Yeast

A Newsletter for Persons Interested in Yeast

ISSN 0513-5222

Official Publication of the International Commission on Yeasts of the International Union of Microbiological Societies (IUMS)

JUNE 2013 **Volume LXII, Number I**

Marc-André Lachance, Editor
University of Western Ontario, London, Ontario, Canada N6A 5B7
<lachance@uwo.ca>

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

Editorial

Tibor Deák (1936-2013)

I regret to announce the recent death of our colleague Tibor Deák on March 3 of this year. Tibor was very dear to many of us and is best known for his contributions to food microbiology. He was also an enthusiastic member of the International Commission on Yeasts, having hosted two ISSYs, one in Keszthely in 1977 and another in Budapest in 2003. Gábor Péter has kindly provided an obituary.

M.A. Lachance, Editor

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

Recent publications.

1 Golubev WI. 2013. Action spectrum of *Kluyveromyces lactis* mycocins. Microbiology 82:77-84.

New mycocinogenic strains of the yeast *Kluyveromyces lactis* were found. They have fungicidic activity at pH from 5 to 7. This activity was eliminated by UV irradiation. Among over 260 species tested, ones sensitive to these mycocins were revealed mainly in the families Saccharomycetaceae and Wickerhamomycetaceae of the order Saccharomycetales.

2 Golubev WI. 2013. Fungicidal activity of yeast isolated from chal. Appl Biochem Microbiol 49:176-181.

A *Kluyveromyces* strain secreting a fungicidal proteinaceous toxin has been isolated. Its maximal activity is observed at pH 5.0 and an increased osmotic pressure. This agent has been identified as a mycocin; it is active towards species belonging to the genus *Kluyveromyces* and some representatives of taxonomically related taxa.

3 Golubev WI. 2013. A *Kluyveromyces lactis* mycocin active at neutral pH. Microbiology 82:290-294.

A strain of *Kluyveromyces lactis* was found to secrete a fungicidal mycocin active in the pH range from 6 to 9 and exhibiting the highest activity at pH of approximately 7. A few yeast species of the families Saccharomycetaceae and Wickerhamomycetaceae were sensitive to the mycocin. Some genera and species are heterogeneous in this respect. UV treatment of the mycocinogenic strain resulted in loss of its antifungal activity. Although prokaryotes were not sensitive to the mycocin, the strain under study inhibited growth of some bacteria.

4 Golubev WI. 2013. Heterogeneity of the genus *Kazachstania* by sensitivity toward the mycocins of *Pichia membranifaciens*. Mykologia Phytopathologia 47:89-91 (in Russian).

According to their sensitivity patterns toward *Pichia membranifaciens* mycocins, *Kazachstania* species fall into five groups. The species of this genus also exhibit a great variety of morphological, physiological, molecular characteristics and natural habitats.

II Department of Biology, Faculty of Medicine, Masaryk University, Kamenice 5, 62500 Brno, Czech Republic. Communicated by Marie Kopecká. <mkopecka@med.muni.cz> http://www.med.muni.cz/~mkopecka/

Journal paper published in 2013.

1 Marie Kopecká, Susumu Kawamoto & Masashi Yamaguchi. 2012. A new F-actin structure in fungi: actin ring formation around the cell nucleus of *Cryptococcus neoformans*. J Electron Microsc (Tokyo) - doi: 10.1093/jmicro/dfs074 [PDF].

The F-actin cytoskeleton of *Cryptococcus neoformans* is known to comprise actin cables, cortical patches and cytokinetic ring. Here, we describe a new F-actin structure in fungi, a perinuclear F-actin collar ring around the cell nucleus, by fluorescent microscopic imaging of rhodamine phalloidin-stained F-actin. Perinuclear F-actin rings form in *Cryptococcus neoformans* treated with the microtubule inhibitor Nocodazole or with the drug solvent dimethyl sulfoxide (DMSO) or grown in yeast extract peptone dextrose (YEPD) medium, but they are absent in cells treated with Latrunculin A. Perinuclear F-actin rings may function as 'funicular cabin' for the cell nucleus, and actin cables as intracellular 'funicular' suspending nucleus in the central position in the cell and moving nucleus along the polarity axis along actin cables.

III State Scientific-Research Institute for Genetics and Selection of Industrial Microorganisms (GosNIIgenetika), I-Dorozhnyi 1, Moscow 117545, Russia. Communicated by GI Naumov and ES Naumova <gnaumov@yahoo.com>.

We are grateful to Dr. Kyria Boundy-Mills for hosting our visit to the Herman J. Phaff Yeast Culture Collection at University of California (Davis, USA) in May 2013 and fruitful collaboration.

The following are papers for 2012–2013.

1 Chang CF, Liu YR, Chen SF, Naumov GI, Naumova ES, Lee CF. 2012. Five novel species of the anamorphic genus *Candida* in the *Cyberlindnera* clade isolated from natural substrates in Taiwan. Antonie van Leeuwenhoek. 102: 9–21.

2 Daniel HM, Redhead SA, Schnürer J, Naumov GI, Kurtzman CP. 2012. (2049–2050) Proposals to conserve the name *Wickerhamomyces* against *Hansenula* and to reject the name *Saccharomyces sphaericus* (Ascomycota:Saccharomycotina). Taxon. 61: 459–461.

3 Naumov GI, Lee CF, Naumova ES. 2013. Molecular genetic diversity of the *Saccharomyces* yeasts in Taiwan: *S. arboricola, S. cerevisiae* and *S. kudriavzevii*. Antonie van Leeuwenhoek 103: 217–228.

4 Naumov GI, Naumova ES, Martynenko NN & Korhola M. 2013. Reidentification of chromosomal *CUP1* translocations in wine yeasts *Saccharomyces cerevisiae*. Microbiology (Moscow). 82(2):201–209. © Pleiades Publishing, Ltd.

5 Naumova ES, Sadykova AZh, Martynenko NN & Naumov GI. 2013. Molecular and genetic characterization of distillers' yeasts *Saccharomyces cerevisiae*. Microbiology (Moscow). 82(2):175–185. © Pleiades Publishing, Ltd.

6 Naumov GI, Naumova ES, Tjurin OV & Kozlov DG. 2013. *Komagataella kurtzmanii* sp. nov., a new sibling species of *Komagataella* (*Pichia*) *pastoris* in accordance with multigene sequence analysis. Antonie van Leeuwenhoek (submitted).

7 Naumov GI, Fernandez JE, Naumova ES & Boundy-Mills K. 2013. Biogeography and ecology for sibling species of the yeast genus *Komagataella* (in preparation).

IV Technical University of Lodz, Institute of Fermentation Technology and Microbiology, Wolczanska 171/173, 90-924 Lodz, Poland. Communicated by Dorota Kregiel <dorota.kregiel@p.lodz.pl>.

Recent book chapter.

1 Kregiel D. 2012. Succinate dehydrogenase of *Saccharomyces cerevisiae* – the unique enzyme of TCA cycle – current knowledge and new perspectives. In: Dehydrogenases, RA Canuto (Ed), ISBN 978-953-307-019-3, INTECH. DOI: 10.5772/48413.

The following posters were presented recently.

2 Berlowska J, Dziugan P, Kregiel D & Witonska I. 2013. Yeast vitality in fermentation medium supplemented by thick juice from sugar beet. 3rd International Conference Sustainable Postharvest and Food Technologies Inoptep 2013, Vrnjacka Banja, Serbia.

Sugar beet and intermediates from beet-processing are very good raw materials for different biotechnological processes, due to their content of fermentable sugars which can be directly used for fermentation, without any pretreatment. Raw juice contains about 15–20% of dry solids. Its purity ranges between 85 and 90% that means there are about 85–90% of sugars and 10–15% of non-sugars in dry matter. Considering these facts, raw juice can be used straightaway after pH adjustment for fermentation both as main fermentable source and as adjunct. All these properties together with a relatively low price in comparison with other intermediates from beet processing make the raw

juice a very profitable material for many processes. Raw extraction juice ha the lowest price from beet processing intermediates, but its disadvantage is low storability. Thick juice is more expensive than extraction juice , but its storability is excellent, that is comparable with molasses. However, think sugar beet contains also saponins - natural antibiotics with a tendency to ward off microbes, especially yeast and moulds. Aim of this study was to examine the influence of adjunct of sugar beet thick juice on the dynamic of the fermentation process, and yeast physiological state in wort broth supplemented in think beet juice. The several strains *Saccharomyces pastorianus* from LOCK105 and NCYC collections for brewery applications were used in this study. To monitor the yeast vitality, in brewery malt medium supplemented in think beet juice, the measurement of intracellular ATP (adenoside-5 -triphosphate) were used. ATP content in yeast cells was measured using the luciferin–luciferase bioluminescent method. Because of its high stability and simplicity, the luminometer Hy-LiTE2 with special bioassay kits (Merck) were used. The presence of saponin compounds from supplement – think beet juice did not reduce the vitality of used yeast in fermentation media. Moreover, higher amount of thick juicefrom sugar beet resulted also in increased alcohol content.

The following papers were published in journals.

3 Piotrowska M, Nowak A, Czyzowska A. 2013. Removal of ochratoxin A by wine *Saccharomyces cerevisiae* strains. Eur Food Res Technol 3:441-447.

The aim of this work was to examine two wine strains of *Saccharomyces cerevisiae* (Syrena LOCK 0201 and Malaga LOCK 0173 strains) and thermally inactivated biomass of bakery yeast (BS strain) for their ability to remove ochratoxin A (OTA) from model YPG, white grape GM, and blackcurrant BM media. The media was initially contaminated by 1 μg/mL OTA. The influence of OTA on yeast growth parameters, kinetic of fermentation, and amount of ethanol, glycerol, and acids were determined. It was found that both yeast strains were able to decrease the toxin amount in YPG, GM, and BM media. Strain Malaga LOCK 0173 was able to remove 82.8 and 10.7 % ochratoxin A from grape and blackcurrant medium, respectively. In case of Syrena LOCK 0201 strain, the OTA reduction was higher: 85.1 % for grape and 65.2 % for blackcurrant media. From 54.1 to 64.4 % of initial ochratoxin A concentration was removed after the contaminated wine treatment by thermally inactivated baker's yeast strain (BS) cells. The elongation of lag phase in contaminated YPG medium compared on toxin-free medium was noted. In white grape and blackcurrant medium, the differences between the final cell number, fermentation rate, moreover the ethanol, glycerol, and acids production in the medium with OTA and the control were not statistically significant. The results showed that the application of selected strains of yeasts in winemaking involving raw material contaminated with OTA might reduce the toxin contamination as well as the health risk related to human exposure to this toxin. Moreover, the application of heat-inactivated yeast's biomass for toxin adsorption gives new possibilities in oenology.

4 Piotrowska M. 2012. Adsorption of ochratoxin a by *Saccharomyces cerevisiae* living and non-living cells. Acta Alimentaria 1:1-7.

In presented work the ability of *Saccharomyces cerevisiae* cells to binding of ochratoxin A was evaluated. The viable and thermally inactivated cells at various densities were incubated with ochratoxin A in PBS buffer and the toxin residue in supernatant was determined using HPLC method. The amount of OTA removed after 24 h of contact equalled 20, 29 and 75% for 1, 5 and 50 mg of dry biomass/ml, respectively. It was proved that killed biomass remove OTA from buffer in higher quantities than viable cells. The process of adsorption proved to be very fast; 30 min after mixing the cells with toxin, its amount significantly decreased. It was stated that incubation of the samples under static conditions is more effective than incubation with shaking. The releasing from 11 to 22% of initially binding toxin after three washing of biomass indicates the reversibility of bond between cells and toxins. The complex of killed cells-ochratoxin A is less firm than it is in case of viable biomass. Adsorption of toxin is closely related to the components of yeast's cell wall. Cells without cell wall (protoplasts) lost the ability to adsorption of ochratoxin A.

5 Berłowska J, Kręgiel D, Ambroziak W. 2013. Enhancing adhesion of yeast brewery strains to chamotte carriers through aminosilane surface modification. World J Microbiol Biotechnol - DOI 10.1007/s11274-013-1294-4.

The adhesion of cells to solid supports is described as surface-dependent, being largely determined by the properties of the surface. In this study, ceramic surfaces modified using different organosilanes were tested for proadhesive properties using industrial brewery yeast strains in different physiological states. Eight brewing strains were tested: bottom-fermenting Saccharomyces pastorianus and top-fermenting Saccharomyces cerevisiae. To determine adhesion efficiency light microscopy, scanning electron microscopy and the fluorymetric method were used. Modification of chamotte carriers by 3-(3-anino-2-hydroxy-1-propoxy) propyldimethoxysilane and 3-(N, N-dimethyl-N-2-hydroxyethyl) ammonium propyldimethoxysilane groups increased their biomass load significantly.

6 Balcerek M, Pielech-Przybylska K, Patelski P, Sapińska E, Ksiezopolska M. 2013. The usefulness of intermediate products of plum processing for alcoholic fermentation and chemical composition of the obtained distillates. J Food Sci - DOI: 10.1111/1750-3841.12097.

In this study, an evaluation of intermediate products of plum processing as potential raw materials for distillates production was performed. Effects of composition of mashes on ethanol yield, chemical composition and taste, and flavor of the obtained spirits were determined. The obtained results showed that spontaneous fermentations of the tested products of plum processing with native microflora of raisins resulted in lower ethanol yields, compared to the ones fermented with wine yeast *Saccharomyces bayanus*. The supplementation of mashes with 120 g/L of sucrose caused an increase in ethanol contents from 6.2 ± 0.2 to 6.5 ± 0.2% v/v in reference mashes (without sucrose addition, fermented with S. bayanus) to ca. 10.3 ± 0.3% v/v, where its highest yields amounted to 94.7 ± 2.9 to 95.6 ± 2.9% of theoretical capacity, without negative changes in raw material originality of distillates. The concentrations of volatile compounds in the obtained distillates exceeding 2000 mg/L alcohol 100% v/v and low content of methanol and hydrocyanic acid, as well as their good taste and aroma make the examined products of plum processing be very attractive raw materials for the plum distillates production.

V Industrial Biotechnology, Department of Chemical and Biological Engineering, Chalmers University of Technology, Kemivägen 10, SE-412 96, Gothenburg, Sweden. Communicated by Prof. Lisbeth Olsson <lisbeth.olsson@chalmers.se>.

Peer reviewed publications.

Book chapter.

1 V Mapelli, CJ Franzén & L. Olsson. 2013. Systems biology methods and developments for *Saccharomyces cerevisiae* and other industrial yeasts in relation to the production of fermented food and food ingredients. DOI: 10.1533/9780857093547.1.42. Chapter 3 in Microbial production of food ingredients, enzymes and nutraceuticals, edited by B McNeil, D Archer, I Giavasis and L Harvey. Woodhead Publishing, ISBN 0 85709 343 6, ISBN-13: 978 0 85709 343 1.

