulin J. 2019. Bioprospecting for brewers: exploiting natural diversity for naturally diverse beers. *Yeast* 36: 383-398.

The burgeoning interest in archaic, traditional and novel beer styles has coincided with a growing appreciation of the role of yeasts in determining beer character as well as a better understanding of the ecology and biogeography of yeasts. Multiple studies in recent years have highlighted the potential of wild *Saccharomyces* and non-*Saccharomyces* yeasts for production of beers with novel flavour profiles and other desirable properties. Yeasts isolated from spontaneously-fermented beers as well as from other

food systems (wine, bread, kombucha) have shown promise for brewing application and there is evidence that such cross-system transfers have occurred naturally in the past. We review here the available literature pertaining to the use of non-conventional yeasts in brewing, with a focus on the origins of these yeasts, including methods of isolation. Practical aspects of utilizing non-domesticated yeasts are discussed and modern methods to facilitate discovery of yeasts with brewing potential are highlighted.

- 4 Dahabieh M, Thevelein J. & Gibson B. 2019. Multimodal microorganism development: Integrating top-down biological engineering with bottom-up rational design. *Trends in Biotechnology* - <https://doi.org/10.1016/j.tibtech.2019.09.006>

Biological engineering has unprecedented potential to solve society's most pressing challenges. Engineering approaches must consider complex technical, economic, and social factors. This requires methods that confer gene/pathway-level functionality and organism-level robustness in rapid and cost-effective ways. This article compares foundational engineering approaches – bottom-up, gene-targeted engineering, and top-down, whole-genome engineering – and identifies significant complementarity between them. Cases drawn from

engineering *Saccharomyces cerevisiae* exemplify the synergy of a combined approach. Indeed, multimodal engineering streamlines strain development by leveraging the complementarity of whole-genome and gene-targeted engineering to overcome the gap in design knowledge that restricts rational design. As biological engineers target more complex systems, this dual-track approach is poised to become an increasingly important tool to realize the promise of synthetic biology.

- 5 Krogerus K, Magalhães F, Kuivanen J & Gibson B. 2019. A deletion in the *STAI* promoter determines maltotriose and starch utilization in *STAI+* *Saccharomyces cerevisiae* strains. *Applied Microbiology and Biotechnology* 18: 7597-7615.

Diastatic strains of *Saccharomyces cerevisiae* are common contaminants in beer fermentations and are capable of producing an extracellular *STAI*-encoded glucoamylase. Recent studies have revealed variable diastatic ability in strains tested positive for *STAI*, and here we elucidate genetic determinants behind this variation. We show that poorly diastatic strains have a 1162 bp deletion in the promoter of *STAI*. With CRISPR/Cas9-aided reverse engineering, we show that this deletion greatly decreases the ability to grow in beer and consume dextrin, and the expression of *STAI*. New PCR primers were designed for differentiation of highly and poorly diastatic strains based on the presence of the deletion in the *STAI* promoter. In addition, using publically available whole genome sequence data, we show that the *STAI* gene is

prevalent in among the ‘Beer 2’/‘Mosaic Beer’ brewing strains. These strains utilize maltotriose efficiently, but the mechanisms for this have been unknown. By deleting *STAI* from a number of highly diastatic strains, we show here that extracellular hydrolysis of maltotriose through *STAI* appears to be the dominant mechanism enabling maltotriose use during wort fermentation in *STAI+* strains. The formation and retention of *STAI* is an alternative evolutionary strategy for efficient utilization of sugars present in brewer’s wort. The results of this study allow for the improved reliability of molecular detection methods for diastatic contaminants in beer, and can be exploited for strain development where maltotriose use is desired.

- 6 Krogerus K, Holmström S & Gibson B. 2018. Enhanced wort fermentation with de novo lager hybrids adapted to high ethanol environments. *Applied and Environmental Microbiology* 84: e02302-17.

Interspecific hybridization has been shown to be a valuable tool for developing and improving brewing yeast in a number of industry-relevant aspects. However, the genomes of newly formed hybrids have been shown to be unstable. Here, we exploited this notion 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 2L-scale wort fermentations replicating industrial conditions. The fermentations 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 larger improvements in fermentation performance. Interestingly, it was not only the hybrid strains, but also the *S. cerevisiae* parent strain, that appeared to adapt and showed considerable changes in genome size. Genome sequencing and ploidy analysis revealed that changes had occurred both at chromosome and single nucleotide level 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 that are relevant to industrial lager beer fermentation.

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Recently published papers.

- 1 Passer AR, Coelho MA, Billmyre RB, Nowrousian M, Mittelbach M, Yurkov AM, Averette AF, Cuomo CA, Sun S. and Heitman J. 2019. Genetic and genomic analyses reveal boundaries between species closely related to *Cryptococcus* pathogens. *mBio* 10: e00764-19.

