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# Yeast

## A Newsletter for Persons Interested in Yeast

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# Editorial

## What's in a (double) name?

Dr JP Sampaio recently reported on current discussions within the Special Committee on Fungal Nomenclature, formed during the last International Mycological Congress, with the mandate of examining the revision of Article 59 of the International Code of Botanical Nomenclature, which concerns the dual nomenclature of fungi.

Specifically, Dr David Hawksworth proposed to redraft Art. 59 as follows:

(183) Proposal to prohibit the introduction of new formal dual nomenclature in pleomorphic fungi from January 2008

Add a new Art. 59.7:

"59.7. A separate name, proposed on or after 1 January 2008, for an anamorph associated with a pre-existing named teleomorph, or for a teleomorph associated with a pre-existing named anamorph, is illegitimate (Art. 52.1) and to be rejected. Where the earliest legitimate name is that of an anamorph, an epitype exhibiting the teleomorphic state is to be selected so that the anamorph name can be used as the name of the holomorph (see Art. 59.8)".

For more details on this proposal please refer to Taxon 53(2): 596-598.

Dr Sampaio expressed concerns with the potential impact of this proposal on asexual and extremely polyphyletic genera like *Candida*, *Cryptococcus*, or *Rhodotorula*. Several active systematists were consulted and the very strong consensus is that the dual nomenclature of fungi should be phased out. However, it was felt that Dr. Hawksworth's proposal to use anamorph names to designate holomorphs weakens the proposal. The outcome would be that a large number of species currently included in large polyphyletic anamorph genera would forever be branded with uninformative genus names. In addition, it is felt that the significance of the current articles on epitypification is generally not well understood in the community of yeast systematists.

Readers who wish to participate in this discussion should communicate with me or Dr Sampaio <**jss@fct.unl.pt**>.

MA Lachance, Editor

**I CBS Fungal Biodiversity Centre, Department of Yeast and Basidiomycete Research, Uppsalalaan 8, NL-3584CT Utrecht, The Netherlands. Communicated by Ferry Hagen <f.hagen@cbs.knaw.nl>.**

Recent publications.

1 De Barros JD, Do Nascimento SM, De Araujo FJ, Braz RD, Andrade VS, Theelen B, Boekhout T, Illnait-Zaragozi MT, Gouveia MN, Fernandes MC, Monteiro MG, Barreto de Oliveira MT In press *Kodamaea* (*Pichia*) *ohmeri* fungemia in a pediatric patient admitted in a public hospital. Med Mycol. PMID: 19466675

2 de Garcia V, Brizzio S, Russo G, Rosa CA, Boekhout T, Theelen B, Libkind D, van Broock M In press *Cryptococcus spencermartinsiae* sp. nov., a basidiomycetous yeast isolated from glacial waters and apple fruits. Int J Syst Evol Microbiol. PMID: 19656921

3 Passoth V, Andersson AC, Olstorpe M, Theelen B, Boekhout T, Schnürer J 2009 *Cryptococcus cerealis* sp. nov. a psychrophilic yeast species isolated from fermented cereals. Antonie van Leeuwenhoek 96:635-643.

4 Hagen F, Assen SV, Luijckx GJ, Boekhout T, Kampinga GA In press Activated dormant *Cryptococcus gattii* infection in a Dutch tourist who visited Vancouver Island (Canada): a molecular epidemiological approach. Med Mycol. PMID: 19824880

5 Tore O, Akcaglar S, Kazak E, Heper Y, Akalin H, Hakyemez B, Ener B, Boekhout T, Hagen F 2009 Multiple intracranial abscesses due to *Cryptococcus neoformans*: an unusual clinical feature in an immunocompetent patient and a short review of reported cases. Med Mycol 21:1-5.

6 Ma H, Hagen F, Stekel DJ, Johnston SA, Sionov E, Falk R, Polacheck I, Boekhout T, May RC 2009 The fatal fungal outbreak on Vancouver Island is characterized by enhanced intracellular parasitism driven by mitochondrial regulation. Proc Natl Acad Sci USA 106:12980-12985.

7 Meyer W, Aanensen DM, Boekhout T, Cogliati M, Diaz MR, Esposto MC, Fisher M, Gilgado F, Hagen F, Kaocharoen S, Litvintseva AP, Mitchell TG, Simwami SP, Trilles L, Viviani MA, Kwon-Chung J 2009 Consensus multi-locus sequence typing scheme for *Cryptococcus neoformans* and *Cryptococcus gattii*. Med Mycol 12:1-14.

8 Taj-Aldeen SJ, Al-Ansari N, El Shafei S, Meis JF, Curfs-Breuker I, Theelen B, Boekhout T 2009 Molecular identification and susceptibility of *Trichosporon* species isolated from clinical specimens in Qatar: isolation of *Trichosporon dohaense* Taj-Aldeen, Meis & Boekhout sp. nov. J Clin Microbiol 47:1791-1799.

9 Bovers M, Hagen F, Kuramae EE, Boekhout T 2009 Promiscuous mitochondria in *Cryptococcus gattii*. FEMS Yeast Res 9:489-503.

10 Botes A, Boekhout T, Hagen F, Vismer H, Swart J, Botha A 2009 Growth and mating of *Cryptococcus neoformans* var. *grubii* on woody debris. Microb Ecol 57:757-765.

**II Department of Soil Biology, Faculty of Soil Science, Moscow State University, Leninckie Gory, Moscow 119899, Russia. Communicated by IYu Chernov <soilyeast@mail.ru>.**

The following papers have been published recently.

1 Kachalkin AV, Glushakova AM, Yurkov AM, and Chernov IYu 2008 Characterization of yeast groupings in the phyllosphere of Sphagnum mosses. Microbiology 77:474–481.

Significant differences were revealed in the taxonomic structure of the epiphytic yeast communities formed on *Sphagnum* mosses and on the leaves of vascular plants. On mosses, low abundance of red yeasts was found (the most typical epiphytes on vascular plant leaves), along with a relatively high content and diversity of nonpigmented dimorphic basidiomycetes related to the order Leucosporidiales. The species composition of epiphytic yeasts from mosses is different from that of both forest and meadow grasses and of the parts of vascular plants submerged in the turf. The specific composition of the *Sphagnum* mosses yeast community is probably determined by the biochemical characteristics of this environment, rather than by the hydrothermal regime in the turf.

2 Glushakova AM, Chernov IYu 2009 Yeast communities dynamics in fruits of Hedge rose (*Rosa canina*). Mikologia i fitopatoligia (Mycology and Phytopathology) 43:193-199 (in Russian).

Composition of yeast communities in fruits of hedge rose (*Rosa canina* L.) was investigated during all ontogenetic periods from primordium to fruits` destruction. Yeasts were found to be numerous and diverse not only on surface of fruits but also inside. The whole number of yeasts inside fruits gradually increased during ripening and was maximal in winter before their destruction. Species composition of yeasts inside fruits and on fruits surface was similar. The dominant species were represented by *Cryptococcus albidus* and related filobasidious species, *Cystofilobasidium capitatum, Merschnikowia pulcherrima* and *Hanseniaspora guilliermondii*. The relative abundance of these species changed during fruits ripening, and each species was characterized by its own type of dynamic. The abundance of basidiomycetous yeasts was higher on fruit's surface while ascomycetous yeasts were more numerous inside ripe fruits. So the outgoing of ascomycetous yeasts inside fruits in winter is assumed to be the strategy to escape negative factors.

3 Isaeva OV, Glushakova AM, Yurkov AM, and Chernov IYu 2009 The yeast *Candida railenensis* in the fruits of English oak (*Quercus robur* L.). 78:355-359.

The cotyledons of whole intact acorns were shown to contain yeasts; their number increased sharply before acorn germination. The yeasts in the cotyledons are mainly represented by one species, *Candida railenensis*, with the number in the germinating cotyledons reaching $10^7$ CFU/g. After germination or exocarp destruction, the cotyledons were colonized by the usual epiphytic and litter yeasts *Cryptococcus albidus, Rhodotorula glutinis*, and *Cystofilobasidium capitatum*.

4 Maksimova IA, Yurkov AM, and Chernov IYu 2009 Spatial structure of epiphytic yeast communities on fruits of *Sorbus aucuparia* L. Biology Bulletin, 2009, Vol. 36, No. 6, pp. 613–618.

The subject of this research is epiphytic yeast communities formed on the surface of *Sorbus aucuparia*. The object is to make quantitative assessment of the yeast communities' differentiation of the same but distant substratum. Results of the nested ANOVA demonstrated that with increase in distances, there are increases in the variation of total number and relative abundance of the dominant yeast communities. The average similarity between groups of single fruits (Sørensen's Similarity Coefficient) regularly decreased with distance. The results demonstrate that the number and structure of separate yeast groups depend not only on ecological factors but also on proximity to other communities. Such aggregation in the distribution of the microorganisms' species caused by migration and colonial resettlement should be taken into account when analyzing their diversity in natural habitats.

5 Isaeva OV, Glushakova AM, Garbuz SA, Kachalkin AV, and Chernov IYu 2010 Endophytic yeast fungi in plant storage tissues. Biology Bulletin 37:26–34.

It was found that plant storage tissues (fleshy sugar-containing fruits, subsurface metamorphically altered plant organs (storage roots, tubers, etc.), and starch-containing seed lobes) nearly always contain yeasts that are able to actively reproduce in these tissues causing no visible damage. Within storage tissues, yeast cells were detected both in the intercellular space and inside plant cells. In the tissues of fleshy fruits, endophytic yeasts are represented by the same species as epiphytic ones; cryptococci of the order Filobasidiales and ascomycetes belonging to the genera *Hanseniaspora* and *Metschnikowia* are predominant. In subsurface plant organs, red pigmented basidiomycetous yeasts of the genus *Rhodotorula* prevail. Selective growth of representatives of one species, *Candida railenensis*, is typical of starch-containing storage tissues of seeds. The results obtained change the established notion of the distributional patterns of yeast fungi in natural habitats and suggest that internal storage tissues of plants can be considered as a new interesting model for studies of coevolving plant-microbial associations.