Journal articles.

2 Ylitervo P, Franzén CJ, Taherzadeh MJ. 2013. Impact of Furfural on Rapid Ethanol Production Using a Membrane Bioreactor, Energies. 6:1604-1617.

3 Kazemi Seresht A, Cruz AL, de Hulster E, Helby M, Palmqvist EA, van Gulik W, Daran JM, Pronk J & Olsson L. 2013. Long-term adaptation of *Saccharomyces cerevisiae* to the burden of recombinant insulin production. Biotechnol Bioeng (in press).

4 Otero JM, Cimini D, Patil KR, Poulsen SG, Olsson L, Nielsen J 2013. Industrial Systems Biology of *Saccharomyces cerevisiae* enables novel succinic acid cell factory, PLOS One 8, e54144.

5 Thörn C, Gustafsson H, Olsson L. 2013. QCM-D as a method for monitoring enzyme immobilization in mesoporous silica particles. Microporous Mesoporous Materials 176:71-77.

6 Kazemi Seresht A, Palmqvist EA, Schluckebier G, Pettersson I, Olsson L. 2013 The challenge of improved secretory production of active pharmaceutical Ingredients in *Saccharomyces cerevisiae:* A Case study on Human Insulin Analogs. Biotechnol Bioeng (in press).

7 Kazemi Seresht A, Nørgaard P, Palmqvist EA, Andersen AS, Olsson L. 2013. Modulating heterologous protein production in yeast: the applicability of truncated auxotrophic markers. Appl Microbiol Biotechnol 97:3939-3948.

8 Ask M, Bettiga M, Mapelli V & Olsson L. 2013. The influence of HMF and furfural on redox-balance and energy-state of xylose-utilizing *Saccharomyces cerevisiae*. Biotechnol Biofuels 6:22.

9 Koppram R, Nielsen F, Albers E, Olsson L, Lambert A, Wännström S, Welin L, Zacchi G & Olsson L. 2013. Simultaneous saccharification and co-fermentation for bioethanol production usin corncobs at lab, PDU and demo scales. Biotechnol Biofuels 6:2.

10 Thörn C, Carlsson N, Gustafsson H, Holmberg K, Åkerman B, Olsson L. 2013. A method to measure pH inside mesoporous particles using protein-bound SNARF1 fluorescent probe. Microporous Mesoporous Materials 165:240-246.

11 Mapelli C, Mapelli V, Olsson L, Mombelli D, Gruttadauria A & Barella S. 2013. Viability study of the use of cast iron open cell foam as microbial fuel cell electrodes. Advanced Engineering Materials 15:112-117.

12 Koppram R, Albers E, Olsson L. 2012. Evolutionary engineering strategies to enhance tolerance of xylose utilizing recombinant yeast to inhibitors derived from spruce biomass. Biotechnology Biofuels 5:32.

13 Ask M, Olofsson K, Di Felice T, Ruohonen L, Penttilä M, Lidén G & Olsson L. 2012. Challenges in enzymatic hydrolysis and fermentation of pretreated *Arundo donax* revealed by a comparison between SHF and SSF. Process Biochem 47:1452-1459.

14 Scalcinati G, Otero JM, van Vleet JRH, Jeffries TW, Olsson L & Nielsen J. 2012. Evolutionary engineering of *Saccharomyces cerevisiae* for efficient aerobic xylose consumption. FEMS Yeast Res 12:582-597.

15 Udatha GDBRK, Mapelli V, Panagiotou G & Olsson L. 2012. Common and distant structural characteristics of feruloyl esterase families from *Aspergillus oryzae*. PLoSOne, 7, e39473.

16 Udatha GDBRK, Sugaya N, Olsson L & Panagiotou G 2012 How well do the substrates KISS the enzyme? Molecular docking program selection for feruloyl esterases. Science Reports 2:232.

17 Dimarogona M, Topakas E, Olsson L and Christakopoukos P. 2012. Lignin boosts the cellulose performance of a GH-61 enzyme from *Sporotrichum thermophile.* Bioresource Technol 110:480-487.

18 Westman, J.O, Taherzadeh, M.J, Franzén, C.J (2012) Inhibitor tolerance and flocculation of a yeast strain suitable for 2nd generation bioethanol production. *Electronic J Biotechnol.* 15(3):8.

19 Ylitervo P, Franzén CJ, Taherzadeh MJ. 2012. Mechanically robust polysiloxane-ACA capsules for prolonged ethanol production. J Chem Technol Biotechnol - in press.

20 Westman JO, Manikondu RB, Franzén CJ, Taherzadeh MJ. 2012. Encapsulation-induced stress helps *Saccharomyces cerevisiae* resist convertible lignocellulose derived inhibitors. Int J Mol Sci, 13: 11881-11894.

21 Westman JO, Taherzadeh MJ, Franzén CJ. 2012. Proteomic analysis of the increased stress tolerance of *Saccharomyces cerevisiae* encapsulated in liquid core alginate-chitosan capsules. PLoS ONE 7(11):e49335.

22 Westman JO, Ylitervo P, Franzén CJ, Taherzadeh MJ. 2012.. Effects of encapsulation of microbial cells on product formation during microbial fermentations. Appl Microbiol Biotechnol 96:1441–1454.

Presentations.

23 Olsson L, Anasontzis GE, Thanh DT, Thuy NT, Hang DTM & Thanh VN. 2013. Linking growth on lignocellulosic carbon sources to gene expression through secretome and transcriptome analysis in novel enzyme producing filamentous fungi from Vietnamese habitats. Oral presentation. 35th Symposium on Biotechnology for Fuels and Chemicals, Portland, OR, USA, April 29 – May 2.

24 Ask M, Duraiswamy VR, Mapelli V, Bettiga M & Olsson L. 2013. Intracellular redox state as key target for *Saccharomyces cerevisiae* tolerance to lignocellulosic hydrolysate inhibitors. Oral presentation. 35th Symposium on Biotechnology for Fuels and Chemicals, Portland, OR, USA, April 29–May 2.

25 Tomás-Pejó E. 2013. Obtaining barcoded xylose fermenting strains for ethanol production at industrial scale. Oral presentation. 2nd IberoAmercian congress on Biorefineries, Jaen, Spain, April 10–12.

26 Olsson L. 2013. Robust microorganisms and process strategies – The key to successful lignocellulose ethanol production. Oral presentation. 2nd IberoAmercian congress on Biorefineries, Jaen, Spain, April 10–12.

27 Xiros C, Claesson K, Larsson C & Olsson L. 2012. High Gravity Biofuels: Process amelioration methods as tools to deepen our knowledge on the toxicity of lignocellulosic hydrolysates. 2nd Symposium on biotechnology applied to lignocelluloses, Fukuoka, Japan, October 14-17.

28 Seresht AK, Palmqvist EA & Olsson L. 2012. The impact of phosphate scarcity on pharmaceutical protein production and cellular physiology in *Saccharomyces cerevisiae*. Oral presentation. 13th International congress on Yeasts, Madison, Wisconsin, Aug 26–30.

29 Ask M, Bettiga M, Mapelli V & Olsson L. 2012. HMF and furfural stress results in drainage of redox and energy charge of *Saccharomyces cerevisiae*. Oral presentation. 13th International congress on Yeasts, Madison, Wisconsin, Aug 26–30.

30 Bettiga M & Olsson L. 2012. Robust microorganisms and process strategies – The key to successful lignocellulose based production. Oral presentation. 13th International congress on Yeasts, Madison, Wisconsin, Aug 26–30.

31 Tomás-Pejó E & Olsson L. 2012. Evaluation of evolved xylose fermenting strains for bioethanol production - Comparison of single cells and mixed populations. Oral presentation. 2nd BioPro Symposium on Inhomogeneities in large-scale bioprocesses: System biology and process dynamics, Berlin, Germany, March 14–16.

Summary of a recently completed project.

The NEMO project provides novel efficient enzymes and microbes for 2nd generation bioethanol production. It generates through metabolic engineering and mutagenesis & screening approaches robust yeast strains that have a broad substrate range and can (co-) ferment C6 and C5 sugars to ethanol with high productivity (rate and yield), and that are significantly more stress tolerant, i.e. inhibitor, ethanol, and thermo-tolerant than the current *S. cerevisiae* strains used in ethanol production. The NEMO project also identifies and improves enzymes for hydrolysis of biomass relevant for Europe. Novel enzymes are identified and improved through various approaches, based on screening, broad comparative genomics analyses, and protein engineering. These efforts will generate more thermostable enzymes for high temperature hydrolysis, more efficient enzymes for hydrolysis of the resistant structures in lignocellulose such as crystalline cellulose and lignin-hemicellulose complexes, enzymes with reduced affinity for lignin, and efficient thermo and mesophilic enzymes mixtures that are optimised and tailor-made for the relevant biomass for Europe and European industry. These novel biocatalysts are tested in an iterative manner in process relevant conditions, including pilot-scale operations, which ensure that the novel enzymes and microbes will be superior in real process conditions. Furthermore, optimal enzyme, microbe and process regime combinations are identified, providing basis for the development of the most economic and eco-efficient overall processes. The impact of the NEMO project on 2nd generation bioethanol production is significant because it provides most realistic but widely applicable technologies that could be exploited broadly by European industry. Its impact goes also much beyond bioethanol because NEMO provides technology improvements that are directly applicable and crucial for efficient and economic production of also other biofuels and bulk chemicals.

PhD defense.

Magnus Ask, a PhD student and a member of Industrial Biotechnology group, Chalmers University of Technology, is scheduled to defend his PhD in the area of lignocellulose bioethanol production: Insights into yeast physiology to improve robustness of fermentation process. To request thesis and to know the presentation time and venue please contact Magnus Ask, magnus.ask@chalmers.se.

VI Microbial Genomics and Bioprocessing Research, National Center for Agricultural Utilization Research, ARS-USDA, 1815 N. University Street, Peoria, IL 61604, USA. Communicated by CP Kurtzman <Cletus.Kurtzman@ars.usda.gov>.

Recent publication.

1 Kurtzman, CP & Robnett CJ. 2013. *Alloascoidea hylecoeti* gen. nov., comb. nov., *Alloascoidea africana* comb. nov., *Ascoidea tarda* sp. nov. and *Nadsonia starkeyi-henricii* comb. nov., new members of the Saccharomycotina (Ascomycota). FEMS Yeast Res. In press.

Phylogenetic analysis of concatenated nuclear gene sequences for large and small subunit rRNAs, translation elongation factor 1-α and the two large subunits of RNA polymerase II (RPB1, RPB2) demonstrated that species assigned to the yeast genus *Ascoidea* represent two separate and distantly related clades, i.e., *Ascoidea* (*A. asiatica*, NRRL Y-17632, CBS 377.68; *A. rubescens*, NRRL Y-17699, CBS 116.35, type species; *A. tarda* sp. nov., NRRL Y-2393, CBS 12609, type strain), which is near the genus *Saccharomycopsis*, and *Alloascoidea* gen. nov. (*Al. africana* comb. nov., NRRL Y-6762-3, CBS 12606, *Al. hylecoeti* comb. nov., NRRL Y-17634, CBS 355.80, type species), which is near *Nadsonia* and related genera. From these analyses and from comparison of herbarium specimens, it appears that type strains of *A. asiatica* and *Al. africana* had been reversed. Sequence analysis further showed that *Schizoblastosporion starkeyi-henricii* is a sister species of *Nadsonia fulvescens* and it is proposed for transfer to *Nadsonia*.

VII Department of Botany and Plant Pathology, Purdue University, 915 W. State Street, West Lafayette, Indiana, USA. Communicated by MC Aime <maime@purdue.edu>.

Recently published.

1 Toome M, Roberson RW, Aime MC. 2013. *Meredithblackwellia eburnea* gen. et sp. nov, *Kriegeriaceae* fam. nov. and Kriegeriales ord. nov.—toward resolving higher-level classification in Microbotryomycetes. Mycologia 105: 485-495.

A field survey of ballistosporic yeasts in a Neotropical forest yielded a new species isolated from a fern leaf. The isolate is a cream-colored butyrous yeast that reproduces by budding. Budding occurs at both the apical and basal cell poles; occasionally multiple budding events co-occur, giving rise to rosette-like clusters of cells at both poles of the yeast mother cell. DNA sequences of large and small subunit and the internal transcribed spacer regions of the nuclear ribosomal DNA cistron indicated an affinity to Microbotryomycetes, Pucciniomycotina. A new genus, *Meredithblackwellia*, is proposed to accommodate the new species, *M. eburnea* (type strain MCA4105). Based on phylogenetic analyses, *Meredithblackwellia* is related to *Kriegeria eriophori*, a sedge parasite, to an aquatic fungus *Camptobasidium hydrophilum* and to several recently described anamorphic yeasts that have been isolated from plant material or psychrophilic environments. Morphological and ultrastructural studies confirm the relatedness of *M. eburnea* to these taxa and prompted the re-evaluation of higher-level classification within Microbotryomycetes. We propose here a new order, Kriegeriales, and place two families, Kriegeriaceae fam. nov. and Camptobasidiaceae R.T. Moore, within it. Our study re-emphasizes the need for systematic revision of species described in *Rhodotorula*.

2 Rush TA, Aime MC. 2013. The genus *Meira*: phylogenetic placement and description of a new species. Antonie Van Leeuwenhoek 103:1097-1106.

The genus *Meira* currently contains three recently described species of mite-associated basidiomycete yeasts from Israel and Japan and is placed in the Exobasidiomycetes (Ustilaginomycotina) *Incertae sedis*. A previously undescribed species of *Meira* was isolated from the phylloplane of a magnolia leaf in Louisiana, USA. Herein, we describe *Meira miltonrushii* sp. nov. and include phylogenetic analyses from three rDNA loci to resolve the placement of *Meira*. This study provides evidence that *Meira* belongs to the family Brachybasidiaceae in the

Exobasidiales and supports the placement of another mite-associated yeast genus, *Acaromyces*, within Cryptobasidiaceae (Exobasidiales). We also examine sequences produced by numerous environmental studies that suggest *Meira* species can be found as endophytes of many plant species. To our knowledge, this is the first record of a member of the genus *Meira* in North America.

VIII Division of Biotechnology and Forensic Sciences, School of Contemporary Sciences, University of Abertay Dundee, Bell Street, Dundee DD1 1HG, Scotland, UK. Communicated by Ashok K Adya <A.Adya@abertay.ac.uk>.

The following will be presented at the 30th International Specialised Symposium on Yeast in Stará Lesná, June 18-22, 2013.

1 Nayyar A, Walker G, Canetta E, Wardrop F, Adya A. 2013. Understanding cell-surface structure-function relationships in industrial yeasts.