Speciation is a central mechanism of biological diversification. While speciation is well studied in plants and animals, in comparison, relatively little is known about speciation in fungi. One fungal model is the *Cryptococcus* genus, which is best known for the pathogenic *Cryptococcus neoformans*/*Cryptococcus gattii* species complex that causes >200,000 new human infections annually. Elucidation of how these species evolved into important human-pathogenic species remains challenging and can be advanced by studying the most closely related nonpathogenic species, *Cryptococcus amyloletus* and *Tsuchiyaea wingfieldii*. However, these species have only four known isolates, and available data were insufficient to determine species boundaries within this group. By analyzing full-length chromosome assemblies, we reappraised the phylogenetic relationships of the four available strains, confirmed the genetic separation of *C. amyloletus* and *T. wingfieldii* (now *Cryptococcus*

wingfieldii), and revealed an additional cryptic species, for which the name *Cryptococcus floricola* is proposed. The genomes of the three species are ~6% divergent and exhibit significant chromosomal rearrangements, including inversions and a reciprocal translocation that involved intercentromeric ectopic recombination, which together likely impose significant barriers to genetic exchange. Using genetic crosses, we show that while *C. wingfieldii* cannot interbreed with any of the other strains, *C. floricola* can still undergo sexual reproduction with *C. amyloletus*. However, most of the resulting spores were inviable or sterile or showed reduced recombination during meiosis, indicating that intrinsic postzygotic barriers had been established. Our study and genomic data will foster additional studies addressing fungal speciation and transitions between nonpathogenic and pathogenic *Cryptococcus* lineages.

- 2 Kachalkin AV, Turchetti B, Inácio J, Carvalho C, Mašínová T, Pontes A, Röhl O, Glushakova AM, Akulov A, Baldrian P, Begerow D, Buzzini P, Sampaio JP, Yurkov AM. 2019. Rare and undersampled dimorphic basidiomycetes. *Mycological Progress* 18: 945-971.

The diversity of yeasts has grown rapidly as the discovery of new species has benefited from intensified sampling and largely improved identification techniques. An environmental study typically reports the isolation of yeast species, some of which are new to science. Rare species represented by a few isolates often do not result in a taxonomic description. Nucleic acid sequences from these undescribed yeasts remain in public sequence databases, often without a proper taxonomic placement. This study presents a constrained phylogenetic analysis for many rare yeasts from unpublished but publicly available DNA sequences and from studies previously conducted by the authors of this work. We demonstrate that single isolates are an important source of taxonomic findings such as including new genera and species. Independent surveys performed during the last 20 years on a large geographic scale yielded a number of single strains, which were proved to be conspecific in the phylogenetic analyses presented here. The following new species were resolved and described: *Vustinia terrea* Kachalkin, Turchetti & Yurkov gen. nov. et sp. nov.; *Udeniomyces caspiensis* Kachalkin sp. nov.; *Udeniomyces orazovii* Kachalkin sp. nov.; *Tausonia rosea* Kachalkin sp. nov.; *Itersonilia diksonensis* Kachalkin sp. nov.; *Krasilnikovozyma fibulata*

Glushakova & Kachalkin, *Kwoniella fici* Turchetti sp. nov.; *Heterocephalacria fruticeti* f.a. Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Heterocephalacria gelida* f.a. Turchetti & Kachalkin sp. nov.; *Heterocephalacria hypogea* f.a. Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Heterocephalacria lusitanica* f.a. Inacio, Carvalho, Roehl, Yurkov & Sampaio sp. nov.; *Piskurozyma arborea* Yurkov, Kachalkin, Mašínová & Baldrian sp. nov.; *Piskurozyma silvicultrix* Turchetti, Mašínová, Baldrian & Yurkov sp. nov.; *Piskurozyma stramentorum* Yurkov, Mašínová & Baldrian sp. nov.; *Naganishia nivalis* Turchetti sp. nov.; and *Yurkovia nerthusi* Yurkov & Begerow, sp. nov. In addition, two new combinations were proposed *Krasilnikovozyma curviuscula* (Babeva, Lisichkina, Reshetova & Danilevich) Yurkov, Kachalkin & Sampaio comb. nov. and *Hannaella taiwanensis* (F.L. Lee & C.H. Huang) Yurkov comb. nov. The order Cyphobasidiales T. Spribille & H. Mayrhofer is rejected in favor of the older name Erythrobasidiales R. Bauer, Begerow, J.P. Sampaio, M. Weiss & Oberwinkler. Other potential novel species identified in this paper await future description. Phylogenetic placement of yet unpublished sequences is believed to facilitate species descriptions and improve classification of yeasts from environmental sequence libraries.

- 3 Richter C, Yurkov AM, Boekhout T, Stadler M. 2019. Diversity of *Tilletiopsis*-like fungi in Exobasidiomycetes (Ustilaginomycotina) and description of six novel species. *Frontiers in Microbiology* 10: 2544.

