ISSN 0513-5222

Y E A S T

A Newsletter for Persons Interested in Yeast

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

JUNE 1995 **Volume XLIV, Number I**

Marc-André Lachance, Editor
University of Western Ontario, London, Ontario, Canada N6A 5B7

Notice to our readers

I shall be on sabbatical leave from July 1 1995 to June 30 1996. As a result, some delays can be expected in the publication of the December 1995 and the June 1996 issues. I therefore ask our readers for their patience in the circumstances.

M. A. Lachance
Editor

I. American Type Culture Collection. 12301 Parklawn Drive, Rockville, Maryland 20852-1776, U.S.A. Communicated by S.C. Jong.

Complete information of the following strains may be obtained upon request from the Mycology and Botany Department at the ATCC.

NAME	ATCC#	DEPOSITOR/STRAIN	SIGNIFICANCE/REFERENCE
C. albicans	90819	P.G. Sohnle CATW 4/19	Human isolate; inhibition by host defense system (J. Infect. Dis. 163:187-192, 1991; Acta Derm. Venereol. (Stockh). 72:241-244, 1992; J. Lab. Clin. Med. 121:235-243, 1993)
C. albicans	96108	T. Suzuki SRT1	Phototrophic, polyploid (J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96109	T. Suzuki NARA2	Phenotype:Met- Pro-; diploid (J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96110	T. Suzuki SGY126	Requires adenine (Mol. Microbiol. 6:171-177, 1992; J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96111	T. Suzuki 126A1	Genotype: ade2; phenotype: Met-; diploid (J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96112	T. Suzuki A5153	Phenotype: His- Lys- Trp-; diploid (Yeast 2:53-58, 1986; J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96113	T. Suzuki NUM51	Prototrophic, polyploid (J. Gen. Microbiol. 132:443-453, 1986; J. Gen. Appl. Microbiol. 34:409-416, 1988; J. Bacteriol. 176:3345-3353, 1994)
C. albicans	96114	T. Suzuki NUM961	Serotype A, produces both germ tubes and chlamydospores (J. Gen. Microbiol. 135:425-434, 1989). Prototroph, near 3N (J. Bacteriol. 176:3345-3353, 1994)
C. albicans	90873	H. Dermoumi B62	In vitro susceptibility (MIC): 0.125 mg/L itraconazole; 0.25 mg/L fluconazole; 0.25 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
C. albicans	96351	M. Butler HOG839	Genotype: ade2 pro3 met+/met- lys+/lys-. Transformation host (Mol. Gen. Genet. 235:453-457, 1992)
C. apicola	96134	R.K.Hommel IMET 43747	Produces sophorose lipid (Biotechnol. Lett. 15:853-858, 1993; J. Biotechnol. 33:147-155, 1994)
C. caseinolytica	90544	H.J. Phaff UCD 81-494.4	Characterization (Int. J. Syst. Bacteriol. 44:641-645, 1994)
C. caseinolytica	90545	H.J. Phaff UCD 81-665.2	Characterization (Int. J. Syst. Bacteriol. 44:641-645, 1994)
C. caseinolytica	90546	H.J. Phaff UCD 83-438.3	Type culture (Int. J. Syst. Bacteriol. 44:641, 1994)
C. glabrata	90876	H. Dermoumi B73	In vitro susceptibility (MIC): 2 mg/L itraconazole; 32 mg/L fluconazole; 0.5 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
C. guilliermondii	96042	M. Maiwald & R. Kappe HD 4094/92	18S-rRNA sequence, EMBL M60304 (J. Med. Vet. Mycol. 32:115-122, 1994)
C. guilliermondii	90877	H. Dermoumi B77	In vitro susceptibility (MIC): 0.06 mg/L itraconazole; 2 mg/L fluconazole; 0.125 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
C. krusei	90878	H. Dermoumi	In vitro susceptibility (MIC):0.25 mg/L itraconazole; 64 mg/L fluconazole; 0.5 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
C. lusitaniae	96040	M. Maiwald & R. Kappe HD 1764/92	18S-rRNA sequence, EMBL M55526 (J. Med. Vet. Mycol. 32:115-122, 1994)
C. parapsilosis	96137	P.F. Lehmann MCO441	RAPD patterns (J. Clin. Microbiol. 30:3249-3254, 1993). Produces extracellular proteinase rDNA sequence, GenBank U10987 (P.F. Lehmann, personal communication)
C. parapsilosis	96138	P.F. Lehmann MCO433	RAPD and electrophoretic karyotype (J. Clin. Microbiol. 30:3249-3254, 1992; Curr. Genet. 23:463-467, 1993). Sequence of 5.8S rDNA, GenBank L11352 (Yeast 9:1199-1206, 1993)
C. parapsilosis	96139	P.F. Lehmann MCO457	Sequence of rDNA, GenBank U10988 (P.F. Lehmann, personal communication)
C. parapsilosis	96140	P.F. Lehmann MCO471	RAPD patterns (J. Clin. Microbiol. 30:3249-3254, 1992). Sequence of rDNA, GenBank U10988 (P.F. Lehmann, personal communication)