Cell surface adhesion properties of yeasts are crucial for many biological processes, such as sexual reproduction, tissue or substrate invasion, biofilm formation and flocculation. Understanding and controlling this latter phenomenon is of commercial interest to yeast biotechnology industries. For example, flocculation in brewing yeasts can determine the degree of attenuation of the wort. Early or premature flocculation is a common cause of 'hung' or 'stuck' fermentations giving rise to exceedingly sweet beer, whereas a lack or delay in flocculation can cause beer clarification problems. In this study we used a modified flocculation assay [1] to determine flocculation capabilities of four industrial yeast strains employed for winemaking, fuel alcohol, brewing and champagne production. We also investigated cell surface hydrophobicity characteristics in these yeast strains and were able to correlate flocculation behaviour with hydrophobicity as determined using the Hydrophobicity Microsphere Assay (HMA Assay) and the MATHS test (Microbial Adhesion to Hydrocarbons). It was found that the highly flocculent beer producing yeast strain with 42% flocculation ability exhibited concomitantly high cell-surface hydrophobicity index of 66%. Adhesion (adhesion force and energy) and elastic (Young's modulus) properties, and ultra-structure of cell walls (surface morphology and roughness) of the same yeast strains were then investigated at the nanoscale using Atomic Force Microscopy (AFM). This work is providing new information regarding surface morphology, nanomechanical properties of yeast cell walls and their physiological behaviour. This work will hopefully lead to greater understanding about the onset of yeast flocculation, and the various factors that may be responsible for the process in industrial fermentations.

[1] Bony, M., Barre, P. & Blondin, B. 1998. Distribution of the flocculation protein, Flop, at the cell surface during yeast growth: the availability of flop determines the flocculation level. Yeast, 14: 25-35.

IX University of Stellenbosch, Private Bag X1, Matieland 7602, South Africa. Communicated by Bernard Prior <bap@sun.ac.za>.

Recent publications.

The publication (abstract below) in PLoS One by Setati et al. (2012) on the vineyard yeast microbiome attracted considerable attention by the international media with an interest in wine production. It is seldom that the impact of a yeast publication is reported in such international popular periodicals such as New York Times, Daily Express (UK) amongst many others. Results showed that grapes produced using three different farming methods such as conventional, organic and biodynamic had differences in the diversity of the yeast population on the skin surfaces. Organic wine grapes had greater yeast diversity than those produced with conventional farming methods whereas biodynamic grapes had the most. Exposure to sun and temperature variation could also impact on the diversity. The differences could impact on wine aroma and complexity.

1 Setati ME, Jacobson D, Andong U-C, Bauer FF. 2012. The vineyard yeast microbiome, a mixed model microbial map. PLoS ONE 7(12): e52609. doi:10.1371/journal.pone.0052609

Vineyards harbour a wide variety of microorganisms that play a pivotal role in pre- and post-harvest grape quality and will contribute significantly to the final aromatic properties of wine. The aim of the current study was to investigate the spatial distribution of microbial communities within and between individual vineyard management units. For the first time in such a study, we applied the Theory of Sampling (TOS) to sample gapes from adjacent and well established commercial vineyards within the same terroir unit and from several sampling points within each individual vineyard. Cultivation-based and molecular data sets were generated to capture the spatial heterogeneity in microbial populations within and between vineyards and analysed with novel mixed-model networks, which combine sample correlations and microbial community distribution probabilities. The data demonstrate that farming systems

have a significant impact on fungal diversity but more importantly that there is significant species heterogeneity between samples in the same vineyard. Cultivation-based methods confirmed that while the same oxidative yeast species dominated in all vineyards, the least treated vineyard displayed significantly higher species richness, including many yeasts with biocontrol potential. The cultivatable yeast population was not fully representative of the more complex populations seen with molecular methods, and only the molecular data allowed discrimination amongst farming practices with multivariate and network analysis methods. Importantly, yeast species distribution is subject to significant intra-vineyard spatial fluctuations and the frequently reported heterogeneity of tank samples of grapes harvested from single vineyards at the same stage of ripeness might therefore, at least in part, be due to the differing microbiota in different sections of the vineyard.

2 Styger G, Jacobson D, Prior BA & Bauer FF. 2013. Genetic analysis of the metabolic pathways responsible for aroma metabolite production by *Saccharomyces cerevisiae*. Appl Microbiol Biotechnol 97: 4429-4442.

During alcoholic fermentation, higher alcohols, esters and acids are formed from amino acids via the Ehrlich pathway by yeast, but many of the genes encoding the enzymes have not yet been identified. When the *BAT1/2* genes, encoding transaminases that deaminate amino acids in the first step of the Ehrlich pathway are deleted, higher metabolite formation is significantly decreased. Screening yeast strains with deletions of genes encoding decarboxylases, dehydrogenases and reductases revealed nine genes whose absence had the most significant impact on higher alcohol production. The seven most promising genes (*AAD6*, *BAT2, HOM2*, *PAD1*, *PRO2*, *SPE1* and *THI3*) were further investigated by constructing double and triple deletion mutants. All double deletion strains showed a greater decrease in isobutanol, isoamyl alcohol, isobutyric and isovaleric acid production than the corresponding single deletion strains with the double deletion strains in combination with *bat2* and the *hom2- aad6* strain revealing the greatest impact. *BAT2* is the dominant gene in these deletion strains and this suggests the initial transaminase step of the Ehrlich pathway is rate-limiting. The triple deletion strains in combination with *BAT2* (*bat2- thi3- aad6* and *bat2- thi3- hom2*) had the greatest impact on the end metabolite production with the exception of isoamyl alcohol and isovaleric acid. The strain deleted for two dehydrogenases and a reductase (*hom2- pro2- aad6*) had a greater effect on the levels of these two compounds. This study contributes to the elucidation of the Ehrlich pathway and its significance for aroma production by fermenting yeast cells.

3 Willenburg E & Divol B. 2012. Quantitative PCR: An appropriate tool to detect viable but not culturable *Brettanomyces bruxellensis* in wine. Int J Food Microbiol 160:131-136.

Quantitative PCR as a tool has been used to detect *Brettanomyces bruxellensis* directly from wine samples. Accurate and timely detection of this yeast is important to prevent unwanted spoilage of wines and beverages. The aim of this study was to distinguish differences between DNA and mRNA as template for the detection of this yeast. The study was also used to determine if it is possible to accurately detect cells in the viable but not culturable (VBNC) state of *B. bruxellensis* by qPCR. Several methods including traditional plating, epifluorescence counts and qPCR were used to amplify DNA and mRNA. It was observed that mRNA was a better template for the detection in terms of standard curve analysis and qPCR efficiencies. Various primers previously published were tested for their specificity, qPCR efficiency and accuracy of enumeration. A single primer set was selected which amplified a region of the actin-encoding gene. The detection limit for this assay was 10 cells mL^{-1}. *B. bruxellensis* could also be quantified in naturally contaminated wines with this assay. The mRNA gave a better indication of the viability of the cells which compared favourably to fluorescent microscopy and traditional cell counts. The ability of the assay to accurately estimate the number of cells in the VBNC state was also demonstrated.

4 Reid VJ, Theron LW, du Toit M & Divol B. 2012. Identification and partial characterization of extracellular aspartic protease genes from *Metschnikowia pulcherrima* IWBT Y1123 and *Candida apicola* IWBT Y1384. Appl Environ Microbiol 78:6838-6849.

The extracellular acid proteases of non-*Saccharomyces* wine yeasts may fulfil a number of roles in winemaking, which include increasing the available nitrogen sources for the growth of fermentative microbes, affecting the aroma profile of the wine, and potentially reducing protein haze formation. These proteases, however, remain poorly characterized, especially at genetic level. In this study, two extracellular aspartic protease-encoding genes were identified and sequenced, from two yeast species of enological origin: one gene from *Metschnikowia pulcherrima* IWBT Y1123, named MpAPr1, and the other gene from *Candida apicola* IWBT Y1384, named CaAPr1. In silico analysis of these two genes revealed a number of features peculiar to aspartic protease genes, and both the MpAPr1 and CaAPr1 putative proteins showed homology to proteases of yeast genera. Heterologous expression of MpAPr1 in *Saccharomyces cerevisiae* YHUM272 confirmed that it encodes an aspartic protease. MpAPr1

production, which was shown to be constitutive, and secretion were confirmed in the presence of bovine serum albumin (BSA), casein, and grape juice proteins. The MpAPr1 gene was found to be present in 12 other *M. pulcherrima* strains; however, plate assays revealed that the intensity of protease activity was strain dependent and unrelated to the gene sequence.

5 Favaro L, Jooste T, Basaglia M, Rose SH, Saayman M, Görgens JF, Casella S & van Zyl WH. 2013. Designing industrial yeasts for the consolidated bioprocessing of starchy biomass to ethanol. Bioengineered 4: 97-102.

Consolidated bioprocessing (CBP), which integrates enzyme production, saccharification and fermentation into a one step process, is a promising strategy for the effective ethanol production from cheap lignocellulosic and starchy materials. CBP requires a highly engineered microbial strain able to both hydrolyze biomass with enzymes produced on its own and convert the resulting simple sugars into high-titer ethanol. Recently, heterologous production of cellulose and starch-degrading enzymes has been achieved in yeast hosts, which has realized direct processing of biomass to ethanol. However, essentially all efforts aimed at the efficient heterologous expression of saccharolytic enzymes in yeast have involved laboratory strains and much of this work has to be transferred to industrial yeasts that provide the fermentation capacity and robustness desired for large scale bioethanol production. Specifically, the development of an industrial CBP amylolytic yeast would allow the one-step processing of low-cost starchy substrates into ethanol. This article gives insight in the current knowledge and achievements on bioethanol production from starchy materials with industrial engineered *S. cerevisiae* strains.

6 Smith JJ, Burke A, Bredell H, van Zyl WH & Görgens JF. 2012. Comparing cytosolic expression to peroxisomal targeting of the chimeric L1/L2 (ChiΔH-L2) gene from human papillomavirus type 16 in the methylotrophic yeasts *Pichia pastoris* and *Hansenula polymorpha*. Yeast 29: 385-93.

The chimeric ChiΔH-L2 gene from human papillomavirus type 16, consisting of structural proteins L1 and L2, was successfully expressed in the cytosol of both *Pichia pastoris* and *Hansenula polymorpha* during methanol induction. In addition, a novel approach was employed whereby ChiΔH-L2 was targeted to the peroxisome using peroxisomal targeting sequence 1 (PTS1) to compare ChiΔH-L2 yields in the peroxisome vs the cytosol. The ChiΔH-L2 gene was yeast-optimized and cloned into plasmids aimed at genomic integration. Levels of intracellular ChiΔH-L2 accumulation in the cytosol were highest in *P. pastoris* KM71 strain KMChiΔH-L2 (1.43 mg/l), compared to the maximum production level of 0.72 mg/l obtained with *H. polymorpha*. ChiΔH-L2 targeting to the peroxisome was successful; however, it appeared to negatively affect ChiΔH-L2 production in both *P. pastoris* and *H. polymorpha*.

7 van Zyl WH, Bloom M & Viktor MJ. 2012. Engineering yeasts for raw starch conversion. Appl Microbiol Biotechnol 95:1377-1388.

Next to cellulose, starch is the most abundant hexose polymer in plants, an import food and feed source and a preferred substrate for the production of many industrial products. Efficient starch hydrolysis requires the activities of both α-1,4 and α-1,6-debranching hydrolases, such as endo-amylases, exo-amylases, debranching enzymes, and transferases. Although amylases are widely distributed in nature, only about 10 % of amylolytic enzymes are able to hydrolyse raw or unmodified starch, with a combination of α-amylases and glucoamylases as minimum requirement for the complete hydrolysis of raw starch. The cost-effective conversion of raw starch for the production of biofuels and other important by-products requires the expression of starch-hydrolysing enzymes in a fermenting yeast strain to achieve liquefaction, hydrolysis, and fermentation (Consolidated Bioprocessing, CBP) by a single organism. The status of engineering amylolytic activities into *Saccharomyces cerevisiae* as fermentative host is highlighted and progress as well as challenges towards a true CBP organism for raw starch is discussed. Conversion of raw starch by yeast secreting or displaying α-amylases and glucoamylases on their surface has been demonstrated, although not at high starch loading or conversion rates that will be economically viable on industrial scale. Once efficient conversion of raw starch can be demonstrated at commercial level, engineering of yeast to utilize alternative substrates and produce alternative chemicals as part of a sustainable biorefinery can be pursued to ensure the rightful place of starch converting yeasts in the envisaged bio-economy of the future.

8 Njokweni AP, Rose SH & van Zyl WH. 2012. Fungal β-glucosidase expression in *Saccharomyces cerevisiae*. J Indust Microbiol Biotechnol 39:1445-1452.

Recombinant *Saccharomyces cerevisiae* strains expressing β-glucosidases from *Thermoascus aurantiacus* (Tabgl1) and *Phanerochaete chrysosporium* (PcbglB and Pccbgl1) were constructed and compared to *S. cerevisiae*

Y294[SFI], previously identified as the best β-glucosidase-producing strain. The PcbglB was also intracellularly expressed in combination with the lac12 lactose permease of *Kluyveromyces lactis* in S. cerevisiae Y294[PcbglB + Lac12]. The recombinant extracellular β-glucosidases indicated maximum activity in the pH range 4-5 and temperature optima varying from 50 to 75 °C. The *S. cerevisiae* Y294[Pccbgl1] strain performed best under aerobic and anaerobic conditions, producing 2.6 times more β-glucosidase activity than *S. cerevisiae* Y294[SFI] and an ethanol concentration of 4.8 g l(-1) after 24 h of cultivation on cellobiose as sole carbohydrate source. *S. cerevisiae* Y294[Tabgl1] was unable to grow on cellobiose (liquid medium), whereas S. cerevisiae Y294[PcbglB + Lac12] exhibited limited growth.

9 van Rensburg E, den Haan R, Smith J, van Zyl WH, Görgens JF. 2012. The metabolic burden of cellulase expression by recombinant *Saccharomyces cerevisiae* Y294 in aerobic batch culture. Appl Microbiol Biotechnol 96:197-209.

Two recombinant strains of *Saccharomyces cerevisiae* Y294 producing cellulase using different expression strategies were compared to a reference strain in aerobic culture to evaluate the potential metabolic burden that cellulase expression imposed on the yeast metabolism. In a chemically defined mineral medium with glucose as carbon source, *S. cerevisiae* strain Y294[CEL5] with plasmid-borne cellulase genes produced endoglucanase and β-glucosidase activities of 0.038 and 0.30 U mg dry cell weight(-1), respectively. Chromosomal expression of these two cellulases in strain Y294[Y118p] resulted in no detectable activity, although low levels of episomally co-expressed cellobiohydrolase (CBH) activity were detected. Whereas the biomass concentration of strain Y294[CEL5] was slightly greater than that of a reference strain, CBH expression by Y294[Y118p] resulted in a 1.4-fold lower maximum specific growth rate than that of the reference. Supplementation of the growth medium with amino acids significantly improved culture growth and enzyme production, but only partially mitigated the physiological effects and metabolic burden of cellulase expression. Glycerol production was decreased significantly, up to threefold, in amino acid-supplemented cultures, apparently due to redox balancing. Disproportionately higher levels of glycerol production by Y294[CEL5] indicated a potential correlation between the redox balance of anabolism and the physiological stress of cellulase production. With the reliance on cellulase expression in yeast for the development of consolidated bioprocesses for bioethanol production, this work demonstrates the need for development of yeasts that are physiologically robust in response to burdens imposed by heterologous enzyme production.