In 2006 several yeast-like fungi were isolated from apples that showed a postharvest disorder named 'white haze'. These strains were morphologically and molecularly assigned to the genus *Tilletiopsis*. Following the recent reclassification of yeasts in Ustilaginomycotina and the genus *Tilletiopsis* in particular, species that caused 'white haze' disorder were re-identified based on the phylogenetic analysis of five DNA-loci (ITS, LSU, SSU, *RPB2* and *TEF1*) and analysis of D1/D2 domains of the 26S/28S rRNA (LSU). Six novel species belonging to three orders in the Exobasidiomycetes, namely *Entyloma belangeri* (holotype: CBS 111600; ex-type: DSM 29114) MB

823155, *E. davenportii* (holotype: CBS 111604; ex-type: DSM 100135) MB 823154, *E. elstari* (holotype: CBS 111593; ex-type: DSM 29113) MB 823153, *E. randwijkense* (holotype: CBS 111606; ex-type: DSM 100136) MB 823156, *Jamesdicksonia mali* (holotype: CBS 111625; ex-type: DSM 29121) MB 823151 and *Golubevia heteromorpha* (holotype: CBS 111610; ex-type: DSM 100176) MB 823152 are proposed to accommodate these strains. In addition, sequences representing phylogenetically related but yet undescribed fungi were obtained from GenBank in order to show the diversity of *Tilletiopsis*-like yeast states in Exobasidiomycetes.

- 4 Yurkov AM, Püschner HM, Scholz AH. 2019. DSMZ: the European Union's first Registered Collection under the Nagoya Protocol. *Microbiology Australia* 40: 108-113.

The Convention on Biological Diversity and the Nagoya Protocol have created new challenges for international microbiological research. With the implementation of the Nagoya Protocol in 2014, the European Union created a new voluntary legal mechanism, the Register of Collections, to help users of collections, including culture collections, have an easier path to Nagoya Protocol compliance by using a

so-called 'registered collection'. The Leibniz Institute DSMZ is the first, and so far only, collection to successfully be entered into the Register. The challenges and lessons learned during this process can be informative for culture collections and users of microbial resources beyond the EU and indeed around the world.

Papers accepted for publication.

- 5 Yurkov AM, Sannino C, Turchetti B. 2019. *Mrakia fibulata* sp. nov, a psychrotolerant yeast from temperate and cold habitats. *Antonie van Leeuwenhoek*: in press.
- 6 He MQ, Zhao RL, Hyde K, Begerow D, Kemler M, Yurkov AM et al. 2019. Notes, outline and divergence times of Basidiomycota. *Fungal Diversity*, in press.

XIII Laboratory of Genetics, DOE Great Lakes Bioenergy Research Center, Wisconsin Energy Institute, Genome Center of Wisconsin, J. F. Crow Institute for the Study of Evolution, University of Wisconsin, Madison, WI 53726, USA. Communicated by Chris Todd Hittinger <chittinger@wisc.edu>.

Recent publications.

- 1 Langdon QK, Peris D, Baker EP, Opulente DA, Nguyen HV, Bond U, Goncalves P, Sampaio JP, Libkind D, Hittinger CT@. 2019. Fermentation innovation through complex hybridization of wild and domesticated yeasts. *Nat Ecol Evol* 3: 1576-1586. <https://doi.org/10.1038/s41559-019-0998-8>

@ = Corresponding author

The most common fermented beverage, lager beer, is produced by interspecies hybrids of the brewing yeast *Saccharomyces cerevisiae* and its wild relative *S. eubayanus*. Lager-brewing yeasts are not the only

example of hybrid vigour or heterosis in yeasts, but the full breadth of interspecies hybrids associated with human fermentations has received less attention. Here we present a comprehensive genomic analysis of 122

Saccharomyces hybrids and introgressed strains. These strains arose from hybridization events between two to four species. Hybrids with *S. cerevisiae* contributions originated from three lineages of domesticated *S. cerevisiae*, including the major wine-making lineage and two distinct brewing lineages. In contrast, the undomesticated parents of these interspecies hybrids were all from wild Holarctic or European lineages. Most hybrids have inherited a mitochondrial genome from a parent other than *S. cerevisiae*, which recent functional studies suggest could confer adaptation to

colder temperatures. A subset of hybrids associated with crisp flavour profiles, including both lineages of lager-brewing yeasts, have inherited inactivated *S. cerevisiae* alleles of critical phenolic off-flavour genes and/or lost functional copies from the wild parent through multiple genetic mechanisms. These complex hybrids shed light on the convergent and divergent evolutionary trajectories of interspecies hybrids and their impact on innovation in lager brewing and other diverse fermentation industries.

- 2 Krassowski T, Kominek J, Shen XX, Ofulente DA, Zhou X, Rokas A, Hittinger CT, Wolfe KH. 2019. Multiple reinventions of mating-type switching during budding yeast evolution. *Curr Biol* 29: 2555-2562.

Cell type in budding yeasts is determined by the genotype at the mating-type (*MAT*) locus, but yeast species differ widely in their mating compatibility systems and life cycles. Among sexual yeasts, heterothallic species are those in which haploid strains fall into two distinct and stable mating types (*MATa* and *MAT α*), whereas homothallic species are those that can switch mating types or that appear not to have distinct mating types. The evolutionary history of these mating compatibility systems is uncertain, particularly regarding the number and direction of transitions between homothallism and heterothallism, and regarding whether the process of mating-type switching had a single origin. Here, we inferred the mating compatibility systems of 332 budding yeast species from their genome sequences. By reference to

a robust phylogenomic tree, we detected evolutionary transitions between heterothallism and homothallism, and among different forms of homothallism. We find that mating-type switching has arisen independently at least 11 times during yeast evolution and that transitions from heterothallism to homothallism greatly outnumber transitions in the opposite direction (31 versus 3). Although the 3-locus *MAT-HML-HMR* mechanism of mating-type switching as seen in *Saccharomyces cerevisiae* had a single evolutionary origin in budding yeasts, simpler “flip/flop” mechanisms of switching evolved separately in at least 10 other groups of yeasts. These results point to the adaptive value of homothallism and mating-type switching to unicellular fungi.