## III 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 2009 Anti-Tremellomycetes activity of *Cryptococcus pinus* mycocin. Mikrobiologiya 78(3):355-361.

The mycocin secreted by *Cryptococcus pinus* had molecular mass no less 15 kDa and showed fungicidal activity under acidic conditions. It was thermolabile and resistant to proteases. Sensitive to this mycocin are tremellomycetous species concentrated in the Filobasidiales and Tremellales.

2 Kulakovskaya TV, Kulakovskaya EV, Golubev WI 2009 Antifungal activities of glycolipids secreted by the yeasts. In: Fungicides: Chemistry, Environmental Impact and Health Effects (P. De Costa and P. Bezerra, eds.). Nova Science Publishers, Inc., NY. (in press).

Many yeasts secrete glycolipids. Among these compounds, sophorolipids, cellobiose lipids, and mannosylerythritols are best studied. Cellobiose lipids differ in their structures, including the number of OH-groups in fatty acid residue and number and structures of O-substituents in cellobiose residue. For example, *Cryptococcus humicola* secretes mainly 16-(tetra-O-acetyl-2-O-(3-hydroxyhexanoyl)-beta-cellobiosyloxy)-2,15-dihydrooxyhexadecanoic acid. Recently it has been found that these compounds, known as surfactants, are highly active against many species of ascomycetous and basidiomycetous fungi. They exhibit maximal activity at pH about 4.0. The effective concentrations against basidiomycetes (*Filobasidiella neoformans*) and ascomycetes (Candida spp.) are 0.03 mM and 0.1-0.4 mM, respectively. The mechanism of cellobiose lipid action on yeast cells is based on enhancement of nonspecific permeability of the cytoplasmic membrane, which results in the rapid leakage of ATP and potassium ions from the cells treated with these compounds. The broad spectrum of activity, pH and temperature stability allow one to consider cellobiose lipids as promising natural biocontrol agents of yeast and mycelial fungi.

3 TV Kulakovskaya, WI Golubev, MA Tomashevskaya, EV Kulakovskaya, AS Shashkov, AA Grachev, AS Chizhov and NE Nifantiev 2010 Production of antifungal cellobiose lipids by *Trichosporon porosum*. Mycopathologia (in press).

The yeast *Trichosporon porosum* suppresses growth of ascomycetes and basidiomycetes belonging to 52 genera. It is due to secretion of a thermostable fungicidal agent. The suppression was maximal at pH 3.5–4.0. Fungicidal preparation obtained from the culture broth was shown to be a mixture of cellobiosides

of dihydrodecane acid with different degree of acetylation of cellobiose residue. The preparation caused the death of *Candida albicans* and *Filobasidiella neoformans* cells in the concentrations of 0.2 and 0.03 mM, respectively.

4 Golubev WI, Sampaio JP 2010 New filobasidiaceous yeasts found in the phylloplane of a fern. J Gen Appl Microbiol (in press).

Nitrate-positive strains of anamorphic yeasts representing the genus *Cryptococcus* were isolated on fern infusion agar from *Athyrium filix-femina*. Phylogenetic analyses of the D1/D2 domain of the LSU rRNA and of the ITS region placed them in *Cylindricus* clade in the Filobasidiales. Morphological and physiological characteristics, as well as mycocinotyping and molecular analysis, show a close affinity between strains. Subsequent comparative studies of new isolates revealed that they were not conspecific with any other known *Cryptococcus* species, and the cultures represented an undescribed species with two varieties, for which the names *Cryptococcus filicatus* var. *filicatus* (type strain VKM Y-2954 = CBS 10874) and *Cryptococcus filicatus* var. *pelliculosus* (type strain VKM Y-2955 = CBS 10875) are proposed.

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**IV Department of Biology, Faculty of Medicine Masaryk University, Kamenice 5, A6, 62500 Brno, Czech Republic. Communicated by Marie Kopecká <mkopecka@med.muni.cz>.**

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Recently published papers.

1 Kopecká M, Gabriel M 2009 Microtubules and actin cytoskeleton of potentially pathogenic basidiomycetous yeast as targets for antifungals. Chemotherapy 55:278-286.

**Background:** The cytoskeleton was investigated as a potential target for the inhibition of cell division in *Fellomyces fuzhouensis* CBS 8243 related to *Cryptococcus neoformans*. **Methods:** Vincristine, vinblastine, paclitaxel, methyl benzimidazole-2-yl carbamate (BCM), thiabendazole, cytochalasins A, B and D and latrunculin A were added to yeast extract peptone dextrose medium containing cells, investigated by phase contrast and fluorescence microscopy, counted in a Bürker chamber and absorbance was measured. *Results:* Vincristine, vinblastine, paclitaxel, cytochalasins A, B and D transiently blocked proliferation. BCM disrupted microtubules and inhibited mitosis, but F-actin patches and cables persisted and neck-less conidia appeared without stalks. Latrunculin disrupted F-actin, cells became spherical, and stalks and necks degenerated; microtubules persisted, but mitosis, cytokinesis and conidiogenesis were blocked. The combined application of latrunculin and BCM disrupted F-actin and microtubules, and inhibited cells became spherical and did not divide. **Conclusions:** Microtubules and F-actin are effective targets for permanent inhibition of nuclear and cell division and conidiogenesis by BCM and latrunculin A.

2 Yamaguchi M, Kopecká M 2009 Ultrastructural disorder of the secretory pathway in temperature-sensitive actin mutants of *Saccharomyces cerevisiae*. J Electron Microscopy doi: 10.1093/jmicro/dfp050

Phenotypes of the two temperature-sensitive actin mutants of *Saccharomyces cerevisiae act1-1* and *act1-2* at permissive, restrictive and semirestrictive temperatures were studied by freeze fracture and thin section electron microscopy, and fluorescent microscopy. In contrast to secretory mutants where accumulations of either secretory vesicles, Golgi apparatus, or endoplasmic reticulum were reported, *act1-1* and *act1-2* mutants revealed accumulation of all the three components, even at permissive temperature. However, more distinct accumulation of secretory organelles was evident during cultivation at the sub-restrictive temperature of 30°C. At the restrictive temperature of 37°C, many cells died, and their empty cell walls remained. Some of the few living cells showed features of apoptosis. From the present study, actin cables are concluded to be necessary for (i) correct spatial positioning and orientation of secretary pathway to the bud and septum, and (ii) vectorial movement of vesicles of the secretory pathway along the actin cables to the bud and septum.

3 Kopecká M, Svoboda A - In preparation - Ten years of activity of the Department of Biology, Faculty of Medicine, Masaryk University, Brno (chapter for monograph on 50 Years of Activity in Czech and Slovak Yeast Research, 1999-2009.

## V Wouter J. Middelhoven. Retired from Laboratory of Microbiology, Wageningen University, The Netherlands <woutermid@online.nl>.

In December 2009 a book entitled "Yeast Biotechnology: Diversity and Applications" will appear at Springer. Its editors are Kunze and Satyanaryana. I contributed Chapter 7, entitled "Assimilation of unusual carbon compounds". It deals with most of my research on non-*Saccharomyces* yeasts over the last thirty years and related work by other authors. Reprints are available upon request.

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

We are grateful to Eui-Sung Choi (Daejeon) and Isabelle Masneuf-Pomarède (Bordeaux) for fruitful collaboration during our stay in their labs in July and September 2009.

The following are papers for 2009 or in press.

1 Naumov GI 2009 New wine yeasts: on the publication of the book Modern Preparative Forms of Yeasts for Wine-Making by NN Martynenko, Moscow: Rossel'khozizdat 2006. Microbiology (Moscow) 78(4):520-521.

2 Naumov GI, Naumova ES, Masneuf-Pomarède I 2009 Genetic identification of new biological species *Saccharomyces arboricolus* Wang et Bai. Antonie van Leeuwenhoek (in press).

Direct genetic testing for hybrid sterility unambiguously showed that the newly described yeast *S. arboricolus* Wang et Bai is reproductively isolated from *S. cerevisiae*, *S. bayanus*, *S. cariocanus*, *S. kudriavzevii*, *S. mikatae* and *S. paradoxus* and, therefore, represents a new biological species of the genus *Saccharomyces*. Combined phylogenetic analysis of the rDNA repeat sequences (18S, 26S, ITS), nuclear *ACT1* and mitochondrial *ATP9* genes revealed that *S.arboricolus*, along with *S. kudriavzevii* and *S. bayanus*, is distantly related to other four biological species.

3 Naumova ES, Naumov GI, Barrio E, Querol A 2009 Mitochondrial DNA polymorphism of the yeast *Saccharomyces bayanus* var. *uvarum*. Microbiology (Moscow) (submitted).

Genetic relationships among forty-one strains of *Saccharomyces bayanus* var. *uvarum* isolated in different wine regions of Europe and four wild isolates were investigated by restriction analysis (RFLP) of mitochondrial DNA (mtDNA) with four restriction endonucleases, *Alu*I, *Dde*I, *Hinf*I and *Rsa*I. No clear correlation between origin and source of isolation of *S. bayanus* var. *uvarum* strains and their mtDNA restriction profiles was found. On the whole, the mtDNA of *S. bayanus* var. *uvarum* is much less polymorphic than that of *S. cerevisiae*. This observation is in good agreement with results obtained by electrophoretic karyotyping. Unlike wine *S. cerevisiae*, strains of *S. bayanus* var. *uvarum* display a low level of chromosome length polymorphism.