X Food Science and Technology, University of California Davis, Davis, California, USA 95616. Communicated by Kyria Boundy-Mills <klbmills@ucdavis.edu>.

The Department of Food Science and Technology recently celebrated the 100th anniversary of the birth of Herman J Phaff, mentor to many yeast students, founder of the Phaff Yeast Collection, and Editor of the Yeast Newsletter for 34 years. The following posting marked the occasion:

http://foodscience.ucdavis.edu/remembering-fst-professor-emeritus-herman-phaff/

Recent publications.

1 Sitepu IR, Ignatia L, Franz AK, Wong DM, Faulina SA, Tsui M, Kanti A & Boundy-Mills K. 2012. An improved high-throughput Nile red fluorescence assay for estimating intracellular lipids in a variety of yeast species. J Microbiol Meth 91:321-328.

A rapid and inexpensive method for estimating lipid content of yeasts is needed for screening large numbers of yeasts samples. Nile red is a fluorescent lipophilic dye used for detection and quantification of intracellular lipid droplets in various biological system including algae, yeasts and filamentous fungi. However, a published assay for yeast is affected by variable diffusion across the cell membrane, and variation in the time required to reach maximal fluorescence emission. In this study, parameters that may influence the emission were varied to determine optimal assay conditions. An improved assay with a high-throughput capability was developed that includes the addition of dimethyl sulfoxide (DMSO) solvent to improve cell permeability, elimination of the washing step, the reduction of Nile red concentration, kinetic readings rather than single time-point reading, and utilization of a black 96-well microplate. The improved method was validated by comparison to gravimetric determination of lipid content of a broad variety of ascomycete and basidiomycete yeast species.

2 Boundy-Mills K. 2012. Yeast culture collections of the world: meeting the needs of industrial researchers. J Ind Microbiol Biotechnol 39:673-680.

The importance of selecting optimal yeast strains for research or industrial applications is often underestimated. For example, utilizing a strain background that already provides the desired stress tolerance or nutrient utilization profile can eliminate costly strain optimization. Yeast culture collections can provide not only the yeast strains but also data and curator expertise to help narrow the search for the optimal strain. While some collections are known for a broad range of cultures and services, other "boutique" collections can provide a broader selection of strains of certain categories, a surprising amount of characterization data, and assistance in selecting strains. This article provides information on dozens of yeast collections of the world, profiles of selected yeast culture collections, and the services that they provide: e.g., strain preservation for patent or safe deposit purposes, species identification service, training workshops, and consulting on yeast identification and physiology. Utilization of these services can save industrial researchers valuable time and resources.

3 Golomb BL, Morales V, Jung A, Yau B, Boundy-Mills KL & Marco ML. 2012. Effects of pectinolytic yeast on the microbial composition and spoilage of olive fermentations. Food Microbiol 33:97-106.

This study resulted in the identification of pectinolytic yeasts in directly brined Sicilian-style green olive fermentations and examination of the influence of those yeasts on the microbial composition and quality of fermented olives. Firstly, defective olives processed in Northern California from 2007 to 2008 and characterized by high levels of mesocarp tissue degradation were found to contain distinct yeast and bacterial populations according to DNA sequence-based analyses. Strains of (pectinolytic) *Saccharomyces cerevisiae*, *Pichia manshurica*, *Pichia kudriavzevii*, and *Candida boidinii* isolated from directly brined olives were then inoculated into laboratory-scale olive fermentations to quantify the effects of individual yeast strains on the olives. The pH, titratable acidity, and numbers of lactic acid bacteria (LAB) and yeasts varied between the fermentations and fermentations inoculated with *P. kudriavzevii* and *C. boidinii* promoted the development of LAB populations. Olive tissue structural integrity declined significantly within 30, 74, and 192 days after the inoculation of pectinolytic *S. cerevisiae*, *P. manshurica* and *C. boidinii*, respectively. In comparison, tissue integrity of olives in control fermentations remained intact although pectinolytic yeasts were present. Notably, pectinolytic yeasts were not found in fermentations inoculated with (non-pectinolytic) *P. kudriavzevii* and olives exposed to a 1:1 ratio of *P. kudriavzevii* and *P. manshurica* exhibited no significant tissue defects. This study showed that pectinolytic yeast are important components of directly brined green olive fermentations and damage caused by pectinolytic yeasts might be prevented by other microbial colonists of the olives.

4 Hamby KA, Hernandez A, Boundy-Mills K & Zalom FG. 2012. Associations of yeasts with spotted-wing *Drosophila* (*Drosophila suzukii;* Diptera: Drosophilidae) in cherries and raspberries. Appl Environ Microbiol 78:4869-4873.

A rich history of investigation documents various *Drosophila-yeast* mutualisms, suggesting that *Drosophila suzukii* similarly has an association with a specific yeast species or community. To discover candidate yeast species, yeasts were isolated from larval frass, adult midguts, and fruit hosts of *D. suzukii*. Terminal restriction fragment length polymorphism (TRFLP) technology and decimal dilution plating were used to identify and determine the relative abundance of yeast species present in fruit juice samples that were either infested with *D. suzukii* or not infested. Yeasts were less abundant in uninfested than infested samples. A total of 126 independent yeast isolates were cultivated from frass, midguts, and fruit hosts of *D. suzukii,* representing 28 species of yeasts, with *Hanseniaspora uvarum* predominating. This suggests an association between *D. suzukii* and *H. uvarum* that could be utilized for pest management of the highly pestiferous *D. suzukii.*

5 Stamps JA, Yang LH, Morales VM & Boundy-Mills KL. 2012. *Drosophila* regulate yeast density and increase yeast community similarity in a natural substrate. PLoS One 7: e42238

Drosophila melanogaster adults and larvae, but especially larvae, had profound effects on the densities and community structure of yeasts that developed in banana fruits. Pieces of fruit exposed to adult female flies previously fed fly-conditioned bananas developed higher yeast densities than pieces of the same fruits that were not exposed to flies, supporting previous suggestions that adult *Drosophila* vector yeasts to new substrates. However, larvae alone had dramatic effects on yeast density and species composition. When yeast densities were compared in pieces of the same fruits assigned to different treatments, fruits that developed low yeast densities in the absence of flies developed significantly higher yeast densities when exposed to larvae. Across all of the fruits, larvae regulated yeast

densities within narrow limits, as compared to a much wider range of yeast densities that developed in pieces of the same fruits not exposed to flies. Larvae also affected yeast species composition, dramatically reducing species diversity across fruits, reducing variation in yeast communities from one fruit to the next (beta diversity), and encouraging the consistent development of a yeast community composed of three species of yeast (*Candida californica*, *C. zemplinina*, and *Pichia kluyveri*), all of which were palatable to larvae. Larvae excreted viable cells of these three yeast species in their fecal pools, and discouraged the growth of filamentous fungi, processes which may have contributed to their effects on the yeast communities in banana fruits. These and other findings suggest that *D. melanogaster* adults and their larval offspring together engage in 'niche construction', facilitating a predictable microbial environment in the fruit substrates in which the larvae live and develop.

XI VTT Technical Research Centre of Finland, P.O. Box 1000, FI-02044 VTT, Finland. Communicated by Brian Gibson <brian.gibson@vtt.fi>.

Recent publications.

1 Ekberg J, Rautio J, Mattinen L, Vidgren V, Londesborough J & Gibson BR. 2013. Adaptive evolution of the lager brewing yeast *Saccharomyces pastorianus* for improved growth under hyperosmotic conditions and its influence on fermentation performance. FEMS Yeast Res 13:335-349.

An adaptive evolution method to obtain stable *Saccharomyces pastorianus* brewing yeast variants with improved fermentation capacity is described. The procedure involved selection for rapid growth resumption at high osmotic strength. It was applied to a lager strain and to a previously isolated ethanol-tolerant strain. Fermentation performance of strains was compared at 15 °P wort strength. A selected osmotolerant variant of the ethanol-tolerant strain showed significantly shorter fermentation time than the parent strain, producing 6.45 % alcohol by volume beer in 4-5 days with mostly similar organoleptic properties to the original strain. Diacetyl and pentanedione contents were 50-75 % and 3-methylbutyl acetate and 2-phenylethyl acetate 50 % higher than with the original strain, leading to a small flavour change. The variant contained significantly less intracellular trehalose and glycogen than the parent. Transcriptional analysis of selected genes at 24 h revealed reduced transcription of hexose transport genes and increased transcription of the *MALx1* and *MALx2* genes, responsible for α-glucoside uptake and metabolism. It is suggested that an attenuated stress response contributes to the improved fermentation performance. Results show that sequential selection for both ethanol tolerance and rapid growth at high osmotic strength can provide strains with enhanced fermentation speed with acceptable product quality.

2 Krogerus K & Gibson BR 2013. Influence of valine and other amino acids on total diacetyl and 2,3-pentanedione levels during fermentation of brewer's wort. Appl Microbiol Biotechnol - 10.1007/s00253-013-4955-1.

Undesirable butter-tasting vicinal diketones are produced as by-products of valine and isoleucine biosynthesis during wort fermentation. One promising method of decreasing diacetyl production is through control of wort valine content since valine is involved in feedback inhibition of enzymes controlling the formation of diacetyl precursors. Here, the influence of valine supplementation, wort amino acid profile and free amino nitrogen content on diacetyl formation during wort fermentation with the lager yeast *Saccharomyces pastorianus* was investigated. Valine supplementation (100 to 300 $mg \cdot L^{-1}$) resulted in decreased maximum diacetyl concentrations (up to 37% lower) and diacetyl concentrations at the end of fermentation (up to 33% lower) in all trials. Composition of the amino acid spectrum of the wort also had an impact on diacetyl and 2,3-pentanedione production during fermentation. No direct correlation between the wort amino acid concentrations and diacetyl production was found, but rather a negative correlation between the uptake rate of valine (and also other branched-chain amino acids) and diacetyl production. Fermentation performance and yeast growth were unaffected by supplementations. Amino acid addition had a minor effect on higher alcohol and ester composition, suggesting that high levels of supplementation could affect the flavour profile of the beer. Modifying amino acid profile of wort, especially with respect to valine and the other branched-chain amino acids, may be an effective way of decreasing the amount of diacetyl formed during fermentation.

3 Toivari M, Vehkomäki ML, Nygård Y, Penttilä M, Ruohonen L & Wiebe MG. 2013. Low pH d-xylonate production with *Pichia kudriavzevii*. Bioresource Technol 133:555-562.

d-Xylonic acid is one of the top 30 most desirable chemicals to be derived from biomass sugars identified by the US Department of Energy, being applicable as a non-food substitute for d-gluconic acid and as a platform

chemical. We engineered the non-conventional yeast *Pichia kudriavzevii* VTT C-79090T to express a d-xylose dehydrogenase coding gene from *Caulobacter crescentus*. With this single modification the recombinant *P. kudriavzevii* strain produced up to 171 g L^{-1} of d-xylonate from 171 g L^{-1} d-xylose at a rate of 1.4 g L^{-1} h^{-1} and yield of 1.0 g [g substrate consumed]$^{-1}$, which was comparable with d-xylonate production by Gluconobacter oxydans or Pseudomonas sp. The productivity of the strain was also remarkable at low pH, producing 146 g L^{-1} d-xylonate at 1.2 g L^{-1} h^{-1} at pH 3.0. This is the best low pH production reported for d-xylonate. These results encourage further development towards industrial scale production.

XII CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, the Netherlands. Communicated by Teun Boekhout and Marizeth Groenewald <m.groenewald@cbs.knaw.nl>.

Recent publications.

1 Chen M, Pan WH & Boekhout T. 2013. *Cryptococcus gattii* infections in China: extent of the problem? Chin Med J 126:203-205.

2 Eddouzi J, Hofstetter V, Groenewald M, Manai M & Sanglard S. 2013. Characterization of a new clinical yeast species isolated from a strain collection of Tunisian hospitals. J Clinic Microbiol 51:31-39.

3 Gioti A, Nystedt B, Li W, Xu J, Andersson A, Averette AF, Münch K, Wang X, Kappauf C, Kingsbury JM, Kraak B, Walker LA, Johansson HJ, Holm T, Lehtiö J, Stajich JE, Mieczkowski P, Kahmann R, Kennell JC, Vardenas-Corona ME, Lundeberg J, Saunders CW, Boekhout T, Dawson TL, Munro CA, de Groot PWJ, Butler G, Heitman J & Scheynius A. 2013. Genomics insights into the atopic eczema-associated skin commensal yeast *Malassezia sympodialis*. mBIO 4: e00572-12.

4 Groenewald M, Boekhout T, Gaillardin C, Neuvéglise C, van Dijck PWM & Wyss M. 2013. *Yarrowia lipolytica* – Safety assessment of an oleaginous yeast with a great industrial potential. Crit Rev Microbiol 14 (epub).

5 Groenewald M, Smith MTh. 2013. The teleomorph state of *Candida deformans* Langeron & Guerra and validation of *Candida yakushimensis*. Anthonie van Leeuwenhoek 103:1023-1028.

6 Kolecka A, Khayhan K, Groenewald M, Theelen B, Arabatzis M, Velegraki A, Kostrzewa M, Mares M, Taj-Aldeen SJ & Boekhout T. 2013. MALDI-TOF MS identification of medically relevant species of arthroconidial yeasts belonging to *Trichosporon* and *Geotrichum.* J Clin Microbiol (accepted).

7 Limtong S, Kaewwichian R & Groenewald M. 2013. *Ogataea kanchanaburiensis* sp. nov. and *Ogataea wangdongensis* sp. nov., two novel methylotrophic yeast species from phylloplane in Thailand. Anthonie van Leeuwenhoek 103:551-558.

8 Nyanga LK, Gadaga TH, Nout MJR, Smid EJ, Boekhout T & Zwietering MH. 2013. Nutritive values of masau (*Ziziphus mauritiana*) fruits from Zambezi Valley in Zimbabwe. Food Chemistry 138:168-172.

9 Schoffelen T, Illnait-Zaragozi MT, Joosten LAB, Netea MG, Boekhout T, Meis JF & Sprong T. 2013. *Cryptococcus gattii* induces a cytokine pattern that is distinct from other cryptococcal species. PlosOne 8: e55579.