- 3 Labella AL, Ofulente DA, Steenwyk JL, Hittinger CT, Rokas A. 2019. Variation and selection on codon usage bias across an entire subphylum. *PLoS Genet* 15: e1008304. <https://doi.org/10.1371/journal.pgen.1008304>

Variation in synonymous codon usage is abundant across multiple levels of organization: between codons of an amino acid, between genes in a genome, and between genomes of different species. It is now well understood that variation in synonymous codon usage is influenced by mutational bias coupled with both natural selection for translational efficiency and genetic drift, but how these processes shape patterns of codon usage bias across entire lineages remains unexplored. To address this question, we used a rich genomic data set of 327 species that covers nearly one third of the known biodiversity of the budding yeast subphylum Saccharomycotina. We found that, while genome-wide relative synonymous codon usage (RSCU) for all codons was highly correlated with the GC content of the third codon position (GC3), the

usage of codons for the amino acids proline, arginine, and glycine was inconsistent with the neutral expectation where mutational bias coupled with genetic drift drive codon usage. Examination between genes' effective numbers of codons and their GC3 contents in individual genomes revealed that nearly a quarter of genes (381,174/1,683,203; 23%), as well as most genomes (308/327; 94%), significantly deviate from the neutral expectation. Finally, by evaluating the imprint of translational selection on codon usage, measured as the degree to which genes' adaptiveness to the tRNA pool were correlated with selective pressure, we show that translational selection is widespread in budding yeast genomes (264/327; 81%). These results suggest that the contribution of translational selection and drift to patterns of

synonymous codon usage across budding yeasts varies across codons, genes, and genomes; whereas drift is the primary driver of global codon usage across the

subphylum, the codon bias of large numbers of genes in the majority of genomes is influenced by translational selection.

- 4 Peris D, Moriarty RV, Alexander WG, Wrobel RL, Hittinger CT[@]. Synthetic hybrids of six yeast species. bioRxiv - resubmitted. <https://doi.org/10.1101/597633>

Allopolyploidy generates diversity by increasing the number of copies and sources of chromosomes. Many of the best-known evolutionary radiations, crops, and industrial organisms are ancient or recent allopolyploids. Allopolyploidy promotes differentiation and facilitates adaptation to new environments, but the tools to test its limits are lacking. Here we develop an iterative method to combine the genomes of multiple budding yeast species, generating *Saccharomyces* allopolyploids of an unprecedented scale. Chromosomal instability and

cell size increased dramatically as additional copies of the genome were added, but we were able to construct synthetic hybrids of up to six species. The six-species hybrids initially grew slowly, but they rapidly adapted when selection to a novel environment was applied, even as they retained traits from multiple species. These new synthetic yeast hybrids have potential applications for the study of polyploidy, genome stability, chromosome segregation, cancer, and bioenergy.

- 5 Landgon QK, Peris D, Eizaguirre JI, Oplente DA, Buh KV, Sylvester K, Jarzyna M, Rodríguez ME, Lopes CA, Libkind D[@], Hittinger CT[@]. Genomic diversity and global distribution of *Saccharomyces eubayanus*, the wild ancestor of hybrid lager-brewing yeasts. bioRxiv - under revision. <https://doi.org/10.1101/709535>

S. eubayanus, the wild, cold-tolerant parent of hybrid lager-brewing yeasts, has a complex and understudied natural history. The exploration of this diversity can be used both to develop new brewing applications and to enlighten our understanding of the dynamics of yeast evolution in the wild. Here, we integrate whole genome sequence and phenotypic data of 200 *S. eubayanus* strains, the largest collection to date. *S. eubayanus* has a multilayered population structure, consisting of two major populations that are further structured into six subpopulations. Four of these subpopulations are found exclusively in the Patagonian region of South America; one is found predominantly in Patagonia and sparsely in Oceania and North America; and one is specific to the Holarctic ecozone. *S. eubayanus* is most abundant and genetically diverse in Patagonia, where some locations harbor more genetic diversity than is found outside of

South America. All but one subpopulation shows isolation-by-distance, and gene flow between subpopulations is low. However, there are strong signals of ancient and recent outcrossing, including two admixed lineages, one that is sympatric with and one that is mostly isolated from its parental populations. Despite *S. eubayanus*' extensive genetic diversity, it has relatively little phenotypic diversity, and all subpopulations performed similarly under most conditions tested. Using our extensive biogeographical data, we constructed a robust model that predicted all known and a handful of additional regions of the globe that are climatically suitable for *S. eubayanus*, including Europe. We conclude that this industrially relevant species has rich wild diversity with many factors contributing to its complex distribution and biology.