C. parapsilosis	96141	P.F. Lehmann MCO456	RAPD and electrophoretic karyotype (J. Clin. Microbiol. 30:3249-3254, 1992; Curr. Genet. 23:463-467, 1993). Sequence of 5.8S rDNA, GenBank L11352 (Yeast 9:1199-1206, 1993)
C. parapsilosis	96142	P.F. Lehmann MCO462	RAPD patterns (J. Clin. Microbiol. 30:3249-3254, 1992). Sequence of 5.8S rDNA, GenBank L11352 (Yeast 9:1199-1206, 1993)
C. parapsilosis	96143	P.F. Lehmann MCO429	RAPD patterns (J. Clin. Microbiol. 30:3249-3254, 1992). Sequence of rDNA, GenBank U10989 (P.F. Lehmann, personal communication)
C. parapsilosis	96144	P.F. Lehmann MCO448	RAPD patterns and electrophoretic karyotype (J. Clin. Microbiol. 30:3249-3254, 1992; Curr. Genet. 23:463-467, 1993). Sequence of rDNA, GenBank U10989 (P.F. Lehmann, personal communication)
C. parapsilosis	90875	H. Dermoumi B78	In vitro susceptibility (MIC): 0.06 mg/L itraconazole; 2 mg/L fluconazole; 0.25 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
C. parapsilosis	96041	M. Maiwald & R. Kappe HD 3931/91	18S-rRNA sequence, EMBL M60307 (J. Med. Vet. Mycol. 32:115-122, 1994)
C. sphaerica	96222	I. Spencer-Martins IGC 3208	Transport of L(-)malic acid and other dicarboxylic acids (Appl. Microbiol. Biotechnol. 31:551-555, 1989). Mating type a.
C. tropicalis	20962	Henkel Research Corp. H5343	Genotype: pox5:ura3A pox5:ura3A pox4A:ura3A pox4B:URA3A. Produces dicarboxylic acids (U.S. Pat. 5,254,466).
C. tropicalis	20913	Henkel Research Corp. SU-2	Transformation host for site-specific modification of genome (U.S. Pat. 5,254,466).
C. tropicalis	90874	H. Dermoumi B79	In vitro susceptibility (MIC): 0.125 mg/L itraconazole; 1 mg/L fluconazole; 0.25 mg/L amphotericin B (Chemotherapy 40:92-98, 1994)
Cr. curvatus	96219	P.J. Blanc UfaM3	Unsaturated fatty acid auxotroph. Produces lipids (Appl. Microbiol. Biotechnol. 40:483-488, 1993)