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11 Brink J. van den, Samson RA, Hagen F, Boekhout T & Vries RP de. 2012. Genetic and physiological diversity within the industrial relevant, thermophilic genera *Myceliophthora* and *Corynascus*. Fung Divers 52:197-207 - doi:10.1007/s13225-011-0107-z.

12 Cendejas-Bueno E, Kolecka A, Alastruey-Izquierdo A, Theelen B, Groenewald M, Kostrzewa M, Cuenca-Estrella M, Gómez-López A & Boekhout T. 2012. Reclassification of the *Candida haemulonii* complex; *C. haemulonii* (*C. haemulonii* group I), *C. duobushaemulonii* sp. nov. (*C. haemulonii* group II) and *C. haemulonii* var. *vulnera* var. nov., three multiresistant human pathogenic yeasts. J Clin Microbiol 50:3641-3651 - doi 10.1128/JCM.02248-12.

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14 Colom FM, Hagen F, Gonzalez A, Mellado A, Morera N, Linares C, García DM, Peñataro JS, Boekhout T & Sánchez, M. 2012. *Ceratonia siliqua* (Carob) trees as natural habitat and source of infection by *Cryptococcus gattii* in the Mediterranean environment. Med Mycol 50:67-73 - blog http://curiosidadesdelamicrobiologia.blogspot.com/2011/05/historia-de-weber.html.

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16 Desnos-Ollivier M, Robert V, Raoux-Barbot D, Groenewald M & Dromer F. 2012. Antifungal Susceptibility Profiles of 1698 Yeast Reference Strains Revealing Potential Emerging Human Pathogens PLoS ONE 7: e32278.

17 Gringhuis SI, Kaptein TM, Wevers BA, Theelen B, van der Vlist M, Boekhout T & Geijtenbeek TBH. 2012 Dectin-1 is an extracellular danger sensor for induction and processing of IL-1β through activation of a Malt1-ASC-caspase-8 complex. Nature Immunol. 13:246-255 - News and Views Nature Immunology 13:211-212.

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19 Hagen F, Illnait-Zaragozi M.-T, Meis JF, Chew WHM, Curfs-Breuker I, Mouton JW, Hoepelman AL, Spanjaard L, Verweij PE, Kampinga, GA, Kuijper EJ, Boekhout T & Klaassen CHW. 2012. Extensive genetic diversity within the Dutch clinical *Cryptococcus neoformans* population. J Clin Microbiol 50:1918-1926.

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28 Pan WH, Khayhan K, Hagen F, Wahyuningsih R, Chakrabarti A, Chowdhary A, Ikeda R, Taj-Aldeen SJ, Khan Z, Imran D, Sjam R, Sriburee PJ, Liao, WQ, Chaicumpar K, Ingviya N, Mouton JW, Curfs-Breuker I, Boekhout T, Meis JF & Klaassen CHW. 2012. Resistance of Asian *Cryptococcus neoformans* serotype A is confined to few microsatellite genotypes. PlosONE 7: e32868.

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31 Vu TD, Eberhardt U, Szoke S, Groenewald M, Robert V. 2012. A laboratory information management system for DNA barcoding workflows. Interg. Biol. 4:744-755.

32 Wang QM, Boekhout T & Bai FY. 2012. *Bensingtonia rectispora* sp. nov. and *Bensingtonia bomiensis* sp. nov, novel ballistoconidium-forming yeast species from plant leaves collected in Tibet. Int J Syst Evol Microbiol 62:2039-2044.

33 Valente P, Boekhout T, Fontes Landell M, Crestani J, Pagnocca FC, Durães Sette L, Zambrano Passarini MR, Rosa CA, Brandão LR, Pimenta RS, Ribeiro, JR, Marques Garcia K, Lee CF, Suh SO, Blackwell M, Péter G, Dlauchy D, Fell JW, Scorzetti G, Theelen B & Vainstein MH. 2012. *Bandoniozyma* gen. nov, a new genus composed of fermentative and non-fermentative Tremellaceous yeast species. PLOSOne 7:e46060.

34 Zheng XW, Yan Z, Han BZ, Zwietering MH, Samson RA, Boekhout T & Nout MJR. 2012. Complex microbiota of a Chinese "Fen" liquor fermentation starter (*Fen-Daqu*), revealed by culture-dependent and culture-independent methods. Food Microbiol. 120:159-166.

XI School of Environmental Science, Bovey Building, Room 3218, University of Guelph, Guelph, Ontario Canada N1G 2W1. Communicated by Hung Lee <hlee@uoguelph.ca>.

The following are the abstracts of papers published recently.

1 Bajwa PK, Ho CY, Chan CK, Martin VJJ, Trevors JT & Lee H. 2013. Transcriptional profiling of *Saccharomyces cerevisiae* T2 cells upon exposure to hardwood spent sulphite liquor: comparison to acetic acid, furfural and hydroxymethylfurfural. Antonie van Leuwenhoek (In press - http://dx.doi.org/10.1007/s10482-013-9909-1).

Global gene expression was analyzed in *Saccharomyces cerevisiae* T2 cells grown in the presence of hardwood spent sulphite liquor (HW SSL) and each of the three main inhibitors in HW SSL, acetic acid, hydroxymethyfurfural (HMF) and furfural, using a *S. cerevisiae* DNA oligonucleotide microarray. The objective was to compare the gene expression profiles of T2 cells in response to the individual inhibitors against that elicited in response to HW SSL. Acetic acid mainly affected the expression of genes related to the uptake systems of the yeast as well as energy generation and metabolism. Furfural and HMF mainly affected the transcription of genes involved in the redox balance of the cell. On the other hand, the effect of HW SSL on *S. cerevisiae* T2 cells was distinct and considerably more diverse as compared to the effect of individual inhibitors found in lignocellulosic hydrolysates. This is not surprising as HW SSL contains a complex mixture of inhibitors which may act synergistically. HW SSL elicited significant changes in expression of genes involved in diverse and multiple effects on several aspects of the cellular structure and function. A notable response to HW SSL was decreased expression of the ribosomal protein genes in T2 cells. In addition, HW SSL decreased the expression of genes functioning in the synthesis and transport of proteins as well as metabolism of carbohydrates, lipids, vitamins and vacuolar proteins. Furthermore, the expression of genes involved in multidrug resistance, iron transport and pheromone response was increased, suggesting that T2 cells grown in the presence of HW SSL may have activated pheromone response and/or activated pleiotropic drug response. Some of the largest changes in gene expression were observed in the presence of HW SSL and the affected genes are involved in mating, iron transport, stress response and phospholipid metabolism. A total of 59 out of the 400 genes differentially expressed in the presence of HW SSL, acetic acid, HMF and furfural, belonged to the category of poorly characterized genes. The results indicate that transcriptional responses to individual lignocellulosic inhibitors gave a different picture and may not be representative of how the cells would respond to the presence of all the inhibitors in lignocellulosic hydrolysates such as HW SSL.

2 Sriwongchai S, Pokethitiyook P, Kruatrachue M, Bajwa PK & Lee H. 2013. Screening of selected oleaginous yeasts for lipid production from glycerol and some factors which affect lipid production by *Yarrowia lipolytica* strains. J Microbiol Biotechnol Food Sci 2:2344-2348

http://www.jmbfs.org/current-issue/jmbfs_0256_salinee/?issue_id=2155&art

The ability of eight yeast strains to utilize glycerol as a sole carbon source and accumulate lipids in a chemically defined medium was screened. Among the yeasts, *Yarrowia lipolytica* strains DSM 70561 and JDC 335 grew to high cell densities on glycerol. These strains were further tested for lipid accumulation under varying nutritional conditions in Erlenmeyer flasks. The results showed that strains DSM 70561 and JDC 335 accumulated lipids up to 37.1 % and 54.4 % of total cell dry weight, respectively, when the defined medium was supplemented with 1 g/L urea and 2 g/L yeast extract. The lipids accumulated by the two yeasts contained a high proportion of C16:0, C18:1, C18:2 and C18:0 fatty acids. The results suggest that *Y. lipolytica* strains DSM 70561 and JDC 335 have the potential for converting crude glycerol into fatty acids which can in turn be utilized as substrate for biodiesel production.

3 Bajwa PK, Harner NK, Richardson TL, Sidhu S, Habash MB, Trevors JT & Lee H. 2013. Genome shuffling protocol for the pentose-fermenting yeast *Scheffersomyces stipitis*. In: Laboratory Protocols in Fungal Biology: Current Methods in Fungal Biology. Eds: Gupta VK, Tuohy M, Ayyachamy M, Turner KM & O'Donovan A. Springer, New York. Pages 447-454 (Chapter 41 - http://dx.doi.org/10.1007/978-1-4614-2356-0_41).

This chapter presents the protocol for genome shuffling based on recursive cross mating in the pentose-fermenting yeast *Scheffersomyces* (*Pichia*) *stipitis*. Genome shuffling involves 2 stages. In the first stage, a pool of mutants with improved phenotypes is selected. Several rounds of random mutagenesis can be done using different mutagens, and mutant selection can be based on different criteria to generate different mutant cell lines. In the second stage, the mutants derived from different lines are mated recursively to allow for genetic recombination, followed by

screening after each mating cycle to select for improved phenotypes in the recombinants. A number of reports have described genome shuffling based on recursive protoplast fusion in bacteria and yeasts. Recently, we developed mating-based genome shuffling in the pentose-fermenting yeast *S. stipitis*. We have used this approach to obtain genetically stable mutants of *S. stipitis* with considerably improved tolerance to hardwood spent sulphite liquor (HW SSL), a pulping waste liquor containing a complex mixture of inhibitory substances. This was achieved in the complete absence of knowledge as to the precise genetic modifications needed to confer HW SSL tolerance. Here we describe the protocols for recursive UV mutagenesis, cross mating, sporulation and isolation of recombinants with improved phenotypic traits.

XII Plant Biology Division, Biosciences Department, University of Helsinki, P.O. Box 65, FI-00014, Helsinki, Finland. Communicated by Kirk Overmyer <kirk.overmyer@helsinki.fi> http://www.helsinki.fi/plantfungal.

Since this is our first appearance in the yeast newsletter, I would like to introduce my research lab, the plant fungal interactions group at the University of Helsinki. We are interested in plant associated yeasts, especially pathogenic yeasts and currently focus on *Taphrina* species. We wish to thank Philippe Hauser and Álvaro Fonseca for the collaboration on their *Taphrina deformans* genome project, the first *Taphrina* genome to be sequenced. Our lab in Helsinki has sequenced and is currently analysing the genome of *Taphrina betulina*, the witches' broom pathogen of birch. We are interested in developing a network of labs interested in the *Taphrinomycotina*, for the purposes of potential lab visits, collaborations, workshops, etc. Those interested please contact me at the above email address.

Recent publication.

1 Cissé OH, Fonseca A, Kumar AA, Salojärvi J, Overmyer K, Hauser PM & Pagni M. 2013. Genome sequencing of the plant pathogen *Taphrina deformans*, the causal agent of peach leaf curl. mBio 4(3): doi:10.1128/mBio.00055-13 (Open Access PDF).

Taphrina deformans is a fungus responsible for peach leaf curl, an important plant disease. It is phylogenetically assigned to the Taphrinomycotina subphylum, which includes the fission yeast and the mammalian pathogens of the genus *Pneumocystis*. We describe here the genome of *T. deformans* in the light of its dual plant-saprophytic/plant-parasitic lifestyle. The 13.3-Mb genome contains few identifiable repeated elements (ca. 1.5%) and a relatively high GC content (49.5%). A total of 5,735 protein-coding genes were identified, among which 83% share similarities with other fungi. Adaptation to the plant host seems reflected in the genome, since the genome carries genes involved in plant cell wall degradation (e.g., cellulases and cutinases), secondary metabolism, the hallmark glyoxylate cycle, detoxification, and sterol biosynthesis, as well as genes involved in the biosynthesis of plant hormones. Genes involved in lipid metabolism may play a role in its virulence. Several locus candidates for putative *MAT* cassettes and sex-related genes akin to those of *Schizosaccharomyces pombe* were identified. A mating-typeswitching mechanism similar to that found in ascomycetous yeasts could be in effect. Taken together, the findings are consistent with the alternate saprophytic and parasitic-pathogenic lifestyles of *T. deformans*. Peach leaf curl is an important plant disease which causes significant losses of fruit production. We report here the genome sequence of the causative agent of the disease, the fungus *Taphrina deformans*. The genome carries characteristic genes that are important for the plant infection process. These include (i) proteases that allow degradation of the plant tissues; (ii) secondary metabolites which are products favoring interaction of the fungus with the environment, including the host; (iii) hormones that are responsible for the symptom of severely distorted leaves on the host; and (iv) drug detoxification enzymes that confer resistance to fungicides. The availability of the genome allows the design of new drug targets as well as the elaboration of specific management strategies to fight the disease.

XIII Cell and Organism Biology, Lund University, Sölvegatan 35, SE-22362 Lund, Sweden. Communicated by Jure Piskur <jure.piskur@biol.lu.se>.

Recent publications.

1 Witzgall P, Proffit M, Rozpedowska E, Becher PG, Andreadis S, Coracini M, Lindblom TU, Ream LJ, Hagman A, Bengtsson M, Kurtzman CP, Piskur J, Knight A. 2012. "This is not an apple" - yeast mutualism in codling moth. J Chem Ecol. 38:949-57 - doi: 10.1007/s10886-012-0158-y.

2 Piškur J, Ling Z, Marcet-Houben M, Ishchuk OP, Aerts A, LaButti K, Copeland A, Lindquist E, Barry K, Compagno C, Bisson L, Grigoriev IV, Gabaldón T, Phister T. The genome of wine yeast *Dekkera bruxellensis* provides a tool to explore its food-related properties. Int J Food Microbiol 157:202-209 - doi: 10.1016/j.ijfoodmicro.2012.05.008.

3 Vigentini I, De Lorenzis G, Picozzi C, Imazio S, Merico A, Galafassi S, Piškur J, Foschino R. 2012. Intraspecific variations of *Dekkera*/*Brettanomyces bruxellensis* genome studied by capillary electrophoresis separation of the intron splice site profiles. Int J Food Microbiol 157:6-15 - doi: 10.1016/j.ijfoodmicro.2012.02.017.

4 Rasmussen A,LvY, Schnackerz KD, Piškur J. 2011. A new expression vector for production of enzymes in the yeast *Saccharomyces* (*Lachancea*) *kluyveri*. Nucleosides Nucleotides Nucleic Acids. 30:1227-1222 - doi: 10.1080/15257770.2011.603713.

XIV Laboratorio de Microbiología Aplicada y Biotecnología (Applied Microbiology and Biotechnology Lab.), Centro Regional Universitario Bariloche, Universidad Nacional del Comahue. Quintral 1250, (8400), Bariloche, Argentina. Communicated by Diego Libkind <diego.libkind@gmail.comar>.

Recent Publications.