4 Naumov GI, Naumova ES, Choi E-S 2009 Natural and industrially important peculiarities of sugars utilization in the yeast *Kluyveromyces marxianus*. Biotechnology (Moscow) (submitted).

5 Naumova ES, Naumov GI, Legras JL, Le Jeune C, Aigle M, Masneuf-Pomarède I 2009 Identification of double and triple hybrids between *S. cerevisiae*, *S. kudriavzevii* and *S. bayanus* var. *uvarum* in wine-making. 27th International Specialized Symposium on Yeasts (ISSY27), August 26-29, 2009, Paris, France, p 104.

6 Naumova ES, Ivannikova YuV, Hayes A, Oliver SG, Naumov GI 2009 Comparative genomics of natural interspecific *Saccharomyces* hybrids. 24th International Conference on Yeast Genetics and Molecular Biology, Manchester, UK, 19-24 July 2009. Yeast, 26(S):80.

## VII Section Applied Microbiology, Universita Degli Studi di Perugia, Perugia 6121, Italy. Communicated by Pietro Buzzini <pbuzzini@unipg.it> .

Recent publications.

1 Del Bove M, Lattanzi M, Rellini, P, Pelliccia C, Fatichenti F and Cardinali G 2009 Comparison of molecular and metabolomic methods as characterization tools of *Debaryomyces hansenii* cheese isolates. Food Microbiol 26: 453-9.

2 Rellini, P, Roscini, L, Fatichenti, F, Morini, P. and Cardinali, G 2009 Direct spectroscopic (FTIR) detection of intraspecific binary contaminations in yeast cultures. FEMS Yeast Res 9:460-7.

3 Ganter PF, Cardinali, G, and Boundy-Mills K 2009 *Pichia insulana* sp. nov., a cactophilic yeast from the Caribbean. Int J Syst Evol Microbiol (*in press*)

4 Romani A, Vignolini P, Isolani L, Tombelli S, Heimler D, Turchetti B. and Buzzini P 2008 *In vitro* radical scavenging and anti-yeast activity of extracts from leaves of *Aloe* spp. growing in Congo. Nat Prod Comm 3:2061-4.

5 Goretti M, Turchetti B, Buratta M, Branda E, Corazzi L, Vaughan A and Buzzini P 2009 *In vitro* antimycotic activity of a *Williopsis saturnus* killer protein against food spoilage yeasts. Int J Food Microbiol 131, 178-82.

6 Bravi E, Perretti G, Buzzini P, Della Sera R. and Fantozzi P 2009 Technological steps and yeast biomass as factors affecting lipid content of beer along the brewing process. J Agric Food Chem 57:6279-84.

7 Rossi M, Buzzini P, Cordisco L, Amaretti A, Sala M, Raimondi S, Ponzoni C. Pagnoni UM, and Matteuzzi D 2009 Growth, lipid accumulation, and fatty acids composition in obligate psychrophilic, facultative psychrophilic and mesophilic yeasts. FEMS Microbiol Ecol 69:363-72.

8 Goretti M, Ponzoni C, Caselli E, Marchegiani E, Cramarossa MR, Turchetti B, Forti L, and Buzzini, P 2009 Biotransformation of electron-poor alkenes by yeasts: asymmetric reduction of *(4S)*-(+)-carvone by yeast enoate reductases. Enzyme Microb Technol 45:463-8.

VIII Department of Cell and Organism Biology, Lund University, SE-22362 Lund, Sweden. Communicated by Jure Piškur <Jure.Piskur@cob.lu.se>.

Recent publication.

1 Poláková S, Blume C, Zárate JA, Mentel M, Jørck-Ramberg D, Stenderup J, Piškur J 2009 Formation of new chromosomes as a virulence mechanism in yeast *Candida glabrata*. Proc Natl Acad Sci USA 106:2688–2693.

In eukaryotes, the number and rough organization of chromosomes is well preserved within isolates of the same species. Novel chromosomes and loss of chromosomes are infrequent and usually associated with pathological events. Here, we analyzed 40 pathogenic isolates of a haploid and asexual yeast, *Candida glabrata*, for their genome structure and stability. This organism has recently become the second most prevalent yeast pathogen in humans. Although the gene sequences were well conserved among different strains, their chromosome structures differed drastically. The most frequent events reshaping chromosomes were translocations of chromosomal arms. However, also larger segmental duplications were frequent and occasionally we observed novel chromosomes. Apparently, this yeast can generate a new chromosome by duplication of chromosome segments carrying a centromere and subsequently adding novel telomeric ends. We show that the observed genome plasticity is connected with antifungal drug resistance and it is likely an advantage in the human body, where environmental conditions fluctuate a lot.

**IX Institut für Angewandte Mikrobiologie, Universität für Bodenkultur, Vienna. Communicated by Hansjörg Prillinger <hansjoerg.prillinger@boku.ac.at>.**

The following is a manuscript sent to International Journal Systematic and Evolutionary Microbiology.

1 Wuczkowski M, Passoth V, Turchetti B, Andersson AC, Olstorpe M, Laitila A, Theelen B, van Broock M, Buzzini P, Prillinger H, Sterflinger K, Schnürer J, Boekhout T, Libkind D *Holtermanniella takashimae* sp. nov., *Holtermanniella* gen. nov. and the new order Holtermanniales accommodating Tremellomycetous yeasts of the *Holtermannia* clade.

A novel genus *Holtermanniella* is proposed here to accommodate four *Cryptococcus* species closely related to *Holtermannia corniformis* that constitutes the *Holtermannia* clade (Basidiomycota, Agaricomycotina). Thus, four novel combinations are proposed: *H. nyarrowii*, *H. festucosa*, *H. mycelialis*, and *H. wattica*. Both *Holtermannia* and *Holtermanniella* genera are included in the new order *Holtermanniales*. In addition, nine strains of a new anamorphic yeast species were isolated from different habitats in Europe and South America (Patagonia, Argentina). Analysis of the sequences of the D1/D2 region of their large subunit ribosomal DNAs showed that the new species is phylogenetically placed within de *Holtermannia* clade of the Tremellomycetes (Agaricomycotina, Basidiomycota). PCR-fingerprinting and sequencing of ITS1-5.8S-ITS2 showed genetic intraspecific variability among the strains: three groups were formed which did not correlate with geographic origin or substrate. This new species is described as *Holtermanniella takashimae* sp. nov., the type strain has been deposited under the code CBS 11174T (=HB 982T).

**X GGStewart Associates, Alcohol Technology Consultants, Brook House, Caerphilly Business Park, Van Road, Caerphilly, Wales, CF83 3GS. Communicated by Graham Stewart <mail@ggstewartassociates.co.uk>.**

The following papers, articles and chapters have recently been published or are in press.

1 Chlup PH, Bernard D, and Stewart GG 2008 Disc stack centrifuge operating parameters and their impact on yeast physiology. J Inst Brewing 114:45-61.

2 Bryce JH, Piggott JR, and Stewart GG 2008 Distilled Spirits Production, Technology and Innovation. Nottingham University Press, Nottingham.

3 Stewart GG 2008 Esters – the most important group of flavour-active compounds in alcoholic beverages. In Distilled Spirits. Production, Technology and Innovation. Bryce JH, Piggott JR and Stewart GG (eds.) Notttingham University Press, Nottingham, UK. pp. 243 – 250.

4 Stewart GG, Leiper KA, and Meidl M 2008 Bioethanol – The current situation. In: Proc. 30th Convention of the Institute of Brewing and Distilling, Asia Pacific Section, Paper 10.

5 Stewart GG 2009 The Horace Brown Medal Lecture – Forty years of brewing research. J Inst Brewing 115:3-29.

6 Stewart GG 2009 High gravity brewing and distilling – Past experiences and future prospects. J Amer Soc Brew Chemists 67:000-000.

7 Hill AE and Stewart GG 2009 A brief overview of brewer's yeast. Brewer & Distiller Internat 5(6):13-15.

8 Lekkas C, Hill AE, Taidi B, Hodgson J, and Stewart GG 2009 The role of small peptides in brewing fermentations. J Inst Brewing, 115:134-139.

9 Stewart G and Murray J 2009 A selective history of high gravity and high alcohol beers. Brewers' Guardian, 138:000-000.

10 Stewart GG 2009 High gravity brewing and distilling – Past experiences and future prospects. J. Amer Soc Brew Chemists 68:000-000.

11 Stewart GG and Priest FG 2010 Beer shelf-life and stabiliy In Food and Beverage Shelf Life and Stability. Kilcast D and Subraman P (eds). Woodhead Publishing Limited pp. 000-000.