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

Fantastic Yeasts (...and where to find them?)

The Editorial Board of *Yeast* has recently decided that the journal will now consider the publication of high-quality descriptions of new taxa. Simultaneously to the publication of the species description below, *Yeast* will release guidelines for authors wishing to

submit such papers. In summary, the guidelines will include: high-quality work using up-to-date literature, compliance with the code of Nomenclature, deposition of ex-types in public collections including the CBS, registration of names in MycoBank, proper name

construction and etymology, a standard list of growth properties, due diligence to characterize the sexual life cycle, high quality micrographs, deposition of barcode sequences, a lucid discussion and application of relevant species concepts, appropriate sequence-based placement of new taxa, geographic and habitat information; strong phylogenetic evidence for assignment to higher taxonomic categories and a strong justification for any name changes. In addition,

authors will be encouraged to base a description on multiple, independent isolates, or in the alternative, a compelling justification for a description based on a single strain. All available strains should be studied to the extent possible, a draft genome assembly should be deposited and annotated, evidence should be given that isolation of new species was part of an ecologically meaningful framework, and karyotype information should be presented.

The following paper will appear in the *Fantastic Yeasts* section of *Yeast*.

- 1 Santos ARO, Lee DK, Ferreira AG, do Carmo MC, Rondelli VM, Barros KO, Hsiang T, Rosa, CA, Lachance MA. 2020. The yeast community of *Conotelus* sp. (Coleoptera: Nitidulidae) in Brazilian passionfruit flowers (*Passiflora edulis*) and description of *Metschnikowia amazonensis* sp. nov., a large-spored clade yeast. *Yeast* (in press).

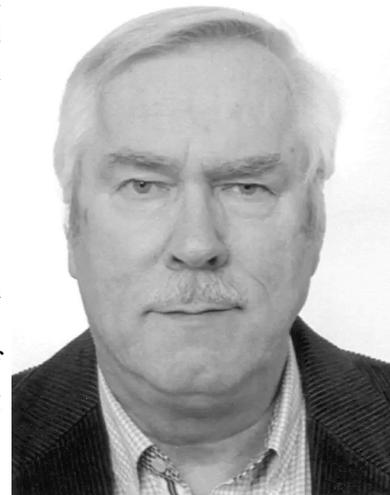
Species of the nitidulid beetle *Conotelus* found in flowers of Convolvulaceae and other plants across the New World and in Hawaii consistently harbour a yeast community dominated by one or more large-spored *Metschnikowia* species. We investigated the yeasts found in beetles and flowers of cultivated passionfruit in Rondônia state, in the Amazon biome of Brazil, where a *Conotelus* species damages the flowers and hinders fruit production. A sample of 46 beetles and 49 flowers yielded 86 and 83 yeast isolates, respectively. Whereas the flower community was dominated by *Kodamaea ohmeri* and *Kurtzmaniella quercitrusa*, the major yeasts recovered from beetles were *Wickerhamiella occidentalis*, which is commonly isolated from this community, and a novel species of

large-spored *Metschnikowia* in the arizonensis subclade, which we describe here as *Metschnikowia amazonensis* sp. nov. Phylogenetic analyses based on barcode sequences (ITS-D1/D2) and a multigene alignment of 11917 positions (genes *ura2*, *msh6*, and *pmt2*) agreed to place the new species as a sister to *Metschnikowia arizonensis*, a rare species known only from one locality in Arizona. The two form sterile asci when mated, which is typical of related members of the clade. The α pheromone of the new species is unique but typical of the subclade. The type of *M. amazonensis* sp. nov. is UFMG-CM-Y6309^T (ex-type CBS 16156^T, mating type a) and the designated allotype (mating type α) is UFMG-CM-Y6307^A (CBS 16155^A). MycoBank MB 833560.

Obituary

Matti Korhola (1946-2019)

On July 20, 2019, Docent of the Faculty of Biological and Environmental Sciences of Helsinki University, Matti P. Korhola, passed away after a serious illness. He was 73 years old. Born on April 1, 1946 in Ristiina, Finland, Matti spent his earlier childhood in the middle of the Finnish forests on a small farm. He attended the University of Helsinki, where he trained in microbiology, genetics and biochemistry. In 1972, Matti earned an M.Sc. degree in General Microbiology. At the beginning of his career, Matti also worked for two years as a teaching assistant in microbial genetics in the Department of Genetics. After graduation, Matti Korhola obtained an ASLA-Fulbright scholarship and continued his Master's thesis studies of DNA replication in *Escherichia coli* at the University of Minnesota. In 1975, he returned to the University of Helsinki as a teaching assistant in General Microbiology, and in 1978 he completed his Ph.D. degree.