1 de Garcia V, Zalar P, Brizzio S, Gunde-Cimerman N & van Broock M. 2012. *Cryptococcus* species (Tremellales) from glacial biomes in the southern (Patagonia) and northern (Svalbard) hemispheres. FEMS Microbiol Ecol 82:523-539.

2 de Garcia V, Brizzio S & van Broock M. 2012. Yeasts from glacial ice of Patagonian Andes, Argentina. FEMS Microbiol Ecol 82:540-550.

3 Tognetti C, Moliné M, van Broock M, Libkind D. 2013. Favored isolation and rapid identification of *Xanthophyllomyces dendrorhous* (*Phaffia rhodozyma*) from environmental samples. J Basic Microbiol 53: 1–7.

4 Libkind D, Moline M, Tognetti C. 2012. Isolation and selection of new astaxanthin producing strains of *Xanthophyllomyces dendrorhous*. In: Microbial carotenoids: Methods and Protocols, Methods in Molecular Biology Series. Barredo JL (Ed.). Chapter 12. Humana Press. ISBN 978-1-61779-918-1. pp. 183-194.

5 Moliné M, Libkind D, van Broock MR. 2012. Production of torularhodin, torulene and B-carotene by *Rhodotorula* yeasts. In: Microbial carotenoids: Methods and Protocols, Methods in Molecular Biology Series. Barredo JL (Ed.). Chapter 19. Humana Press. ISBN 978-1-61779-918-1. pp.275-284.

6 de García V, Moliné M, Libkind D, Giraudo MR. Cold Adapted yeasts in Patagonian Habitats. In: Cold-adapted yeasts: Biodiversity, Adaptation Strategies and Biotechnological Significance. Editors: P Buzzini & Rosa Margesin. Publisher: Springer Verlag, Berlin Heidelberg. Chapter 7. In revision.

7 Moliné M, Libkind D, de García V, Giraudo MR. Production of Pigments and Photo-Protective Compounds by Cold-Adapted Yeasts. En: Cold-adapted yeasts: Biodiversity, Adaptation Strategies and Biotechnological Significance. Editors: Pietro Buzzini and Rosa Margesin Publisher: Springer Verlag, Berlin Heidelberg. Chapters 10. In revision.

XV National Collection of Agricultural and Industrial Microorganisms, Faculty of Food Sciences, Corvinus University of Budapest, 1118, Budapest, Somlói út 14-16. Communicated by Gábor Péter <gabor.peter@uni-corvinus.hu>.

The following articles have been published since our last report.

1 Čadež N, Raspor P, Turchetti B, Cardinali G, Ciafardini G, Veneziani G & Péter G. 2012. *Candida adriatica* sp. nov. and *Candida molendinolei* sp. nov., two novel yeast species isolated from olive oil and its by-products. Int J Syst Evol Microbiol 62:2296-2302.

Thirteen strains isolated from virgin olive oil or its by-products in several Mediterranean countries were found to be phenotypically and genetically divergent from currently recognized yeast species. Sequence analysis of the large subunit (LSU) rDNA D1/D2 domain and internal transcribed spacer regions/5.8S rDNA revealed that the strains represented two novel species described as *Candida adriatica* sp. nov. (type strain ZIM 2334^T=CBS 12504^T=NCAIM Y.02001^T) and *Candida molendinolei* sp. nov. (type strain DBVPG 5508^T=CBS 12508^T=NCAIM Y.02000^T). Phylogenetic analysis based on concatenated sequences of the small subunit rRNA gene, the D1/D2 region of the LSU rDNA and the translation elongation factor-1a gene suggested that *C. adriatica* sp. nov. and *C. molendinolei* sp. nov. should be placed within the *Lindnera* and *Nakazawaea* clades, respectively.

2 Valente P, Boekhout T, Landell MF, Crestani J, Pagnocca FC, Sette LD, Passarini MRZ, Rosa CA, Brandao LR, Pimenta RS, Ribeiro JR, Garcia KM, Lee CF, Suh SO, Péter G, Dlauchy D, Fell JW, Scorzetti G, Theelen B & Vainstein MH. 2012. *Bandoniozyma* gen. nov., a genus of fermentative and non-fermentative tremellaceous yeast species. PLoS ONE 7(10): e46060 - doi:10.1371/journal.pone.0046060.

Background: Independent surveys across the globe led to the proposal of a new basidiomycetous yeast genus within the *Bulleromyces* clade of the Tremellales, *Bandoniozyma* gen. nov., with seven new species.

Methodology/Principal Findings: The species were characterized by multiple methods, including the analysis of D1/D2 and ITS nucleotide sequences, and morphological and physiological/biochemical traits. Most species can ferment glucose, which is an unusual trait among basidiomycetous yeasts.

Conclusions/Significance: In this study we propose the new yeast genus *Bandoniozyma*, with seven species *Bandoniozyma noutii* sp. nov. (type species of genus; CBS 8364^T = DBVPG 4489^T), *Bandoniozyma aquatica* sp. nov. (UFMG-DH4.20^T = CBS 12527^T = ATCC MYA-4876^T), *Bandoniozyma complexa* sp. nov. (CBS 11570^T = ATCC MYA-4603^T = MA28a^T), *Bandoniozyma fermentans* sp. nov. (CBS 12399^T = NU7M71^T = BCRC 23267^T), *Bandoniozyma glucofermentans* sp. nov. (CBS 10381^T = NRRL Y-48076^T = ATCC MYA-4760^T = BG 02-7-15-015A-1-1^T), *Bandoniozyma tunnelae* sp. nov. (CBS 8024^T = DBVPG 7000^T), and *Bandoniozyma visegradensis* sp. nov. (CBS 12505^T = NRRL Y-48783^T = NCAIM Y.01952^T).

3 Dlauchy D, Lee CF & Péter G. 2012. *Spencermartinsiella ligniputridi* sp. nov., a yeast species recovered from rotten wood. Int J Syst Evol Microbiol 62:2799–2804.

Four strains of a novel heterothallic yeast species were isolated from rotten wood samples collected at different locations in Hungary. Analysis of sequences of the D1/D2 domain of the large subunit rRNA gene placed the novel species in the genus *Spencermartinsiella*. The novel species can be distinguished from *Spencermartinsiella europaea*, the single species of the genus, and from *Candida cellulosicola*, the only recognized anamorphic species of the *Spencermartinsiella* clade, on the basis of standard phenotypic characteristics. The relatedness among the four strains of the novel species and two closely related strains representing undescribed yeast species is discussed. The name *Spencermartinsiella ligniputridi* sp. nov. is proposed to accommodate the four novel strains. The type and isotype strains of *Spencermartinsiella ligniputridi* sp. nov. are NCAIM Y.01992^T (=CBS 12585^T =NRRL Y-48818^T) and NCAIM Y.01936^I (=CBS 12586^I=NRRL Y-48819^I), respectively. Two additional strains are NCAIM Y.01991 and NCAIM Y.01993.

4 Péter G, Dlauchy D, Price NPJ & Kurtzman CP. 2012. *Diddensiella caesifluorescens* gen. nov., sp. nov., a riboflavin producing yeast species of the family Trichomonascaceae. Int J Syst Evol Microbiol 62:3081–3087.

Four strains of a novel heterothallic yeast species were isolated from rotten wood collected in or near the Pilis Mountains in Hungary. The strains produced riboflavin in liquid culture. Analysis of gene sequences for the D1/D2 domains of the LSU nuclear rRNA, as well as analysis of concatenated gene sequences for the D1/D2 nuclear LSU

rRNA, mitochondrial SSU rRNA and cytochrome oxidase II placed the novel species in a small clade including only two recognized species, *Candida santjacobensis* and *Candida transvaalensis*, in the family Trichomonascaceae. DNA sequence analyses demonstrated that the novel species was distinct from all currently recognized teleomorphic yeast genera. The name *Diddensiella caesifluorescens* gen nov., sp. nov. is proposed to accommodate the novel genus and species. The new genus proposed here can be recognized only from gene sequence analysis, because the characters of its asexual reproduction and ascospore formation are shared by several members of the genera T*richomonascus*, *Sugiyamaella* and *Spencermartinsiella*. The type and isotype strains of *D. caesifluorescens* are NCAIM Y.01949^{T} (=NRRL Y-48781^{T}=CBS 12613^{T}) and NCAIM Y.01956^{I} (=NRRL Y-48782^{I}=CBS 12614^{I}), respectively. In view of their close relatedness to *D. caesifluorescens*, *C. santjacobensis* and *C. transvaalensis* are transferred to the genus *Diddensiella* as new combinations in accordance with changes in the International Code of Nomenclature for algae, fungi and plants.

5 Deák T & Péter G. 2013. Developments in yeast taxonomy. Acta Alimentaria. 42:55-68.

XVI Department of Biotechnology, VIBT-BOKU, University of Natural Resources and Applied Life Sciences, Muthgasse 11, A-1190 Vienna, Austria. Communicated by Hansjörg Prillinger <Hansjoerg.Prillinger@gmx.at >.

Recent publication.

1 Lopandic K, Rentsendorj U, Prillinger H, Sterflinger K. 2013. Molecular characterization of the closely related *Debaryomyces* species: proposition of *D. vindobonensis* sp. nov. from a municipal wastewater treatment plant. J Gen Appl Microbiol 59:49-58.

A polyphasic molecular approach was used in order to characterize and taxonomically assign *Debaryomyces* yeast isolates of different origins. Actin 1 (*ACT1*) gene sequences coupled with AFLP markers showed that the investigated yeasts belonged to the recently reinstated species *D. hansenii*, *D. fabryi* and *D. tyrocola*. The strain HA1179 was supposed to be a *D. hansenii* strain with introgressed *D. fabryi* DNA segments. This strain acquired ribosomal RNA encoding genes (rDNA) and the *ACT1* gene from the species *D. fabryi* and *D. hansenii* respectively. Comparative sequence analysis of the *ACT1* gene, ITS1-5.8S-ITS2 (5.8S-ITSs) and D1/D2 regions, suggested that five strains isolated from a municipal wastewater treatment plant could represent a new taxon of the genus, for which the name *Debaryomyces vindobonensis* was proposed. The calculated degree of similarity between the AFLP patterns indicated that the strains of *D. vindobonensis* and the closely related species were separated by the values 0.5. New yeast isolates showed very similar morphological and physiological properties to related *Debaryomyces* species. They differed notably only by the assimilation of rhamnose and growth at 50% glucose. In contrast to the other species, *D. vindobonensis* was unable to assimilate starch.

XVII Japan Collection of Microorganisms (JCM), RIKEN BioResource Center, 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan. Communicated by M Takashima <masako@jcm.riken.jp>.

Please note that JCM has moved to the Tsukuba Campus of RIKEN from Wako Campus since October 2012. http://www.jcm.riken.jp/

Recent publication.

1 Endoh R, Suzuki M, Okada G, Takeuchi Y & Futai K. 2011. Fungus symbionts colonizing the galleries of the ambrosia beetle *Platypus quercivorus*. Microb Ecol. 62:106-120 - doi: 10.1007/s00248-011-9838-3

2 Endoh R. 2012. Yeasts associated with coleopteran beetles in forest. J Jpn For Soc 94: 307–315 (in Japanese).

Diverse array of yeasts are associated with Coleopteran beetles in forest. Some yeasts are apparently involved in the life history of beetles, albeit with less scientific attention compared to those for associated filamentous fungi. Thus, yeasts must be important but neglected members inhabiting in the forest ecosystems. In the present review, yeasts associated with Coleopteran beetles in forest are introduced. Nine families and one group of Coleoptera i.e., Buprestidae, Bostrychidae, Cerambycidae, Chrysomelidae, Lucanidae, Nitidulidae, Platypodidae, Rhynchophoridae, Scolytidae, and fungus beetles of interest are selected and discussed in the context

of yeast-beetle symbiosis. Research on yeasts found in natural environment including beetle-associated groups has mainly been weighted on classification, identification and species description. As molecular methods have been developed and as genetic information is increasingly deposited in sequence databases, yeast species discrimination has been getting much easier. Together with these progresses, research on yeasts found from beetles and beetle-associated sources will provide a more comprehensive picture of the nature of the association.

3 Takashima, M, Sugita, T, Van, BH, Nakamura, M, Endoh, R & Ohkuma M. 2012. Taxonomic richness of yeasts in Japan within subtropical and cool temperate areas. PLoS ONE 7(11): e50784 - doi: 10.1371

XVIII CREM – Centro de Recursos Microbiológicos, Departamento de Ciências da Vida, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, 2829-516 Caparica, Portugal. Communicated by JP Sampaio <jss@fct.unl.pt>.

The following papers were recently published or accepted for publication.

1 Guerreiro MA, Springer DJ, Rodrigues JA, Rusche LN, Findley K, Heitman J & Fonseca Á. 2013. Molecular and genetic evidence for a tetrapolar mating system in the Basidiomycetous yeast *Kwoniella mangrovensis* and two novel sibling species. Euk Cell 12:746-760.

Kwoniella mangrovensis has been described as a sexual species with a bipolar mating system. Phylogenetic analysis of multiple genes places this species together with *Kwoniella heveanensis* in the *Kwoniella* clade, a sister clade to that containing two pathogenic species of global importance, *Cryptococcus neoformans* and *Cryptococcus gattii*, within the Tremellales. Recent studies defining the mating type loci (MAT) of species in these clades showed that, with the exception of *C. neoformans* and *C. gattii*, which are bipolar with a single biallelic multigene MAT locus, several other species feature a tetrapolar mating system with two unlinked loci (homeodomain [HD] and pheromone/receptor [P/R] loci). We characterized several strains from the original study describing *K. mangrovensis*; two MAT regions were amplified and sequenced: the STE20 gene (P/R locus) and the divergently transcribed SXI1 and SXI2 genes (HD locus). We identified five different mating types with different STE20/SXI allele combinations that together with results of mating experiments demonstrate that *K. mangrovensis* is not bipolar but instead has a tetrapolar mating system. Sequence and gene analysis for a 43-kb segment of the *K. mangrovensis* type strain MATlocus revealed remarkable synteny with the homolog-ous *K. heveanensis MAT* P/R region, providing new insights into slower evolution of MAT loci in the *Kwoniella* compared to the *Cryptococcus* clade of the Tremellales. The study of additional isolates from plant substrates in Europe and Botswana using a combination of multilocus sequencing with MAT gene analysis revealed two novel sibling species that we name *Kwoniella europaea* and *Kwoniella botswanensis* and which appear to also have tetrapolar mating systems.

2 Coelho MA, Gonçalves C, Sampaio JP & Gonçalves P. Extensive intra-kingdom horizontal gene transfer converging on a fungal fructose transporter gene. PLoS Genetics (accepted).