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**XI Food Microbiology Laboratory, Sikkim Government College, Sikkim University, Tadong 737 102, India. Communicated by Jyoti Prakash Tamang <jyoti_tamang@hotmail.com>.**

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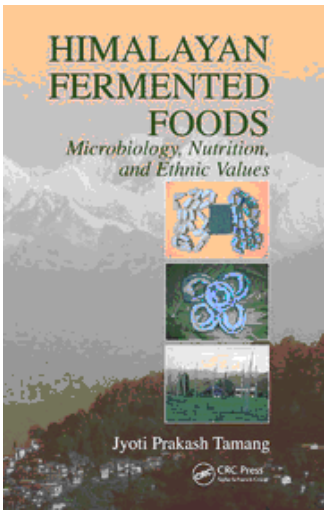
The following are recent publications related to fermented foods and beverages:




1 Tamang JP 2009 Himalayan Fermented Foods: Microbiology, Nutrition, and Ethnic Values. CRC Press, Taylor & Francis, USA, 295 pp. ISBN: 9781420093247; ISBN 10: 142009324X. Price: $149.95. Cat. #: 9324X.\

**www.crcpress.com/product/isbn/9781420093247**

**www.taylorandfrancis.com**

The magnificent Himalayan Mountains, the highest in the world and home to the famed Mount Everest and K2, are also imbued with a rich diversity of ethnic fermented foods. Dr. Jyoti Prakash Tamang, one of the leading authorities on food microbiology, has studied Himalayan fermented foods and beverages for the last twenty-two years. His comprehensive volume, Himalayan Fermented Foods: Microbiology, Nutrition, and Ethnic Values catalogs the great variety of common as well as lesser-known fermented foods and beverages in the Himalayan region. This volume begins with an introduction to the Himalayas and the Himalayan food culture. Using a consistent format throughout the book, Dr. Tamang discusses fermented vegetables, legumes, milk, cereals, fish and meat products, and alcoholic beverages. Each chapter

explores indigenous knowledge of preparation, culinary practices, and microorganisms for each product. Additional information on microbiology and nutritive value supplements each section, and discussions on ethnic food history and values as well as future prospects for these foods complete the coverage. Dr. Tamang demonstrates that fermentation remains an effective, inexpensive method for extending the shelf life of foods and increasing their nutritional content through probiotic function, and therefore remains a valuable practice for developing countries and rural communities with limited facilities.

2 Tamang JP and Fleet GH 2009 Yeasts Diversity in Fermented Foods and Beverages. In: *Yeasts Biotechnology: Diversity and Applications* (Eds: Satyanarayana, T. and Kunze, G.). Springer, New York, pp. 169- 198.

People across the world have learnt to culture and use the essential microorganisms for production of fermented foods and alcoholic beverages. A fermented food is produced either spontaneously or by adding mixed/pure starter culture(s). Yeasts are among the essential functional microorganisms encountered in many fermented foods, and are commercially used in production of baker's yeast, breads, wine, beer, cheese, etc. In Asia, moulds are predominant followed by amylolytic and alcohol-producing yeasts in the fermentation processes, whereas in Africa, Europe, Australia and America, fermented products are prepared exclusively using bacteria or bacteria-yeasts mixed cultures. This chapter would focus on the varieties of fermented foods and alcoholic beverages produced by yeasts, their microbiology and role in food fermentation, widely used commercial starters (pilot production, molecular aspects), production technology of some common commercial fermented foods and alcoholic beverages, toxicity and food safety using yeasts cultures and socio-economy. It is concluded that in fermentation of any substrate, *Saccharomyces* ferments sugar, produces secondary metabolites; inhibits growth of mycotoxin-producing moulds and has several enzymatic activities such as lipolytic, proteolytic, pectinolytic, glycosidasic and urease activities. *Debaryomyces* contributes in sugar fermentation, increases pH of the substrates, and produces growth factors for bacteria. *Hanseniaspora* and *Candida* also contribute in sugar fermentation, production of secondary metabolites, and enzymatic activities. *Yarrowia lipolytica* also plays role in sugar fermentation, lipolytic, proteolytic and urease activities and reduction of fat rancidity in the product.

## XII VTT Technical Research Centre of Finland, P.O.Box 1000, FI-02044 VTT, Finland. Communicated by John Londesborough <john.londesborough@vtt.fi>.

Publications since our last communication include the followng.

1 Jouhten P, Rintala E, Huuskonen A, Tamminen A, Toivari M, Wiebe M, Ruohonen L, Penttilä M, Maaheimo H 2008 Oxygen dependence of metabolic fluxes and energy generation of *Saccharomyces cerevisiae* CEN.PK113-1A. BMC Syst Biol 2:60

**BACKGROUND**: The yeast *Saccharomyces cerevisiae* is able to adjust to external oxygen availability by utilizing both respirative and fermentative metabolic modes. Adjusting the metabolic mode involves alteration of the intracellular metabolic fluxes that are determined by the cell's multilevel regulatory network. Oxygen is a major determinant of the physiology of *S. cerevisiae* but understanding of the oxygen dependence of intracellular flux distributions is still scarce. **RESULTS**: Metabolic flux distributions of *S. cerevisiae* CEN.PK113-1A growing in glucose-limited chemostat cultures at a dilution rate of 0.1 $h^{-1}$ with 20.9%, 2.8%, 1.0%, 0.5% or 0.0% $O_2$ in the inlet gas were quantified by $^{13}$C-MFA. Metabolic flux ratios from fractional [U-13C]glucose labelling experiments were used to solve the underdetermined MFA system of central carbon metabolism of *S. cerevisiae*. While ethanol production was observed already in 2.8% oxygen, only minor differences in the flux distribution were observed, compared to fully aerobic conditions. However, in 1.0% and 0.5% oxygen the respiratory rate was severely restricted, resulting in progressively reduced fluxes through the TCA cycle and the direction of major fluxes to the fermentative pathway. A redistribution of fluxes was observed in all branching points of central carbon metabolism. Yet only when oxygen provision was reduced to 0.5%, was the biomass yield exceeded by the yields of ethanol and $CO_2$.

Respirative ATP generation provided 59% of the ATP demand in fully aerobic conditions and still a substantial 25% in 0.5% oxygenation. An extensive redistribution of fluxes was observed in anaerobic conditions compared to all the aerobic conditions. Positive correlation between the transcriptional levels of metabolic enzymes and the corresponding fluxes in the different oxygenation conditions was found only in the respirative pathway. **CONCLUSION**: 13C-constrained MFA enabled quantitative determination of intracellular fluxes in conditions of different redox challenges without including redox cofactors in metabolite mass balances. A redistribution of fluxes was observed not only for respirative, respiro-fermentative and fermentative metabolisms, but also for cells grown with 2.8%, 1.0% and 0.5% oxygen. Although the cellular metabolism was respiro-fermentative in each of these low oxygen conditions, the actual amount of oxygen available resulted in different contributions through respirative and fermentative pathways.

2 Rintala E, Toivari M, Pitkänen JP, Wiebe MG, Ruohonen L, Penttilä M 2009 Low oxygen levels as a trigger for enhancement of respiratory metabolism in *Saccharomyces cerevisiae* BMC Genomics 10:461.

**BACKGROUND**: The industrially important yeast *Saccharomyces cerevisiae* is able to grow both in the presence and absence of oxygen. However, the regulation of its metabolism in conditions of intermediate oxygen availability is not well characterised. We assessed the effect of oxygen provision on the transcriptome and proteome of *S. cerevisiae* in glucose-limited chemostat cultivations in anaerobic and aerobic conditions, and with three intermediate (0.5, 1.0 and 2.8% oxygen) levels of oxygen in the feed gas. **RESULTS**: The main differences in the transcriptome were observed in the comparison of fully aerobic, intermediate oxygen and anaerobic conditions, while the transcriptome was generally unchanged in conditions receiving different intermediate levels (0.5, 1.0 or 2.8% $O_2$) of oxygen in the feed gas. Comparison of the transcriptome and proteome data suggested post-transcriptional regulation was important, especially in 0.5% oxygen. In the conditions of intermediate oxygen, the genes encoding enzymes of the respiratory pathway were more highly expressed than in either aerobic or anaerobic conditions. A similar trend was also seen in the proteome and in enzyme activities of the TCA cycle. Further, genes encoding proteins of the mitochondrial translation machinery were present at higher levels in all oxygen-limited and anaerobic conditions, compared to fully aerobic conditions. **CONCLUSION**: Global up-regulation of genes encoding components of the respiratory pathway under conditions of intermediate oxygen suggested a regulatory mechanism to control these genes as a response to the need of more efficient energy production. Further, cells grown in three different intermediate oxygen levels were highly similar at the level of transcription, while they differed at the proteome level, suggesting post-transcriptional mechanisms leading to distinct physiological modes of respiro-fermentative metabolism.

3 Toivari MH, Maaheimo H, Penttilä M, Ruohonen L 2009 Enhancing the flux of D-glucose to the pentose phosphate pathway in Saccharomyces cerevisiae for the production of D-ribose and ribitol. Appl. Microbiol. Biotechnol DOI 10.1007/s00253-009-2184-4

Phosphoglucose isomerase-deficient (pgi1) strains of *Saccharomyces cerevisiae* were studied for the production of D-ribose and ribitol from D-glucose via the intermediates of the pentose phosphate pathway. Overexpression of the genes coding for NAD(+)-specific glutamate dehydrogenase (GDH2) of S. cerevisiae or NADPH-utilising glyceraldehyde-3-phosphate dehydrogenase (gapB) of *Bacillus subtilis* enabled growth of the pgi1 mutant strains on D-glucose. Overexpression of the gene encoding sugar phosphate phosphatase (DOG1) of S. cerevisiae was needed for the production of D-ribose and ribitol; however, it reduced the growth of the pgi1 strains expressing GDH2 or gapB in the presence of higher D-glucose concentrations. The CEN.PK2-1D laboratory strain expressing both gapB and DOG1 produced approximately 0.4 g $l^{-1}$ of D-ribose and ribitol when grown on 20 g $l^{-1}$ (w/v) D-fructose with 4 g $l^{-1}$ (w/v) D-glucose. Nuclear magnetic resonance measurements of the cells grown with $^{13}$C-labelled D-glucose showed that about 60% of the D-ribose produced was derived from D-glucose. Strains deficient in both phosphoglucose isomerase and transketolase activities, and expressing DOG1 and GDH2 tolerated only low D-glucose concentrations ($\leq$2 g $l^{-1}$ (w/v)), but produced 1 g $l^{-1}$ (w/v) D-ribose and ribitol when grown on 20 g $l^{-1}$ (w/v) D-fructose with 2 g $l^{-1}$ (w/v) D-glucose.