In 1980, Matti joined Alko Ltd Research Laboratories, a longstanding leader investigating the biochemistry, physiology and structural biology of *Saccharomyces cerevisiae*. From 1987 to 1995, Matti Korhola served as director of the Alko Research Laboratories, including analytical, biomedical and microbial research. As Alko's leader, Matti shifted the direction of the traditional monopoly company's focused on yeast physiology to a diverse study of yeasts and the development of production strains. He hired promising, young scientists from domestic and foreign institutions, and encouraged visits from foreign researchers, among whom were me and my husband Gennadi Naumov. We collaborated with Matti several times both in Alko Research Laboratories and later at the University of Helsinki. In Finland, Matti Korhola organized National Yeast Days, served as a head of the Foundation for Biotechnical and Industrial Fermentation Research which awarded research grants from funds annually provided by Alko Ltd.

In 1995, when Alko was split into three companies and the Research Laboratories closed, Matti moved to the University of Helsinki and established his own company, Alkomohr Biotech Ltd. The company was involved in the EU's extensive EUROFAN program, working on six genes. Alkomohr also conducted commercial product development projects: constructing new baker's and wine yeast strains, as well as developing its own α -galactosidase and methanol dehydrogenase products. Shortly before his departure, Matti donated his vast and valuable collection of yeast strains isolated from industrial processes to the microbial collection of the Faculty of Agriculture and Forestry, University of Helsinki.

Matti had a special sense of humor with word play. The name of his company, Alkomohr, is derived from an anagram of Matti Korhola: Alko pointing to Alko Ltd and Mohr is a West-African gazelle with graceful ringed horns. The first of Matti's grandchild was born six weeks before his untimely departure. He will be remembered as an innovative researcher and administrator, a colleague and a dear friend.

Elena Naumova <lena_naumova@yahoo.com>

We, at Lallemand, are very fortunate to have met Matti some 30 years ago. Our relationship started at yeast-related conferences which led to mutual visits and other meetings, including at a fishing camp where Matti showed us his recipe for 'gravlax' (which we still use). Matti then advised us that his employer, Alko, was selling its industrial activities and we ended taking over their 'mineral enriched yeasts' business,

including their brand 'Alkosel', moving the equipment to our newly acquired Estonian plant. He helped and supported the transfer of the business and related technologies and remained our valued friend and consultant for the last 23 years. He was responsible for many strain improvement attempts and successes of which our leading position in glutathione-rich yeasts (produced still in Estonia partly with the old Alko equipment) is a shining example of his many contributions to our company. One of us (RD) had the opportunity to visit him again in Helsinki in December of last year and he was still eager to contribute to our R&D efforts with a local company.

Here is a quote from his article “Between science and industry-applied yeast research” (FEMS Yeast Research, 18, 2018): "My leading philosophy was to encourage openness, critical thinking and collaboration with colleagues inside and outside of the company" (Alko at the time).

We, at Lallemand, had and still have the same philosophy of openness and collaboration and so it has been a great match between Matti and us during all those years.

Matti also writes that he was very proud to say that three of the speakers he had personally invited to the first Alko Symposium “Gene Expression in Yeast” in 1983 went on to become Nobel Laureates. We believe that Matti belongs to the same category: a gentleman and a world-class scientist who was highly respected by his peers.

Richard Degré and Jean Chagnon <rdegre@lallemand.com> <jchagnon@lallemand.com>

Forthcoming Meetings

International Symposium: Yeasts: at the cross-roads of Systems biology and Biomedicine Madrid, Spain, 23 and 24 January 2020

An international Symposium entitled “*Yeasts: at the cross-roads of Systems biology and Biomedicine*” in memory of Professor Julio Rodríguez-Villanueva (1928-2017) will be held in Madrid on 23 and 24 January 2020, sponsored by the Fundación Ramón Areces. The symposium is coordinated by Carlos Gancedo (Madrid) and César Nombela (Madrid). Featured speakers: J. D. Boeke (New York), J. Arroyo (Madrid), CL. Flores (Madrid), P. Alepuz (Valencia), O. Cohen-Fix, (Bethesda), C. Dargemont, (Montpellier), J. Naglik (London), C. Vázquez de Aldana (Salamanca), V.J. Cid (Madrid), P. San Segundo (Salamanca), Ariño, J (Barcelona), J. Pronk (Delft).

Registration is free and will be soon opened at www.fundacionareces.es

Juana Gancedo <jmgancedo@ext.iib.uam.es>.

International Congress on Yeasts 15 — The Spirit of Yeast August 23-27 2020, Vienna University, Vienna, Austria



It is our great pleasure to invite you to the 15th International Congress on Yeasts to be held at the University of Vienna in the Heart of the City of Vienna, Austria, from August 23 to 27, 2020. The conference is intended to attract all yeast researchers in all fields. The University of Natural Resources and Life Sciences, the Alma Mater Viridis, perceives itself as a teaching and research centre for renewable resources, which are necessary for human life. Today BOKU is one of Austria’s leading centres in yeast research, spanning from fundamental research on yeast ecology to its application in food, feed and biopharmaceutical production, as well as the forefront of synthetic biology for renewable production of chemicals.

The University of Vienna is one of the oldest Universities in the German-speaking world, founded in 1365 by Duke Rudolph IV. The main university building was erected

around 1880 as part of the famous Ringstrasse and is just a few minutes walk from all major sights in the city center.

Major themes: Metabolism • Protein synthesis • Synthetic biology • Fermentation • Evolution, ecology, taxonomy • Growth and stress response • Pathogenesis and health.