Cr. neoformans	96038	M.Maiwald and R.Kappe D52	Serotype D. 18S-rRNA sequence, EMBL X60183 (J. Med. Vet. Mycol. 32:115-122, 1994)
Cr. neoformans	96340	E.S. Jacobson 450	Mating type a, serotype A, melanized only at 25C.
K. lactis	90782	J. Jacoby HK5-8C/tal1Δ2	Genotype: MATα Klpfk1::LEU2 Kleu2 Klpfk2::URA3 Klura3 Kltal1::HIS3 Klhis3. Unable to grow on glucose (Mol. Microbiol. 10:867-876, 1993)
K. lactis	90783	J. Jacoby HK5-8C	Genotype: MATα Klpfk1::LEU2 Klpfk2::URA3 leu2 ura3 his3 trp1 ade. Transformation host (Mol. Microbiol. 10:867-876, 1993)
K. lactis	90735	G.D. Clark-Walker K8	Mating type a (Curr. Genet. 16:429-432, 1989)
K. lactis	90736	G.D. Clark-Walker KF4	Fusion product of *Saccharomyces cerevisiae* FeRho0 and *Kluyveromyces lactis* K25. Petite positive (Curr. Genet. 16:429-432, 1989)
K. lactis	90806	M. Wesolowski-Louvel MW98-8C	Genotype: MATα uraA argA lysA K+ pKD1(0). Transformation host (Curr. Genet. 12:185-192, 1987)
K. lactis	96263	K.D. Breunig JA6	Wild-type genotype: MATα ade ura3 trp1-11 LAC9-2 GAL80. Glucose repression (Mol. Cell. Biol. 13:7566-7576, 1993). Genome map (Yeast 11:211-218, 1995)
K. lactis	96264	K.D. Breunig DL9	Genotype: lac9::URA3 trp1 ade. Glucose repression (Mol. Cell. Biol. 13:7566-7576, 1993). Transcriptional activation (ibid., 7:4400-4406, 1987)
K. lactis	96265	K.D. Breunig KB101	Genotype: MATa ade trp1 ura3 gal80-1. Glucose repression (Mol. Cell. Biol. 13:7566-7576, 1993)
K. lactis	96266	K.D. Breunig JA6/D801R	Genotype: MATα ade trp1 gal80Δ1::ura3. Glucose repression (Mol. Cell. Biol. 13:7566-7576, 1993)
K. lactis	96267	K.D. Breunig JA6/D802R	Genotype: MATα ade trp1 gal80Δ2::ura3. Glucose repression (Mol. Cell. Biol. 13:7566-7576, 1993)
Ph. rhodozyma	96220	J. Adrio FOA-4	Genotype: ura3 (J. Gen. Appl. Microbiol. 39:303-312, 1993)
Ph. rhodozyma	96221	J. Adrio FOA-7	Genotype: ura3 (J. Gen. Appl. Microbiol. 39:303-312, 1993)