4 Vidgren V, Huuskonen A, Virtanen H, Ruohonen L and Londesborough J 2009 Improved fermentation performance of a lager yeast after repair of its *AGT1* maltose and maltotriose transporter genes. Appl Environ Microbiol 75:2333-2345

The use of more concentrated, so-called high gravity and very high gravity (VHG) brewer's worts for the manufacture of beer has economic and environmental advantages. However, many current strains of brewer's yeasts ferment VHG worts slowly and incompletely, leaving undesirably large amounts of maltose and, especially, maltotriose in the final beers. α-Glucosides are transported into *Saccharomyces* yeasts by several transporters, including Agt1, which is a good carrier of both maltose and maltotriose. The *AGT1* genes of brewer's ale strains encode functional transporters, but the *AGT1* genes of studied lager strains contain a premature stop codon and do not encode functional transporters. In the present work, one or more copies of the *AGT1* gene of a lager strain were repaired, by using DNA sequence from an ale strain, and put under the control of a constitutive promoter. Compared to the untransformed strain, the transformants with repaired *AGT1* had higher maltose transport activity, especially after growth on glucose (which represses endogenous α-glucoside transporter genes), and higher ratios of maltotriose transport activity to maltose transport activity. They fermented VHG (24°P) wort faster and more completely, producing beers containing more ethanol and less residual maltose and maltotriose. The growth and sedimentation behaviours of the transformants were similar to those of the untransformed strain, as were the profiles of yeast-derived volatile aroma compounds in the beers.

5 Wiebe MG, Rintala E, Tamminen A, Simolin H, Salusjärvi L, Toivari M, Kokkonen JT, Kiuru J, Ketola RA, Jouhten P, Huuskonen A, Maaheimo H, Ruohonen L, Penttilä M 2008 Central carbon metabolism of *Saccharomyces cerevisiae* in anaerobic, oxygen-limited and fully aerobic steady-state conditions and following a shift to anaerobic conditions. FEMS Yeast Research. 8:140-154.

*Saccharomyces cerevisiae* CEN.PK113-1A was grown in glucose-limited chemostat culture with 0%, 0.5%, 1.0%, 2.8% or 20.9% $O_2$ in the inlet gas ($D$ = 0.10 $h^{-1}$, pH 5, 30°C) to determine the effects of oxygen on 17 metabolites and 69 genes related to central carbon metabolism. The concentrations of tricarboxylic acid cycle (TCA) metabolites and all glycolytic metabolites except 2-phosphoglycerate + 3-phosphoglycerate and phosphoenolpyruvate were higher in anaerobic than in fully aerobic conditions. Provision of only 0.5–1% $O_2$ reduced the concentrations of most metabolites, as compared with anaerobic conditions. Transcription of most genes analyzed was reduced in 0%, 0.5% or 1.0% $O_2$ relative to cells grown in 2.8% or 20.9% $O_2$. Ethanol production was observed with 2.8% or less $O_2$. After steady-state analysis in defined oxygen concentrations, the conditions were switched from aerobic to anaerobic. Metabolite and transcript levels were monitored for up to 96 h after the transition, and this showed that more than 30 h was required for the cells to fully adapt to anaerobiosis. Levels of metabolites of upper glycolysis and the TCA cycle increased following the transition to anaerobic conditions, whereas those of metabolites of lower glycolysis generally decreased. Gene regulation was more complex, with some genes showing transient upregulation or downregulation during the adaptation to anaerobic conditions.

The following thesis has been successfully defended:

6 Laura Salusjärvi 2008 Transcriptome and proteome analysis of xylose-metabolising *Saccharomyces cerevisiae*. Doctoral thesis, University of Helsinki.

## XIII 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 paper was recently published.


1 Gadanho M and Sampaio JP 2009 *Cryptococcus ibericus* sp. nov., *Cryptococcus aciditolerans* sp. nov. and *Cryptococcus metallitolerans* sp. nov., a new ecoclade of anamorphic basidiomycetous yeast species from an extreme environment associated with acid rock drainage in São Domingos pyrite mine, Portugal. Int J Syst Evol Microbiol 59:2375-2379.

2 Hittinger CT, Gonçalves P, Sampaio JP, Dover J, Johnston M and Rokas A Remarkably ancient balanced polymorphisms in a multi-locus gene network. Nature (in press).


Local adaptations within species are often governed by several interacting genes scattered throughout the genome. Single-locus models of natural selection cannot adequately explain the maintenance of such complex variation because recombination breaks apart co-adapted alleles. Here, we report a novel type of multi-locus genetic variation that has been maintained within a species over a vast period of time. The galactose (*GAL*) utilization gene network of the brewer's yeast relative *Saccharomyces kudriavzevii* exists in two very different states: a functional gene network in Portuguese strains and, in Japanese strains, a non-functional gene network comprised of pseudogenes allelic to their functional counterparts. To investigate the origin and maintenance of this variation, we determined the genome sequences of all 18 available *S. kudriavzevii* strains. Surprisingly, none of the functional *GAL* genes in the Portuguese strains were acquired from other species. Rather, the degree of neutral site divergence between these strains suggests that the *GAL* gene network has been maintained in these two very different states for nearly the entire history of the species, despite more recent gene flow throughout the rest of the genome. Conditional fitness assays indicate that inactivation of the *GAL3* and *GAL80* regulatory genes played key roles in the origin and long-term maintenance of the two gene network states. This striking example of a balanced unlinked gene network polymorphism introduces a remarkable type of intraspecific variation that may be widespread.

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

### Essay: GenBank and the boundaries of yeast ubiquity

Under completely different circumstances, I have in recent years come across three extraordinary cases where yeast sequences deposited in GenBank have emerged under the most unexpected headings, enough to suggest extreme cases of horizontal evolution. However, a simpler explanation may have to do with the inconspicuous nature of symbiotic yeasts and the resulting lack of awareness of their existence among the non-initiated.

GenBank accession AF035675 was reported in 1997 to be the ITS/5.8S sequence of *Lacazia loboi*, a fungus belonging to the mitosporic Onygenales and suspected to cause a skin infection in the bottlenose dolphin (Haubold et al. 1998 J med Mycol 36:263-267). A few years after deposition, this sequence was the only one to give a high degree of identity with my query sequence, amplified from the type culture of *Candida zeylanoides*. With the subsequent increase in depositions for yeast ITS/5.8S sequences, it became evident that the authors had indeed amplified the DNA of *C. zeylanoides*, which is apparently associated with bottlenose dolphins (see accession number AB278159 deposited by Yarita and colleagues). The accession labeled *Lacazia loboi* remains unchanged at this time.

In the process of depositing ITS-D1/D2 rDNA sequence FJ744598 for an isolate identified morphologically as *Aureobasidium pullulans*, I queried the database. Among the many deposits giving a significant match were several entries labeled, as expected, *Aureobasidium pullulans*. More interestingly, one entry was labelled "*Zea mays*". At the time, I attributed this to contamination, by the yeast-like fungus, of material used to extract corn DNA. A more recent query indicated that close relatives of *A. pullulans* may in fact be corn endophytes. When sequence FJ744598 is queried with a filter limiting the results to

the taxon *Zea*, a surprisingly long list of matches is obtained that includes deposits purported to represent maize genomic DNA sequences. The possibility that endophytic fungi may act as a source of corn transposable elements is nothing short of bewildering and worth examining in more detail. Alternatively, endophyte DNA may be mixed with the material used in corn genome studies.

My third encounter of the unexpected kind involved the finding of a yeast-like D1/D2 sequence inside an accession annotated as a large rDNA fragment from a nematode. The originating publication (Feldman & Bowman 2007 Lab Animal 36:43-50) featured a phylogenetic tree of nematodes found in the guts of various laboratory animals. Among these was a rabbit commensal called *Passalurus ambiguus*, which sat at the end of a particularly long branch, raising the suspicion of abundant autapomorphies in the sequence used for analysis. A bit of detective work found the autapomorphic part of the sequence to exhibit 95% identity with GenBank accession EF464552, deposited by Kurtzman and Robnett for *Cyniclomyces guttulatus*, which of course is also a rabbit commensal. The sequence is a typical yeast sequence and has no significant identity with any other nematode sequence. The nematodologists had obtained their material by amplification of DNA from washed nematodes. Two overlapping fragments were cloned, sequenced, and assembled. The construct was ostensibly a chimera combining nematode SSU rRNA gene sequences with yeast LSU rRNA gene sequence.

Caveat emptor.

The following paper, whose abstract appeared in the June issue, is now in print.

1 Wardlaw AM, Berkers TE, Man KC and Lachance MA 2009 Population structure of two beetle-associated yeasts: comparison of a New World asexual and an endemic Nearctic sexual species in the *Metschnikowia* clade. Antonie van Leeuwenhoek 96:1-15.

The following seminar was given at the Estación Biológica de Doñana, Sevilla, Spain. I thank Dr. Carlos Herrera and his research team for the kind hospitality provided during my recent visit.

2 Lachance MA Yeasts, flowers, and insects: at the intersection of three kingdoms.

The following paper was accepted recently.

3 Lachance MA, Dobson J, Wijayanayaka DN, Smith AME In press The use of parsimony network analysis for the formal delineation of phylogenetic species of yeasts: *Candida apicola*, Candi*da azyma*, and *Candida parazyma* sp. nov., cosmopolitan yeasts associated with floricolous insects. Antonie van Leeuwenhoek.