Comparative genomics revealed in the last decade a scenario of rampant horizontal gene transfer (HGT) among prokaryotes, but for fungi a clearly dominant pattern of vertical inheritance still stands, punctuated however by an increasing number of exceptions. In the present work, we studied the phylogenetic distribution and pattern of inheritance of a fungal gene encoding a fructose transporter (*FSY1*) with unique substrate selectivity. 109 FSY1 homologues were identified in two sub-phyla of the Ascomycota, in a survey that included 241 available fungal genomes. At least 10 independent inter-species instances of horizontal gene transfer (HGT) involving *FSY1* were identified, supported by strong phylogenetic evidence and synteny analyses. The acquisition of FSY1 through HGT was sometimes suggestive of xenolog gene displacement, but several cases of pseudoparalogy were also uncovered. Moreover, evidence was found for successive HGT events, possibly including those responsible for transmission of the gene among yeast lineages. These occurrences do not seem to be driven by functional diversification of the Fsy1 proteins because Fsy1 homologues from widely distant lineages, including at least one acquired by HGT, appear to have similar biochemical properties. In summary, retracing the evolutionary path of the *FSY1* gene brought to light an unparalleled number of independent HGT events involving a single fungal gene. We propose that the turbulent evolutionary history of the gene may be linked to the unique biochemical properties of the encoded transporter, whose predictable effect on fitness may be highly variable. In general, our results support the most recent views suggesting that inter-species HGT may have contributed much more substantially to shape fungal genomes than heretofore assumed.

XIX Biology Department, Brooklyn College, Brooklyn, New York 11210. Communicated by Nasim A. Khan <nasim.khan4@verizon.net>.

In the yeast *Saccharomyces cerevisiae* there are at least two major α-glucosidases (Yamamoto et.al 2004), namely maltase (E.C.3.2.1.20) and isomaltase (E.C. 3.2.1.10). Khan and Eaton (1967) purified maltase and alpha-methylglucosidase from yeast. These two α-glucosidases were partially characterized, maltase was specific for the hydrolysis of the disaccharide maltose and alpha-methylglucosidase was specific for the hydrolysis of isomaltose and α-methylglucoside. However, both enzymes were able to hydrolyze sucrose and the chromogenic substrate p-nitrophenyl-alpha-D-gucopyranoside (PNPG). We also estimated the molecular weight of maltase as 68,500 and α-methylglucosidase/isomaltase as 64,700. The pupose of this communication is to update the nomenclature of α-methylglucosidase. Both iso-maltase and α-methylglucosidase are now " the other names" for the accepted name oligo-1,6-glucosidase. A request was made to the International Enzyme Commission to give α-methylglucosidase as an " other name " for oligo-1,6-glucosidase, and the request was approved . An updated description for this appears in "ExplorEnzyme-The Enzyme Database" 2013. They have quoted papers by Khan & Eaton (1967) and Yamamoto et al (2004) in support of this update.

References:

1 Khan NA & Eaton NR. 1967. Purification and characterization of maltase and α-methyl-glucosidase from yeast. Biochim Biophys Acta 146:173-178.

2 Yamamoto K, Nakayama A, Yamamoto Y & Tabata S. 2004. Val216 decides the substrate specificity of alpha-glucosidase in *Saccharomyces cerevisiae*. Eur J Biochem 271:3414-4320.

3 ExplorEnz-The Enzyme Database: a MySQL database of the International Union of Biochemistry and Molecular Biology (IUBMB) enzyme nomenclature.

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

Recently accepted papers.

1 Morais CG, Lara CA, Marques S, Fonseca C, Lachance MA & Rosa CA (in press) *Sugiyamaella xylanicola* sp. nov., a xylan-degrading yeast species isolated from rotting-wood in Brazil. Int J Syst Evol Microbiol (Accepted March 2013).

2 Lachance MA & Kurtzman CP (in press) The yeast genus *Tortispora* gen. nov., description of *Tortispora ganteri* sp. nov., *Tortispora mauiana* f.a., sp. nov., *Tortispora agaves* f.a., sp. nov., *Tortispora sangerardonensis* f.a., sp. nov., *Tortispora cuajiniquilana* f.a., sp. nov., *Tortispora starmeri* f.a., sp. nov., and *Tortispora phaffii* f.a., sp. nov., reassignment of *Candida caseinolytica* to *Tortispora caseinolytica* f.a., comb. nov., emendation of *Botryozyma*, and assignment of *Botryozyma*, *Tortispora* gen. nov., and *Trigonopsis* to the family Trigonopsidaceae fam. nov. Int J Syst Evol Microbiol (Accepted May 2013).

We describe the yeast genus *Tortispora* gen. nov., an early diverging lineage in the Saccharomycetales that features the formation of helical ascospores. The genus is based on 16 strains resembling *Candida caseinolytica* that were isolated from necrotic plant tissue in warm regions of the New World. Based on sequences of the D1/D2 domains of the nuclear large subunit rRNA gene, as well as other data, the strains are assigned to eight distinct species. The species are nutritionally specialized and share the unusual ability to hydrolyze casein and to grow on 1-butanol as sole carbon source. One species of the proposed new genus produces a simple ascus with a helical ascospore, whereas other species of the clade have failed to form ascospores. All species in the clade, including *C.caseino-lytica*, are assigned to *Tortispora* gen. nov. The new binomials are *Tortispora ganteri* sp. nov, type species of the genus (SUB 86-469.5 ^{T} = CBS 12581^{T} = NRRL Y-17035^{T}), *Tortispora caseinolytica* f.a., comb. nov. (UCD-FST 83-438.3^{T} = CBS 7781^{T} = NRRL Y-17796^{T}), *Tortispora mauiana* f.a., sp. nov. (UWOPS 87-2430.3^{T} = CBS 12803^{T} = NRRL Y-48832^{T}), *Tortispora agaves* f.a., sp. nov. (UWOPS 94-257.6^{T} = CBS 12794^{T} = NRRL Y-63662^{T}), *Tortispora sangerardonensis* f.a., sp. nov. (UWOPS 00-157.1^{T} = CBS 12795^{T} = NRRL Y-63663^{T}), *Tortispora cuajiniquilana* f.a., sp. nov. (UWOPS 99-344.4^{T} = CBS 12796^{T} = NRRL Y-63664^{T}), *Tortispora starmeri* f.a., sp. nov. (G 91-702.5^{T} = CBS 12793^{T} = NRRL Y-63665^{T}), and *Tortispora phaffii* f.a., sp. nov. (UWOPS 91-445.1^{T} = CBS 12804^{T} = NRRL Y-48833^{T}). In addition, species formerly assigned to *Ascobotryozyma* are reassigned to the genus *Botryozyma*. The genera *Trigonopsis*, *Botryozyma*, and *Tortispora* are assigned to the family Trigonopsidaceae fam. nov.

3 Guzmán B, Lachance MA, Herrera CM. 2013. Phylogenetic analysis of the angiosperm-floricolous insect-yeast association: have yeast and angiosperm lineages co-diversified? Mol Phylogen Evol 68:161-175.

4 Hagler AN, Ribeiro JRA, Pinotti T, Brandão LR, Pimenta RS, Lins U, Lee CF, Hsieh CF, Lachance MA & Rosa CA 2013 *Wickerhamiella slavikovae* sp. nov. and *Wickerhamiella goesii* sp. nov., two yeast species isolated from natural substrates in Brazil and Taiwan. (Accepted May 2013).

The following papers have now appeared in print.

5 Cadete RM, Melo MA, Zilli JE, Vital MJS, Mouro A, Prompt AH, Gomes FCO, Stambuk BU, Lachance MA & Rosa CA. 2013. *Spathaspora brasiliensis* sp. nov., *Spathaspora suhii* sp. nov., *Spathaspora roraimanensis* sp. nov. and *Spathaspora xylofermentans*, sp. nov., four novel D-xylose-fermenting yeast species from Brazilian Amazonian Forest. Antonie van Leeuwenhoek 103:421-431.

6 Safar SVB, Gomes FCO, Guimarães ARM, Lachance MA & Rosa CA. 2013. *Kazachstania rupicola* sp. nov., a yeast species isolated from water tanks of a bromeliad in Brazil. Int J Syst Evol Microbiol 63:1165-1168.

7 Badotti F, Silva PAB, Mendonça MC, Gomes FCO, Morais PB, Lachance MA & Rosa CA. 2013. *Wickerhamiella dulcicola* sp. nov. and Wickerhamiella cachassae sp. nov., two yeasts isolated from cachaça fermentation in Brazil. Int J Syst Evol Microbiol 63:1169-1173.

Obituary
Tibor Deák 1936-2013

Tibor Deák, Professor Emeritus at the Department of Microbiology and Biotechnology, Faculty of Food Science, Corvinus University of Budapest, passed away on March 3 2013 following a long illness. Tibor received his M.Sc. degree from the University of Szeged (at that time József Attila University) in 1957 as a teacher of biology and chemistry and his Ms.C. degree in microbiology from Eötvös Loránd University, Budapest in 1963. He received his Ph.D and D.Sc. degrees in 1970 and 1989, respectively from the Biology Section, Hungarian Academy of Sciences, Budapest. Following a few years of gaining experience at the Budapest Canning Company and the Research Institute for Canning Industry, he joined in 1967 the University of Horticulture and Food Industry, recently integrated into the Corvinus University of Budapest. There, he educated generations of food microbiologists. Students twice awarded him the title *Magister Optimus*. From 1970 to 1993 he served as head of the Department of Microbiology and Biotechnology. From 1986 to 1991 he served as dean of the Faculty of Food Science and from 1993 to 1996 as rector of the University of Horticulture and Food Industry.

Tibor played a major role in establishing the National Collection of Agricultural and Industrial Microorganisms, the first collection receiving the status of International Depositary Authority for patent strains of microorganisms in Central and Eastern Europe.

Among his first research subjects were investigations of the mode of action of sorbic acid and the membrane transport of microorganisms. Later his attention was focused first primarily on the microbial ecology of foods, food spoilage yeasts, yeast biodiversity, and the detection and identification of food spoilage yeasts. Tibor Deák's scientific legacy consists of more than 300 publications, including peer-reviewed articles, books, and book chapters.

He was a member of numerous Hungarian and international organizations, including the International Commission on Yeasts and the International Committee on Food Microbiology and Hygiene. He was a member of the editorial board of the International Journal of Food Microbiology and FEMS Yeast Research. He was the recipient of post-doctoral research fellowships from the Hungarian Academy of

Sciences, the British Council and FAO-UNO and was twice a Senior Fulbright Scholar. He travelled all over the world and established fruitful connections with numerous colleagues.

Professor Deák's outstanding achievement were recognized several times. Among other awards he received the Knight Cross of the Hungarian Republic. In 1996 the University of Szeged conferred upon him an honorary doctorate in recognition of his outstanding scientific contributions.

In recognition of his contributions to yeast research a new yeast species *Ogataea deakii* Péter, Dlauchy & Čadež is being named after him.

In addition of being a great scientist, he was a wonderful colleague and a good friend. Those who knew him enjoyed his company.

Tibor, we miss you very much. We shall keep you in our memory.

Gábor Péter

Forthcoming Meetings

ISSY30 - Cell Surface and Organelles in Yeasts: from Basics to Applications
June 18-22 2013, High Tatras - Stará Lesná, Slovakia

The 30th International Specialized Symposium on Yeast will be held June 18-22, 2013 in Stará Lesná (High Tatras), Slovakia. The theme of the symposium will be: "Cell Surface and Organelles in Yeasts: from Basics to Applications". The conference center of the Slovak Academy of Sciences in Stará Lesná is located at the foothills of the magnificent High Tatras, an area of natural beauty and the rich cultural heritage.

Ivan Hapala and Peter Griac (co-chairs of the 30th ISSY) www.issy2013.org

26th International Conference on Yeast Genetics and Molecular Biology
August 29 - September 3 2013, Frankfurt/M. Germany

The deadline for abstract submission of oral presentations for the 26th International Conference on Yeast Genetics and Molecular Biology (www.yeast-2013.org) was March 31, 2013.

Yeasts are key model organisms in eukaryotic research and in addition play a significant role in many biotechnological processes. Yeast 2013 wants to attract all researchers using yeasts and initiate interdisciplinary exchange. To achieve these aims, we have invited excellent speakers, but the success of the conference will mainly depend on your active and numerous participations.

Frankfurt/M. is located in the middle of Europe and easy to reach. It has a very good infrastructure of plane and train connections to most parts of the world. The conference venue is located on the historical Campus Westend of Goethe University which is one of the most beautiful university locations in Germany with an extraordinary architecture.

The conference will start with a Get-Together on Thursday, August 29, 2013 and lectures will commence from Friday 30, 2013 at 10 a.m. The conference banquet will be combined with a boat cruise on the Middle-Rhine-Valley, which is a world cultural heritage, in the mid-term of the conference (Sunday, September 1st, 2013), followed by two further days of intensive science with lectures and workshops. Although the entire conference is open for contributions from fields of all yeasts, additional satellite symposia on *Kluyveromyces*, *Hansenula*, *Arxula*, *Yarrowia* and other non-conventional yeasts are integrated into the conference programme.

To make the conference affordable for everyone, we have calculated moderate registrations fees which also include the social event. For young scientists there is also a limited number of FEMS grants available. We will depend on your active participation to make sure that the conference will provide the latest developments in yeast research and to reach the goal of an interdisciplinary exchange. We are looking forward to welcome you in Frankfurt.

Karl-Dieter Entian, Eckhard Boles, Markus Bohnsack and the organising team. For further information: <contact@yeast-2013.org> www.yeast-2013.org

Comparative Genomics of Eukaryotic Microorganisms
October 19th -24th 2013, Sant Feliu de Guixols, Spain

For further information, consult: http://events.embo.org/13-comparative-genomics/

PhD course on Industrial Biotechnology for lignocellulose based processes: October 20 – 25, 2013

Aim - To introduce the students to production of biofuels and other chemicals using plant cell wall materials as the raw material with emphasis on the biotechnology aspect of the production process. The course will cover raw material composition and sources, pretreatment and hydrolysis, enzymes that act on plant cell wall material, microorganisms and improvement of microorganisms for production of targeted biofuels and chemicals, the fermentation process and analytics. The perspective of biorefinery solutions will be discussed. Lectures and exercises will be mixed. The course also includes a seminar with hot topics in the area. **Who should attend?** - Students with diverse educational background with interest in industrial biotechnology and sustainable processes are the target group for the course. The course is suitable to PhD students with some background in biotechnology, chemical engineering or biochemistry. Basic knowledge in mathematics and biology is required. It is an intensive course and participants are expected to work vigorously during the course week. The course is accredited with 5 ECTS-points and the course week ends with a written exam. Reading material will be sent out on beforehand. **Course venue** - The course will be held at Chalmers University of Technology, Gothenburg, Sweden. Further information will be announced at:

http://www.chalmers.se/en/departments/chem/research/lifescience/industrial%20biotechnology/Pages/default.aspx.