Plenary Speakers: Jef D. Boeke, New York University, USA; Christina D. Smolke, Stanford University, USA; Hiroshi Takagi, Nara Institute of Science, Japan; Joris Winderickx, KU Leuven, Belgium; Judith E. Berman, Tel Aviv University, Israel; Markus Ralser, The Francis Crick Institute, UK.

Diethard Mattanovich
University of Natural Resources
and Life Sciences, Vienna
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15th International Conference on Culture Collections - ICC15
November 16-20, 2020, Pucón, Chile

The Chilean Culture Collection of Type Strains - CCCT, hosted at the Scientific and Technological Bioresource Nucleus BIOREN-UFRO, of the Universidad de La Frontera (Temuco, Chile) has the honour of announce the 15th International Conference on Culture Collections (ICC15), which will be held in the Campus of Pucón, Chile, from 16th to 20th November 2020.

The meeting is supported by the World Federation for Culture Collections (WFCC).

Please visit the webpage for more information about the conference - <http://www.iccc15.ufro.cl>

ICC15 Secretariat:

CCCT - Chilean Culture Collection of Type Strains (WDCM 1111)
BIOREN-UFRO Núcleo Científico y Tecnológico
Universidad de La Frontera
Av. Francisco Salazar 01145
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Brief News Item

Potentially invalid taxonomic descriptions of yeasts

Dear colleagues,

There has been some confusion around potentially invalid taxonomic descriptions of yeasts. Indeed, the wording used in species descriptions (protologues) was not always conform with the International Code of Nomenclature for algae, fungi, and plants (ICN). Most common problems are incorrect designation of the holotype and incorrect designation of its deposition in a culture collection. As a result, descriptions of a few hundred yeast species were indicated as invalid in the two leading taxonomic repositories, MycoBank and Index Fungorum. This further led to the formal re-description of the yeast genus *Jaminaea* because its description was not conform with the ICN requirements.

Discussions during the ISSY34 meeting brought us to the decision to write a text to comment on the problem of these formally invalid yeast species. We wanted to express our concerns to the International Commission on Taxonomy of Fungi (ICTF) to find a workable solution to the problem. For more than half a year, we have been working on the text. Now, we would like to share this text among scientists working with yeasts to give their opinion and to join forces.

We aim to explain views of yeast taxonomists on the problem. We believe that this text will help to establish a stable approach to cite the reference material in publications. Therefore, we seek input and feedback from the community, experienced researchers and editors and reviewers of journals. Following recommendations from ICTF experts, we added recommendations to protect retroactively many yeast names and reduce name changes due to incorrect typification to a minimum.

Please feel free to contact us if you want to contribute to the discussion. We will send you the text for review and commenting. We will carefully collect all comments and incorporate suggestions. We also expect to receive suggestions from ICTF experts.

With kind regards,

Andrey Yurkov,
Leibniz Institute DSMZ
German Collection of Microorganisms and Cell
Cultures
<andrey.yurkov@dsmz.de>

Teun Boekhout
Westerdijk Fungal Biodiversity Institute,
<t.boekhout@wi.knaw.nl>

Fifty Years Ago

Y E A S T
A News Letter for Persons Interested in Yeast
Official publication of the
International Council of Yeasts and Yeast-like Microorganisms
January 1970 Volume XVIII, Number 2
Editor
Herman J. Phaff, University of California, Davis, California 95616
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Anna Kocková-Kratochvílová, Slovak Academy of Sciences, Bratislava, Czechoslovakia
Associate Editor
F. M. Clark, University of Illinois, Urbana, Illinois
Associate Editor
Richard Snow, Dept. of Genetics, University of California, Davis, California 95616

SPECIAL NOTE

Through the courtesy of Dr. R. C. von Borstal of the Oak Ridge National Laboratory, we have obtained copies of the recent Yeast Genetics Supplement to volume 31 of the Microbial Genetics Bulletin, and are mailing them with this issue of YEAST. This supplement proposes a uniform genetic nomenclature for yeast, and includes a compilation of the presently known products of a large number of genes of Saccharomyces. Since genetic studies of yeast are progressing rapidly, it is very desirable that some standard nomenclature be used, and the editors therefore urge all readers of YEAST to follow the recommendations in their future communications.

National Research Council of Canada, Prairie Regional Laboratory, Saskatoon, Sask., Canada. Communicated by J. F. T. Spencer.

The following list summarize our recent activities concerning yeasts and yeast-like organisms at P.R.L.

We have continued our study of the mannose-containing polysaccharides of yeast by p.m.r. spectroscopy. The following papers have appeared recently, have been accepted or submitted for publication, or are in preparation:

1. "Systematics of the genera Saccharomyces, Schizosaccharomyces, Endomycopsis, Kluyveromyces, Schwanniomyces and Brettanomyces: proton magnetic resonance spectra of the mannans and mannose-containing polysaccharides as an aid in classification." J. F. T. Spencer and P. A. J. Gorin. Antonie van Leeuwenhoek. 35: 361 (1969).