Parsimony network analysis of rDNA sequences was used to delimit phylogenetic species of yeasts in an objective, formal manner. Many strains assigned to *Candida apicola* (*Starmerella* clade), when compared to the type, fell outside the inclusion limits proposed by Kurtzman and Robnett (1998) based on a pair-wise comparison of the large subunit rRNA gene D1/D2 domains. However, when these sequences were analyzed jointly with ITS rDNA sequences by parsimony network analysis, 28 of the 30 strains formed a cohesive set. Two strains, MUCL 45721 and CBS 4353, were excluded from the species, but there was no evident justification to subdivide the rest. A similar analysis of 81 isolates originally assigned to *Candida azyma* (*Wickerhamiella* clade) yielded dramatically different results, giving rise to six independent networks corresponding to *Candida azyma* sensu stricto (18 strains), *Candida azymoides* (2 strains), a pair of isolates from Australian hibiscus flowers, a single isolate from the same substrate, a single isolate from Malaysian bertam palm nectar, and 57 isolates that are assigned to the new species *Candida parazyma* (type = UWOPS 91-652.1$^T$ = CBS 11563$^T$ = NRRL Y-48669$^T$). The strains retained in *C. azyma* sensu stricto differed from one another by up to four substitutions in their D1/D2 sequences, but their polymorphism at the level of the ITS was considerable and suggested a history of divergence resulting from dispersal. Strains of *C. parazyma* fell into seven variant haplotypes based on sequences of the rDNA ITS and D1/D2 regions. The most abundant haplotype occurred across the global range of the species. Others were either endemic to Belize, Costa Rica, Rarotonga, or Tennessee, suggestive of vicariance, or occurred across remote localities, offering partial support to the notion of rapid dispersal.

## XV Geobotany, Faculty of Biology and Biotechnology, Ruhr-University Bochum, Universitätsstraße 150, 44780 Bochum, Germany - http://www.ruhr-uni-bochum.de/geobot/en/ - Communicated by Dominik Begerow <dominik.begerow@rub.de> and Andrey Yurkov <andrey.yurkov@rub.de>.

Recent publications.

1 Bauer R, Metzler B, Begerow D & Oberwinkler F 2009 *Cystobasidiopsis nirenbergiae*, a new agaricostilbomycete (Pucciniomycotina). Mycol Rese 113(9):960-966.

A new genus, *Cystobasidiopsis*, and a new species, *Cystobasidiopsis nirenbergiae*, are described for a fungus isolated from an arable loess soil in Ahlum near Braunschweig, Niedersachsen, Germany. An integrated analysis of morphological, ecological, ultrastructural and molecular data indicates that the new species belongs to the *Chionosphaeraceae* within the *Agaricostilbales*. Relevant characteristics of the new species are discussed and compared with those of related taxa.

2 Maksimova IA, Yurkov AM, & Chernov IYu 2009 Spatial structure of epiphytic yeast communities on fruits of *Sorbus aucuparia* L. Biol Bull 36(6):613-618.

3 Isaeva OV, Glushakova AM, Yurkov AM & Chernov IYu 2009 The yeast *Candida railenensis* in the fruits of English oak (*Quercus robur* L.). Microbiology 78 (3):355-359.

Our studies aimed at characterising yeast communities in soils as part of the German biodiversity exploratories program (www.biodiversity-exploratories.de ) resulted in the isolation of several species which are new to science. Descriptions of two novel ascomycetes have been accepted by Fungal Planet (www.fungalplanet.org):

*Clavispora reshetovae* Yurkov, Schäfer et Begerow, sp. nov. ex-type HEG-9-2 = CBS 11556; GenBank FN428961 (D1/D2 domain of 26S rRNA gene); MycoBank MB 515101.

*Barnettozyma vustinii* Yurkov, Schäfer, et Begerow, sp. nov. ex-type HEW-8-5 = CBS 11554; GenBank FN428955 (D1/D2 domain of 26S rRNA gene); MycoBank MB 515234.

## XVI Laboratorio de Microbiología Aplicada y Biotecnología (Applied Microbiology and Biotechnology Lab.), Instituto de Investigaciones en Biodiversidad y Medio Ambiente (CONICET-UNComahue), Quintral 1250 (8400), Bariloche, Argentina. Communicated by Diego Libkind <libkind@crub.uncoma.edu.ar>.

Recent publications.

1 Moliné M, Libkind D, Diéguez MC, van Broock M 2009 Photo-protective role of carotenoid pigments in yeasts: experimental study contrasting naturally occurring pigmented and albino strains. J Photochem Photobiol B: Biol 95:156–161.

2 Libkind D, Moline M, Sampaio J, van Broock M 2009 Yeasts from high altitude lakes: influence of UV radiation. FEMS Microbiol Ecol 69:353–362.

3 Baeza M, Sanhueza M, Flores O, Oviedo V, Libkind D, Cifuentes V 2009 Polymorphism of viral dsRNA in *Xanthophyllomyces dendrorhous* strains isolated from different geographic areas. Virol J 6:160.

Papers in press.

4 Russo G, Libkind D, Ulloa RJ, de García V, Sampaio JP, van Broock MR 2009 *Cryptococcus agrioensis* sp. nov., a basidiomycetous yeast of the acidic rock drainage ecoclade, isolated from acidic aquatic environments of volcanic origin (River Agrio, Argentina). Int J Syst Evol Microbiol IJS/2009/012534.

5 de Garcia V, Brizzio S, Russo G, Rosa CA, Boekhout T, Theelen B, Libkind D, van Broock M 2009 *Cryptococcus spencermartinsiae* sp. nov., a basidiomycetous yeast isolated from glacial waters and apple fruits. Int J Syst Evol Microbiol IJSEM/2009/013177.

6 de Garcia V, Brizzio S, Libkind D, Rosa C, van Broock M 2009 *Wickerhamomyces patagonicus* sp. nov., a novel teleomorphic ascomycetous yeast from Patagonia, Argentina. Int J Syst Evol Microbiol IJS/2009/015974.

7 Libkind D, Sampaio JP, van Broock M 2009 Cystobasidiomycetes yeasts from Patagonia (Argentina): description of *Rhodotorula meli* sp. nov. from glacial meltwater. Int J Syst Evol Microbiol IJS/2009/018499.

Book chapters.

8 Libkind D, Sampaio JP 2009 *Rhodotorula*. In: Molecular Detection of Foodborne Pathogens. Liu D (Ed.) Chapter 43, CRC Press, Taylor & Francis Group, Boca Raton. pp 603-618.

9 Medeiros A, Rosa CA, Brandão L, Giani A, Ludolf Gomes LN, Libkind D 2009 Microbial quality of freshwater ecosystems of South America. In: Water Quality: Physical, Chemical and Biological Characteristics. Ertuð K, MirzaFrank I (Ed) ISBN: 978-1-60741-633-3. Nova Science Publishers, Inc. In press.

10 Fátima CO, Inayara G, Lacerda CA, Libkind C, Lopes CA, Carvajal J, Rosa CA 2009 Traditional foods and beverages from South America: microbial communities and production strategies. In: Industrial Fermentation: Food Processes, Nutrient Sources and Production Strategies. Krause J, Fleischer O (Eds) ISBN: 978-1-60876-550-8. Nova Science Publishers, Inc. In press.

# Recent Meeting

## 37th Annual Conference on Yeasts of the Czech and Slovak Commission on Yeasts, Smolenice, Slovakia, May 13-15, 2009

The 37th Annual Conference on Yeasts, organized by the Czech and Slovak Commission on Yeasts, Institute of Chemistry, Slovak Academy of Sciences and Department of Biochemical Technology, Slovak University of Technology, took place in the Smolenice Castle, the Congress Center of the Slovak Academy of Sciences, during May 13-15, 2009. Steadily increasing participation of foreign scientists and English as the conference language gave the event a really international character. Several invited speakers were supported by the International VISEGRAD Fund and the organization NATURA associated with the Faculty of Natural Sciences of the Comenius University. Prof. Barbel Hahn-Hägerdal from Lund University in Sweden presented the opening Dr. A. Kocková-Kratochvílová memorial lecture "Pentose fermenting *Saccharomyces cerevisiae*". The conference was attended by 93 scientists, mainly from Czech Republik and Slovakia, although there were also participants from Canada, Hungary, Ireland, Italy, Poland, South Korea, Japan and Spain, among them several invited speakers.

The program consisted of three sessions dedicated to Biotechnology, Genetics and Molecular Biology of Yeasts, and Cell Biology and Medical Mycology. Twenty-eight oral presentations were complemented with 53 posters. The interesting scientific program also featured wine presentations and wine tastings by the wine-producing companies Vino Hruška from the Czech Republic and Villa Vina Rača from the vicinity of Bratislava, capital of Slovakia.

The successful conference ended with a meeting of the Committee of the Czech and Slovak Yeast Commission, during which it was decided that the 38$^{th}$ Annual Yeast Conference will be organized in the Smolenice Castle on May 11-14, 2010. The program will cover Genetics and Molecular Biology of Yeasts, Cell Biology and Medical Mycology, and Biotechnology.

Further information about the activities of the Czech and Slovak Commission for Yeasts can be found on the website **www.chem.sk/yeast**. The titles of lectures and poster of the 37th Annual Yeast Conference are listed below:

**Invited Lecture to the memory of Dr. A. Kocková-Kratochvílová**

1 Hahn-Hägerdal B (Sweden) Pentose fermenting *Saccharomyces cerevisiae*

**Lectures in the session Biotechnology**

2 Suk Hoo Yoon (South Korea) Production and characterization of microbial lipids using oleaginous yeasts.

3 Liu Q, Siloto RMP, Truksa M, Weselake, RJ (Canada) Yeast as model system to study diacylglycerol acyltransferase.

4 Van Zyl, WH, Haan, R.D, Rose, SH, La Grange, DC, Van Wyk, N, Van Rooyen, R, Mcbride, JE, Lynd, LR (South Africa) Construction of cellulolytic *Saccharomyces cerevisiae* strains for consolidated bioprocessing.