Contact person: Maurizio Bettiga, maurizio.bettiga@chalmers.se

Yeasts in Bioeconomy, November 7-8 2013, Madrid, Spain

A two-day International Symposium with the title "Yeasts in Bioeconomy" sponsored by the Fundación Ramón Areces and coordinated by C. Gancedo (Madrid) and J. Pronk (Delft) will be held the 7th and 8th November 2013 in Madrid (Spain). Registration is free but the Fundación requires that a form be filled. The form can be obtained from <cgancedo@iib.uam.es>.

The participants include: Boles E, Germany; Chávez S, Spain; Ferrer P, Spain; Gancedo C, Spain; Kirsten B, USA; Louis E, United Kingdom; McBride J, USA; Madzak C, France; Molina M, Spain; Posas F, Spain; Pronk J, The Netherlands; Querol A, Spain; Revuelta JL, Spain; Sauer U, Switzerland; Siverio JM, Spain; Winderickx J, Belgium.

The 9th International Conference on *Cryptococcus* and Cryptococcosis (ICCC9)
Amsterdam, May15-19 2014

Be our guest at the century old Museum of the Tropics in Amsterdam!

We are pleased to invite you to Amsterdam in the Spring of 2014 for the 9th International Conference on *Cryptococcus* and Cryptococcosis scheduled to be held in the ancient and beautiful 'Tropenmuseum'. We look forward to an exciting meeting focussing on new trends in the research of this important killer yeast. Topics will include clinical perspectives in the developed and developing world, disease management, [access to] treatment, diagnostics, epidemiology, taxonomy, immunology, pathophysiology, molecular biology, and many more.

The old medieval city of Amsterdam is on the UNESCO heritage list and houses many nationalities endowing it a highly international ambience. The scenic area of downtown with its monumental canals and neighbourhoods is very pleasant for just strolling around or taking a boat trip. The Van Gogh Museum and the just renovated Rijksmuseum houses beautiful art collections. The city is known for beautiful hotels, restaurants and bars available in all price categories.

Please note May 15-19, 2014 in your agenda and visit this unique scientific event in Mokum, as Amsterdam is known by the locals.

See http://www.iccc2014.org for further information

Teun Boekhout, Annemarie Brouwer, Ferry Hagen and Jacques Meis

The Congresses of the International Union of Microbiological Societies (IUMS 2014)

The Congresses of the International Union of Microbiological Societies (IUMS 2014) will take place from July 27th to August 1st, 2014 at the Palais des Congrès de Montréal (Montréal's Convention Centre), in Montréal, Canada.

The three congresses [XIVth International Congress of Mycology; XIVth International Congress of Bacteriology and Applied Microbiology; XVIth International Congress of Virology] will be held simultaneously within one week to stimulate cross talk.

The Mycology Division of IUMS is in charge of the International Congress of Mycology and we foresee to expand its scope beyond the fungi. Thus the congress will cover Mycology and other Eukaryotic microorghanisms. The 'Congress of Mycology' in Montreal to also include important aspects of the biology non-fungal eukaryotic microbes.

The congresses will have a key note and bridging sessions across all divisions, shared sessions between de Divisions Bacteriology and 'Mycology', and of course 'Mycology and other Eukaryotic Microbe-oriented' sessions.

The congress will be of interest to all involved or interested in research and training in eukaryotic microbiology, and will cover basic research leading to advancement of knowledge, clinical research bringing new knowledge from the bench to patients, and applied research dealing with the development and use of innovative approaches to prevent and treat microbe-related health problems or to the use of microbes for the benefit of mankind.

See http://www.montrealiums2014.org/

Bridging Sessions: 1. Emerging pathogens: David Denning UK; 2. Host-Pathogens interaction: Theo Geijtenbeek, Netherlands; 3. Vaccins/antimocrobials: Arturo Casadevall, USA; 4. Metagenomics: Alexandra Worden, USA. **Keynotes**: 1. Pathogens; 2. Systems Biology; 3. Models for Human Diseases; 4. Biodiversity & Ecology; 5. Cell & Molecular Biology; 6. Comparative Genomics; 7. Synthetic Biology; 8. Inter Kingdom Crosstalk. **Regular Sessions** will be cover four major domains: 1. Industrial / Systems Biology / Synthetic Biology, Incl. Bioprospecting / secondary metabolism; Food biotechnology; Systems biology; Synthetic biology; Biofuels; Spore biology; Extremophiles. 2. Pathogens: Incl. Genetics; Host - pathogens interactions; Emerging pathogens; Model hosts; Immunity, incl. plants; Resistance; Parasites; Microsporidia; Diagnostics. 3. Cell and Molecular Biology: Incl. Sensing and signaling; Organelle evolution and function; Morphogenesis; Apoptosis; Cell cycle; Sex and asex; Multicellularity; Biofilms. 4. Ecology and Evolution: Incl. Metagenomics; Human microbiome; Indoor microbiome; Biocontrol; Cross kingdom interactions; Mycorrhiza; Tree of Life; Population genomics; Biodiversity.

Teun Boekhout (Chair of the Mycology congress, vice-chair Mycology Division)
Pierre Belhumeur (Vice-chair of the Mycology congress)
Scott Baker (Former chair Mycology congress 2011, Chair Mycology Division

10th International Mycological Congress, August 3-8, 2014, Bangkok, Thailand

We cordially invite you to go to http://www.imc10.kasetsart.org/ and please propose symposium topics for your IMC 10 in Bangkok, August 3-8, 2014, at Queen Sirikit National Convention Center.

Organized by:
Thai Mycological Association
Kasetsart University
National Science and Technology Development Agency

International Mycological Association http://www.ima-mycology.org/
For more information, please visit http://www.imc10.kasetsart.org/

ISSY 31 Yeast Fermentation: From Genes to Application Aspects
Vipava, Slovenia 9-12th October 2014

The conference is organized in the renovated Lanthieri Palace by Lund University, University of Nova Gorica, EU FP7 Cornucopia and Jubilekinase ApS. ISSY 31 is organized under auspices of International Commission on Yeasts (ICY). For further information, contact:

Jure Piskur <Jure.Piskur@biol.lu.se>

http://www.yeast-cornucopia.se/index.php?option=com_content&view=article&id=12&Itemid=24

Brief News Items

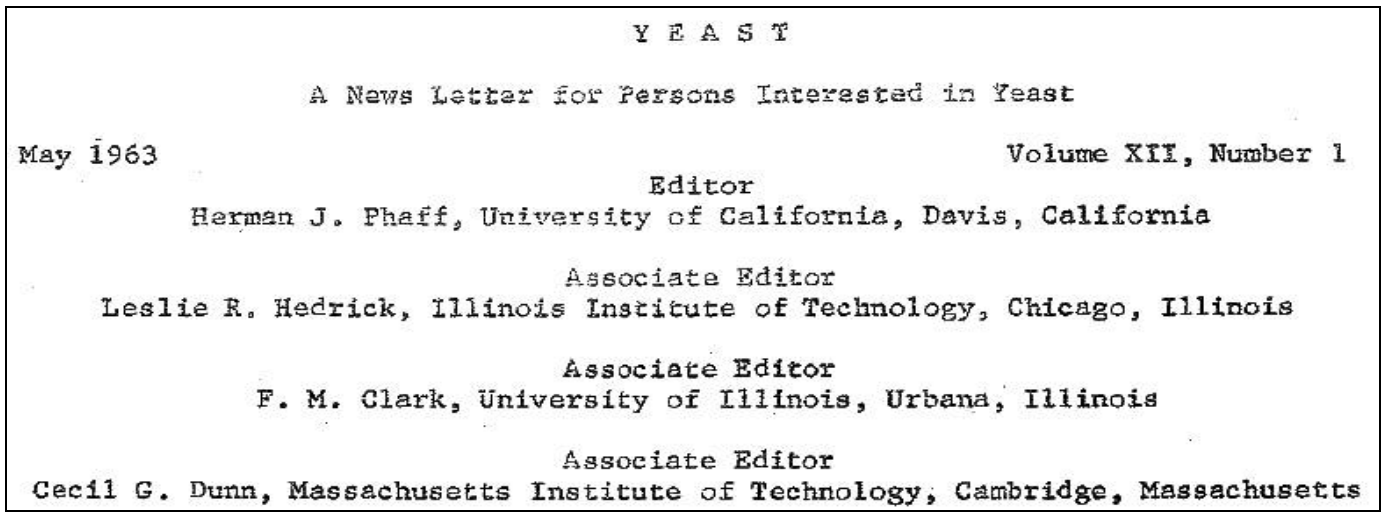
New coordinates: Sakkie Pretorius

I will commence in my new role as Vice President: Research at Macquarie University in Sydney on the 8th July 2013. This email address will be 'disconnected' June 7. I will be off-line from 8 June to 8 July because my family and I are going to Greece for a holiday and when we return to Australia, we will physical move from Adelaide to Sydney. My new contact details are given below. I will continue to be involved with yeast research (yeast omics to be more specific) so please change my email address in your list of contacts.

Isak (Sakkie) S. Pretorius, Deputy Vice Chancellor: Research
Macquarie University
Building E11A, Macquarie University
North Ryde, Sydney NSW 2109
Australia
Tel: +61 2 9850 7887

<sakkie.pretorius@mq.edu.au> www.mq.edu.au

50 Years Ago



Y E A S T

A News Letter for Persons Interested in Yeast

May 1963 Volume XII, Number 1

Editor
Herman J. Phaff, University of California, Davis, California

Associate Editor
Leslie R. Hedrick, Illinois Institute of Technology, Chicago, Illinois

Associate Editor
F. M. Clark, University of Illinois, Urbana, Illinois

Associate Editor
Cecil G. Dunn, Massachusetts Institute of Technology, Cambridge, Massachusetts

Yeast Newsletter - May 1963 - Vol. XII, No. 1

Mrs. **Kreger-van Rij** (CBS) reported that type strains of seven new yeast species were received at CBS, including *Candida guilliermondii, C. viswanthii* and *Rhodotorula nitens*.

Dr. **H. J. Shadomy** (University of California Los Angeles) described exhaustive tests to detect ascspores in 25 strains of *Pityrosporum*, "because of the spore-mother cell sac-like cells seen in preparations of a number of our organisms." No spores were observed, however, leading to the conclusion that *Pityrosporum* is asporogenous.

The main activity in the laboratory of Dr. **N. van Uden** (University of Lisbon, Portugal) is the taxonomic revision of five yeast genera (*Candida, Torulopsis, Trichosporon, Nematospora* and *Metschnikowia*) in preparation for the second edition of Lodder and Kreger-van Rij's "The Yeasts".

4. FELLOWSHIP AVAILABLE:
During the period 1963-64 a Gulbenkian fellowship is available. Applicants should be willing to learn the methods of yeast identification and be interested to do research on marine yeasts, yeasts associated with animals or any other field of yeast ecology. Reasonable fluency in any one of the following languages is required: Portuguese, English, German, Dutch, Spanish or French.

Dr. **Shoji Goto** isolated 847 yeast cultures from 470 wine samples in the wine producing areas of Kofu valley, Japan. Of these 76 could produce alcohol. Some were identified as *Saccharomyces cerevisiae, S. cerevisiae* var. *ellipsoideus, S. steineri, S. oviformis, S. heterogenicus, S. chevalieri,* and *S. italicus.*

Dr. **C. C. Lindegren** listed five recent publications, including

1. Lindegren, C. C. The chromone theory of mitosis. Canadian Journal of Genetics and Cytology 4: 426-439 (1962).

Dr. **Tadashi Hirano** of Southern Illinois University, Carbondale, Illinois, USA announced that he was returning to the Tokyo Metropolitan Isotope Center after working for four years in the laboratory of Carl Lindegren at Southern Illinois University.

Dr. **Fred Sherman** of the University of Rochester published five articles including:

Sherman, F. and H. Roman (1963) Evidence for two types of allelic recombination in yeast. Genetics 48: 375-385.

Dr. **Ericka Friedrich** of Martin Luther University, West Germany described an abbreviated identification procedure for medical yeasts, based on colony morphology:

1st Group: colonies convex, cream-colored, smooth

2nd Group: Colonies smooth, glossy, low convex or flat, greyish-cream, slightly pigmented.

3rd Group: Colonies rough, truncate, low to high convex, greyish cream or whitish, folded or other surface structures.

4th Group: Colonies pigmented red.

Because of the small number of species, which according to general experience are found in clinical material, a more accurate diagnosis is already possible by doing only a few additional tests, after placing the organisms in the four groups listed above. For example, in a large number of such strains one can dispense with the trouble of looking for ascospores and also the assimilation tests are necessary for members of some groups only.

Drs. **J.F.T. Spencer and H. J. Phaff** of the University of California Davis summarized their ecological, taxonomic and physiological studies of yeasts from flowers and water samples. More than half the strains from flowers were identified as *Pullularia*; the remaining belonged to genera *Cryptococcus, Rhodotorula, Candida, Torulopsis, Sporobolomyces* and *Saccharomyces.* Several new species descriptions were being characterized.

Dr. **K. Kodama** of Kodama Brewing Co. Ltd., Japan described culture conditions that could be used to detect contaminants in preparations of sake.

Dr. **Philip Dakin** of the Stroh Brewery Co., Detroit, Michigan, USA published a method for counting yeast in suspensions using haemocrit readings with a microcentrifuge, similar to those used for blood cell analysis in clinical settings.

Dr. **Noboru Kawashami** of Hiroshima University announced two publications, one a "List of Cultures" of yeasts and molds maintained in their laboratory, and one on "Preservation of microorganisms with a simplified lyophil process".

Dr. **M. Woodbine** summarized a paper on the effects of media nutrients on fat production in *Hansenula* yeasts.

T. A. Pedersen published several papers on lipid formation in *Cryptococcus terricolus.*

Researchers at **Universal Foods Corp.** (Red Star Yeast Co., Milwaukee, Wisconsin, USA) announced development of a new compressed yeast product, a new product promising more efficient wine fermentation and higher yield.

R. G. Artagaveytia-Allende donated his collection of several hundred yeast and mold strains to the Faculty of Chemistry, Montevideo, Uraguay.

In a letter of the Editor, **Carl Lindegren** wrote regarding the species designation for the *Saccharomyces* strains that he developed and distributed widely for genetic studies. Many users of the stocks refer to the cultures as *Saccharomyces cerevisiae.* Because many species other than *S. cerevisiae* were incorporated into the cultures, they "should be spoken of simply as the Lindegren *Saccharomyces* Breeding Stock." [Note (KBM): these strains were the progenitors of common lab strain S288C.]

Hiroshi Akamatsu announced that the "JFCC: Catalogue of Cultures. 1962" has been published. This catalog lists 22,300 micoorganisms at 144 institutions in Japan collected over the past 60 years, re-identified over the past 10 years by a team of 40 specialists headed by Dr. Sakaguchi.

Compiled by Kyria Boundy-Mills