Microbiological Laboratory of the Institute of Chemistry of the Slovak Academy of Sciences, Bratislava, Dúbravská cesta, Czechoslovakia. Communicated by Dr. Anna Kocková-Kratochvílová.

The numerical taxonomy of the Genus Saccharomyces (Meyen) Reess was completed after evaluating more than 500 strains and three papers will be published in English under the title "The taxometric study of the Genus Saccharomyces (Meyen) Reess" in the Biological Edition, Publishing House of the Slovak Academy of Sciences, Bratislava, Klemensova 17/:

Georgia State University, 33 Gilmer Street, S. E., Atlanta, Georgia 30303. Communicated by D. G. Ahearn.

An informal colloquium "Recent Trends in Yeast Research" was held at the Miner Center and the State University of New York, College of Arts and Science at Plattsburgh on August 15-16, 1969. The participants who presented papers included: D. G. Ahearn, (Chairman) Georgia State University, Atlanta, W. L. Cook, (Co-Chairman) New York State College of Arts and Sciences, Plattsburgh, S. P. Meyers, (Vice-Chairman) Louisiana State University, Herman J. Phaff, University of California, Davis, L. J. Wickerham, U. S. Department of Agriculture, Peoria, Chun-Juan K. Wang, State University College of Forestry, Syracuse, Vladimir Munk, State University College, Plattsburgh, J. J. Miller, McMaster University, Hamilton, Ontario, Canada, James N. Bicknell, University of Washington, Seattle, Jack W. Fell, University of Miami, Cletus P. Kurtzman, U. S. Department of Agriculture, Peoria, Jean Shadomy, Medical College of Virginia, Richmond, John R. Forro, General Electric Co., Syracuse.

Department of Zoology, University of Edinburgh, West Mains Road, Edinburgh 9, Scotland. Communicated by J. M. Mitchison.

Research topics and papers, mostly on the biochemistry and physiology of the cell cycle of Schizosaccharomyces pombe.

J. M. Mitchison and J. Creanor

Enzyme synthesis during the cell cycle.

Rutgers. The State University of New Jersey, Institute of Microbiology, Waksman Hall, New Brunswick, New Jersey 08903. Communicated by J. O. Lampen.

Two papers related to yeast appeared from this laboratory during the past year:

- (1) The glycoprotein structure of yeast invertase. N. P. Neumann and J. O. Lampen. Biochemistry 8:3352-3356 (1969).

Research Laboratories of the State Alcohol Monopoly (Alko), Helsinki, Finland. Communicated by Prof. Heikki Suomalainen.

Timo Nurminen and Heikki Suomalainen, Enzymatic properties of the isolated cell walls and plasma membrane preparation of baker's yeast. FEBS, Sixth Meeting, Madrid 1969, Abstr. Commun. p. 66.

Laboratoire de Recherches de la Chaire de Génétique - Ecole Nationale Supérieure Agronomique - C.R.A.M. (34) Montpellier, France. Communicated by Pr. P. Galzy.

The following publications have appeared or will be published shortly.

- Variation phénotypique de S. cerevisiae HANSEN au cours d'une culture prolongée sur acide pyruvique.

Laboratory of Cell Biology, Faculty of Science, Osaka City University, Sumiyoshi-ku, Osaka, Japan. Communicated by N. Yanagishima.

AUXIN-INDUCED EXPANSION GROWTH OF CELLS AND PROTOPLASTS OF YEAST. By N. Yanagishima and C. Shimoda, *Physiol. Plantarum* 21, 1122, 1968.

Using an auxin-responsive mutant of *Saccharomyces ellipsoideus*, expansion growth of cells caused by auxin was studied especially in comparison with that of protoplasts.

1. Indole-3-acetic acid induced detectable cell expansion growth in 3 hours in a buffered simple solution where no cell division occurred.
2. The auxin-induced expansion growth was inhibited by an antiauxin, transcinnamic acid.
3. Actinomycin D, chloramphenicol and cycloheximide inhibited the auxin-induced cell expansion growth.
4. Protoplasts did not expand in response to auxin under the condition where intact cells did.
5. The stability of protoplasts was not changed by the low auxin concentration (20 mg/l) which induced cell expansion.
6. High concentrations (100-1000 mg/l) of auxin caused protoplasts to burst even under an osmotically stable condition.

Central Research Laboratory of Ajinomoto Co., Inc., Kawasaki, Japan. Communicated by Takashi Nakase.

Fermentation of η -Paraffins by Yeast. Part I. Fermentative Production of α -Ketoglutaric Acid by *Candida lipolytica*. By Ryuichiro Tsugawa, Takashi Nakase, Tadao Kobayashi, Koichi Yamashita and Shinji Okumura. *Agr. Biol. Chem.*, Vol. 33, No. 2, p. 158-167, 1969.

We can supply to interested persons mating types and a sporulating diploid of *Candida lipolytica*.

I am planning to retire in September 1970 and my wife and I plan to move then to Southern Arizona.

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Our laboratory is studying the energetics of *Schizosaccharomyces pombe* and *Candida lipolytica* as well as the biogenesis of mitochondrial membrane of *Saccharomyces cerevisiae*.

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