5 Ryabova O, Vršanská M, Biely P (Slovakia) Xylanolytic system of xylose-fermenting *Pichia stipitis*.

6 Raspor, P, Ekert, M, Fujs, Š, Jamnik, P, Paš, M, Poljšak, B (Slovenia) Accumulation of minerals in yeasts: How much these interfere with oxidation and antioxidation process in yeast cells?

7 Maráz, A, Kovács M, Pomázi A (Hungary) Stress response of yeasts during fermentation of botrytized wines.

8 Halienová, A, Márová, I, Čarnecká, M, Zdráhal, Z, Müller, L, Breierová, E, Čertík M (Czech Republic and Slovakia) Proteomics and genomics of red yeasts: Separation and partial identification of *Rhodotorula* proteins and DNA.

9 Čertík, M, Breierová, E, Márová, I, Hanusová, V, Dvořáková, T, Čarnecká M (Slovakia and Czech Republic) Characterization of exoglycoproteins and biomass produced by carotenoid yeasts grown under heavy metals.

10 Čarnecká, M, Márová, I, Hároniková, A, Dvořáková, T, Kubáčková, M, Hanusová, V, Čertík, M, Breierová E (Czech Republic and Slovakia) Production of carotene-enriched biomass by red yeasts grown on various waste substrates.

11 Tretinová K (Czech Republic) Introduction and sensorial evaluation of wines from Vino Hruška, s.r.o.

**Lectures in the session Genetics and Molecular Biology of Yeasts**

12 Sullivan D (Ireland) *Candida dubliniensis*: A budding yeast pathogen NATURA Lecture

13 Poláková S, Blume Ch, Zárate J.A, Mentel M, Jørck-Ramberg D, Stenderup J, Piškur J (Slovakia and Sweden) The role of genome architecture in *Candida glabrata*: virulence and lifestyle NATURA Lecture.

14 Monkaityte R. Voegeli S, Chelstowska A, Philippsen P, Rytka J (Poland and Switzerland) Evolution analysis of *Saccharomyces cerevisiae* and *Ashbya gossypii* by functional complementation.

15 Chołbiński P. Gajowniczek A, Hopper AK, Żołądek T (Poland and USA) Localization of Rsp5 ubiquitin ligase to multiple sites in yeast cells depends on C2, WW domains and nuclear localization and export signals in the HECT domain.

16 Popolo L. Rolli E, Calderon J, Ragni E (Italy) The glucan-transferases and their importance in fungal morphogenesis.

17 García R, Rodriguez-Peña J.M, Bermejo C, Arias P, Sanz A.B, Blanco N, Díez S, Nombela C, Arroyo J (Spain) Regulation of cell wall stress responses in yeast: The role of CWI and HOG MAPK pathways.

18 Petrezsélyová S, Herynková P, Hošková B, Sychrová H (Czech Republic) Regulation of plasma-membrane K+ transport cycle in *S. cerevisiae*.

19 Polčic P, Drobcová B, Kiššová I, Polčicová K, Mentel M, Kolarov J (Slovakia) Viral antiapoptotic protein Mhv68-M11 prevents cell death by inhibiting Bax and Bak (Yeast Said).

**Lectures in the session Cell Biology and Medical Mycology**

20 Buc M (Slovakia) Dectin 1 and other pattern recognition receptors in the induction of antifungal immunity.

21 Juchimiuk M, Pasikowska M, Kundzewicz J, Orłowski J, Palamarczyk G (Poland) Dolichol associated defect of *S. cerevisiae* cell wall increases sensitivity towards specified anti-fungals.

22 Bujdáková H. Šimová Z, Paulovičová E, Kolecka A, Neščáková Z. (Slovakia) Role of *Candida albicans* surface antigens in adherence and their potential use in therapy.

23 Hrušková-Heidingsfeldová O. Dostál J, Majer F, Havlíková J, Hradilek M, Pichová I (Czech Republic) Secreted aspartic proteinases of *Candida parapsilosis*: analysis of gene expression and catalytic properties.

24 Wysocka-Kapcinska M, Lutyk-Nadolska J, Kiliszek M, Plochocka D, Maciag M, Leszczynska A, Rytka J, Burzynska B (Poland) Functional expression of human HMG-CoA reductase in *Saccharomyces cerevisiae*: a system to analyse normal and mutated versions of the enzyme in the context of statins treatment.

25 Krejčí L (Czech Republic) DNA repair mechanisms in yeast NATURA lecture.

26 Sipiczki M. (Hungary) Splitting of the *Schizosaccharomyces* septum.

27 Špánová M. Czabany T, Zellnig G, Leitner E, Hapala I, Daum G (Slovakia and Austria) Lipid particles as a storage compartment for squalene in the yeast *Saccharomyces cerevisiae*.

28 Juchimiuk M. Orłowski J, Litwicka P, Ernst J, Palamarczyk G (Poland) Impaired synthesis of dolichol prevents hyphae formation and alters the cell wall of *Candida albicans*.

29 Kolecka A. Thierry F, Rosa H, Thierry B, Steffen R, Bujdáková H (Slovakia, France and Germany) Role of pH in *Candida albicans* biofilm formation.

30 Malík F (Slovakia) Introduction and sensorial evaluation of wines from Villa Vino Rača, a.s.

**List of posters**

31 Abelovská L, Fričová D, Klobučníková, V, Nosek J, Tomáška Systematic screening of the *Saccharomyces cerevisiae* deletion library for ionophore resistant and hypersensitive mutants.

32 Balková K, Hodúrová Z, Hervayová N, Garaiová, M,Gbelská Y The role of KlPdr1p in expression of KlPDR5 encoding the major multidrug resistance transporter.

33 Monika Baťova, Vladimira Džugasova, Silvia Borecka, Eduard Goffa, Julius Šubík Molecular basis of the ScPEL1 mutation and heterologous expression of genes encoding phosphatidylglycerolphosphate synthase in yeast.

34 Norbert Berila, Silvia Borecka-Melkusova, Vladimira Džugasova, Julius Šubík Mutations in the CgPDR1 gene are responsible for azole resistance in *Candida glabrata* clinical isolates.

35 Silvia Borecka, Silvia Novohradska, Julius Šubík Role of chromatin remodeling in virulence of the yeast *Saccharomyces cerevisiae*.

36 Fričová D and Nosek J Mgm101 Protein from the yeast *Candida parapsilosis*.

37 Gunišová Stanislava, Nosek Jozef, Tomáška Ľubomír Identification and characterization of telomere length and sequence composition of pathogenic yeasts *Candida parapsilosis, C. orthopsilosis and C metapsilosis*.

38 Martina Janoskova and Leos Valašek. The load&release mechanism of eif1 mediated by the n-terminal domain of the eif3c subunit plays a critical role in stringent aug selection.

39 Kinský S, Tomáška Ľ Transcription factor Bas1 and its role in cell morphogenesis in the yeast *Yarrowia lipolytica*.

40 Kinský S, Kramara J, Tomáška Ľ *Yarrowia lipolytica* – a novel yeast model for telomere research.

41 Dominika Mániková, Danuša Vlasáková, Lucia Letavayová, Dana Vigašová, Jana Loduhová, Viera Vlčková, Jela Brozmanová, Miroslav Chovanec A role for base excision repair and non-homologous end-joining pathways in sodium selenite-induced toxicity, DNA strand breakage and mutational spectra in yeast.

42 Vanda Munzarová, Josef Pánek, Leoš Valášek Mutagenetic analysis combined with computational structure predictions of the reinitiation-promoting sequences 5' of uORF1 of GCN4 reveal one eIF3a-dependent and two additional eIF3a-independent stimulatory hot spots.

43 Silvia Poláková, Emanuel Procházka, Pavol Sulo, Franz Lang, Jure Piškur A comparison of mitochondrial genomes from two related *Brettanomyces*/*Dekkera* yeast species (distribution of patchy elements, fungal phylogeny).

44 Laurenčík Michal, Sulo Pavol, Poláková Silvia, Lucia Kraková, Sláviková Elena *Geotrichum bryndzae* sp. nov. a novel asexual arthroconidial yeast species related to the genus *Galactomyces*.

45 Viktoria Polakovičová, Elena Tichá, Margita Obernauerová The influence of the pgs1 mutation on the energy-transducing enzymatic system in *Kluyveromyces lactis* and *Saccharomyces cerevisiae* yeasts.

46 Procházka Emanuel, Sulo Pavol, Poláková Silvia. A fate of mtDNA in the interspecies hybrids (Recombination driven by mobile introns is preferred).

47 Procházka Emanuel, Sulo Pavol, Franko Filip, Poláková Silvia A complete sequence of mitochondrial genome from *Saccharomyces paradoxus*.

48 Iga Piekarska, Bozenna Rempola, Roza Kucharczyk, Joanna Rytka Vacuolar sorting protein ccz1 is essential for sporulation of the yeast *Saccharomyces cerevisiae*.

49 Burgess, RC, Šebesta M, Sisaková A, Marini V, Sung P, Klein H, Rothstein R, Krejčí, L The interaction between RAD54 and PCNA is crucial for DNA repair synthesis during homologous recombination.

50 Matúš Valach, Dominika Fričová, Zoltán Farkas, Ilona Pfeiffer, Judit Kucsera, Ľubomír Tomáška, Jozef Nosek Mitochondrial genomes from the yeasts *Candida frijolesensis* and *C. subhashii*.

51 Katarína Višacká, Joachim M. Gerhold, Jana Petrovičová, Slavomír Kinský, Jozef Nosek, Juhan Sedman, Ľubomír Tomáška Gcf1 proteins from *Candida* species: Novel subfamily of mitochondrial HMG-box containing proteins.

52 Dana Vránová, Renata Vadkertiová, Hana Šuranská, Radana Olivová Verification of taxonomy of genus yeasts *Hanseniaspora, Pichia, Saccharomyces, Rhodotorula* during fermentation of white wine from Velké Pavlovice.

53 Micialkiewicz I, Wiek A, Chelstowska Interactions of the Swc4 protein of chromatin remodeling complexes in *Saccharomyces cerevisiae*.

54 Jaromír Zahrádka and Hana Sychrová Substrate specificity of the yeast NHA1 na+/h+ antiporter is influenced by internal-loop residue Asn67.

55 Eva Jánošíková, Igor Zeman, Jozef Nosek Heterologous expression of mitochondrial carriers from *Candida parapsilosis* in baker's yeast.

56 Patrycja B. Zembek, Urszula Perlińska-Lenart, Katarzyna Rawa, Wioletta Górka-Nieæ, Gabriela Smoleńska-Sym, Grażyna Palamarczyk, Joanna S. Kruszewska. Cloning and functional analysis of DPM2 and DPM3 genes from *Trichoderma reesei* expressed in *Saccharomyces cerevisiae* DPM1D mutant.

57 Żaneta Ludwiczak, Piotr Chołbiński, Teresa Żołądek Studies on phosphorylation of Rsp5 ubiquitin ligase by protein kinase A.

58 Joanna Kamińska, Daria Romanyuk, Piotr Jêdrzejak, Marcin Grynberg, Teresa Żołądek Effects of expression of KIAA0404 encoding human Atg2A protein on autophagy in yeast.

59 Zuzana Holešová, Ivana Zavadiaková, and Jozef Nosek MNX1 and MNX2: Genes encoding putative flavoprotein monooxygenases in the pathogenic yeast *Candida parapsilosis*.

60 Ema Paulovičová, Helena Bujdáková, Lucia Paulovičová, Alexander A. Karelin, Yury E Tsvetkov, Nikolay E Nifantiev Pattern of polyclonal recognition of *Candida* cell wall antigenic α-mannosidic sequences in different morphological forms.

61 Halgaš Ondrej, Sulo Pavol, Hapala Ivan Moot petite phenotype is common in systematic deletion mutants.

62 Havelková M, Unger Eberhard Yeast: an appropriate model for the detection of cancerostatics.

63 Markéta Hilská, Vratislav Šťovíček, Blanka Janderová Role of FLO11 gene expression in the wrinkled colonies of *Saccharomyces cerevisiae* Ssh.

64 Csilla Mészárosová, Eva Stratilová, Nadežda Kolarova *Cryptococcus laurentii* glycosidase activities during budding.

65 Paulovičová L, Paulovičová E, Bystrický S, Karelin AA, Tsvetkov YE, Nifantiev NE Immunogenicity of synthetic mannan derived heptamannoside - protein conjugate.

66 Jana Hlousková, Andrea Volejníková, Karel Sigler, Alena Pichová Cellular and mitochondrial respiration of *Saccharomyces cerevisiae* cells of different age.

67 Šimočková M, Sedláková L, Griač P Homeostasis of anionic mitochondrial phospholipids in the yeast *Saccharomyces cerevisiae*.

68 Marta Brlejová, Milan Čertík, Peter Rapta, Vlasta Brezová, Ema Paulovičová The influence of yeast morphology on the antioxidant properties of cell wall glycoproteins.

69 Kregiel D, Rygala A, Berłowska J, Mizerska U, Fortuniak W, Chojnowski J, Ambroziak W Antimicrobial properties of chemically modified surfaces.

70 Kregiel D, Berłowska J, Ambroziak W The viability assessment of yeast cells adhered on different solid carriers.

71 Katarína Furdíková, Peter Rapta, Milan Valach, Dana Dudinská, Fedor Malík, Milan Čertík Autochthonous yeast cultures vs. antioxidant activity of wine.

72 Katarína Furdíková, Katarína Ïurčanská, Jozef Ševcech, Helena Hronská, Fedor Malík. Autochthonous yeast cultures in winemaking.

73 Ondruška V, Matoušková P, Obruča S, Skutek M, Márová I Biomass and pullulan production in *Aureobasidium pullulans* grown under exogenous stress.

74 Duroňová K, Lichnová A, Márová I Use of *Saccharomyces cerevisiae* D7 test system to study of antimutagenicity/genotoxicity of several kinds of honey.

75 Dvořáková T. , Čarnecká M, Vavrysová A, Márová I, Breierová E Production of carotenoids by *Cystofilobasidium capitatum* in optimal and stress condition.

76 Milan Mazúr, Katarína Furdíková, Michal Kaliňák, Marián Valko Minor compounds in grape must, "burčiak", "rampáš" and new wine by quantitative NMR spectroscopy.

77 E. Breierová , J. Pátková-Kaňuchová, K. Nemcová Expression of indigenous grape microflora on the sensory of varietal wine.

78 Omelková J, Zechmeistrová L,Valicová M The influence of technological procedure on the occurrence of microorganisms during the fermentation of red wine.

79 Renata Vadkertiová, Elena Sláviková, Dana Vránová Yeasts colonizing the leaves of fruit trees.

80 Marián Mazáň, Noelia Blanco, Javier Arroyo, Vladimír Farkaš Biochemical characterization of Crh proteins catalyzing transglycosylation in yeast cell wall.

81 Wysocka-Kapcinska M, Lutyk-Nadolska J, Kiliszek M, Plochocka D, Maciag M, Leszczynska A, Rytka J, Burzynska B Localization of Rsp5 ubiquitin ligase to multiple sites in yeast cells depends on C2, WW domains and nuclear localization and export signals in the HECT domain.

82 Tomšíková A Pathogenesis of fungal infection.

83 Postlerová L, Rusková L, Kocmanová I, Mišíková J, Hamal P, Raclavský V Identification of *Candida dubliniensis*: Usefulness of McRAPD technique.

Communicated by Peter Biely

# Forthcoming Meetings

## 23rd VH Berlin Yeast Conference
## Advances in Yeast Technology and Applied Research
## April 26-27, 2010, Vienna, Austria

The 23rd VH Berlin Yeast Conference will be held April 26-27, 2010, at the Austria Trend Hotel Schloss Wilhelminenberg, A-1160 Vienna. Lecturers are invited to present applied research, projects and case studies in fields of food and non food baker's yeast process.

Please look up our website **www.vh-berlin.org** for further details. If any questions remain, please do not hesitate to contact us:

VERSUCHSANSTALT DER HEFEINDUSTRIE E.V.
Research Institute for Baker's yeast
Dr. Michael Quantz
General manager
<**Michael.quantz@vh-berlin.org**>

## ISSY28, Bangkok, Thailand

The first ISSY to be held in South East Asia. The symposium will be held during 15 - 18 September 2010 at Montein Riverside Hotel, Bangkok, Thailand. On-line registration now opened.

The Land of Smile awaits yeast researchers from around the world. Please visit our website:
**www.issy28.org**

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For up-to-date announcements on forthcoming meetings, please see the YNL website
**http://publish.uwo.ca/~lachance/Future%20meetings.html**

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**http://publish.uwo.ca/~lachance/Microbiology%20Group%20Manager.pdf**

# Fifty Years Ago in the Yeast Newsletter
# (Volume VIII Number 2, May 1959)

**Mrs. N. J. W. Kreger-van Rij**

The Yeast Division is now located in a new building and the correct address is [...] Julianalaan 67 A-Delft, Holland

**H. J. Phaff**

[...] the principal yeasts found in the bark beetles *Ips* and *Dendroctonus* by Shifrine and Phaff (Mycologia **48**, 41, 1956 [...] are not present in Scolytus frass and larvae.

Dr. Shifrine and I are attempting to prove previously made hypothesis on the mechanism by which *Saccharomycopsis guttulata* becomes established in the gastrointestinal tract of newly born rabbits.

**Dr. Carl C. Lindegren**

Lindegren, Carl C. Darwinism. Agrobiology (Russia) #5, 740-741 (Sept.-Oct., 1959).

McClary, Dan O., Nulty, W. L. and Miller, G. R. Effect of potassium versus sodium in the sporulation of *Saccharomyces*. J. Bacteriol. **78**, 362-368 (1959).

**Dr. P. K. C. Austwick**

I. F. Keymer and I returned to the site of our isolation of *Candida albicans* from a lawn in July 1958 and on July 28th, 1959 were able to recover the fungus again from the same spot [in Weybridge, England]. This time no young partrides [*sic*] had been near the area and one must assume that this is a real habitat for *C. albicans*. We failed to isolate the yeast from grass in other parts of the same lawn and from the grass in adjacent field.

**Dr. J. A. Barnett**

It is urgent that yeast taxonomists should clarify this kind of information, at least for *S. cerevisiae*, the best known and most important yeast. If they are unable to agree internationally on such major characteristics for this species, they may find themselves in disrepute with biochemists and industrial workers to whom their work should be useful.

**Dr. F. W. Beech**

Would it be possible to draw up an internationally agreed set of methods and media for yeasts [...]? Results could then be discussed without specifying their context. [...] The problem of "weak" reactions might be overcome if the results were expressed quantitatively as yield of yeast on a dry weight basis or checked by chromatographic examination of the growth media.