P. anomala	90522	W.T. Starmer 85-256.2	Ecology (Appl. Environ. Microbiol. 58:990-997, 1992) Erythritol-negative
P. anomala	90724	T. Ogata J-224-H1	Sequence of URA3 gene encoding orotidine-5'-phosphate decarboxylase (J. Ferment. Bioeng. 74:352-357, 1992). Haploid (ibid., 79:1-5, 1995)
Rsp. toruloides	90950	R. Joseph CFR-1	Produces chitosanase (Lett. Appl. Microbiol. 14:1-4, 1992)
Rsp. aurantiaca	90775	W.J. Middelhoven G36	Degrades cresols and benzene compounds (Plant Soil 145:37-43, 1992; Antonie Leeuwenhoek 63:125-144, 1993)
Rh. glutinis	96365	CBS 2367	Type culture of *Mycotorula rosea-corallina* (Nuova G. Bot. Ital. Series 5:546-554, 1928)
S. bayanus	90738	H.V. Nguyen L19-1A	Genetic and karyotype identification (Syst. Appl. Microbiol. 16:274-279, 1993)
S. bayanus	90739	H.V. Nguyen 58I-2B	Genetic and karyotype identification (Syst. Appl. Microbiol. 16:274-279, 1993)
S. bayanus	90740	H.V. Nguyen SCU 13-1B	Genetic and karyotype identification (Syst. Appl. Microbiol. 16:274-279, 1993)
S. bayanus	90919	J.M. Salmon M30	Alcoholic fermentation (Biotechnol. Lett. 16:89-94, 1994)
S. cerevisiae	90665	F. Ahne G36	Genotype: MATα rev2-1 ade2-1 trp1-289 ura3-52 arg4-17 his5-2 lys2-1. DNA double-strand break repair (Curr. Genet. 23:402-407, 1993)
S. cerevisiae	90666	F. Ahne G50	Genotype: MATα RAD ade2-1 trp1-289 ura3-52 arg4-17 his5-2 lys2-1. DNA double-strand break repair (Curr. Genet. 23:402-407, 1993)
S. cerevisiae	90667	F. Ahne G57	Genotype: MATa rad4-4 ade2-1 trp1-289 ura3-52 his5-2. DNA double-strand break repair (Curr. Genet. 23:402-407, 1993)
S. cerevisiae	90630	J. Polaina KPX6-3C	Genotype: MATα ade2 his4 thr1 trp1 kar3-1.
S. cerevisiae	90631	J. Polaina GF4836-8C	Genotype: MATa leu1 thr1 KAR+ (Curr. Genet. 24:369-372, 1993)
S. cerevisiae	90632	J. Polaina 17A-N1/CR4	Genotype: MATα ade2 his4 can1 KAR+
S. cerevisiae	90633	J. Polaina KPX6-2B	Genotype: MATα his4 thr1 kar3-1.
S. cerevisiae	90634	J. Polaina KPX2-6D	Genotype: MATα leu1 ura3 kar1-2.
S. cerevisiae	90635	J. Polaina XW5/1-5D	Genotype: MATα his4 leu1 can1 kar2-1.
S. cerevisiae	90636	J. Polaina KPX5-1A	Genotype: MATa thr1 nysr kar3-1.
S. cerevisiae	90637	J. Polaina KPX1-6A	Genotype: MATa ade2 ura3 kar2-1
S. cerevisiae	90638	J. Polaina KPX1-1A	Genotype: MATα ade2 ura3 kar2-1 (J. Polaina, pers. communication)
S. cerevisiae	90639	J. Polaina XW5/1-7C	Genotype: MATa ade2 thr1 kar2-1
S. cerevisiae	90640	J. Polaina KPX1-3A	Genotype: MATa ura3 kar2-1
S. cerevisiae	90641	J. Polaina XW2-11C	Genotype: MATa ade2 thr1 kar1-2.
S. cerevisiae	90642	J. Polaina XW2-3B	Genotype: MATa leu1 thr1 kar1-2.
S. cerevisiae	90689	A.S. Lewin KKY100	Genotype: MATα ade1-100 his4-519 leu2-3 leu2-112 ura3-52 CIT1::LEU2 CIT2::URA3. Peroxisomal citrate synthase targeting signal (Mol. Cell. Biol. 12:5593-5599, 1992)
S. cerevisiae	90688	A.S. Lewin GK1	Genotype: MATα his3-11 his3-15 leu2-3 leu2-112 CANr CIT1::LEU2. Peroxisomal citrate synthase targeting signal (Mol. Cell. Biol. 12:5593-5599, 1992)
S. cerevisiae	90726	L.L. Sandell LS18	Genotype: MATα kar1-1 aro2 leu2 "control chromosome VII" with URA3 adjacent to VII-L telomere (Cell 75:729-739, 1993)
S. cerevisiae	90727	L.L. Sandell LS19	Genotype: MATα kar1-1 aro2 leu2 "test chromosome VII" with URA3 and recognition sequence for HO endonuclease adjacent to VII-L telomere
S. cerevisiae	90728	L.L. Sandell LS20	Genotype: matΔ his3 ade2 can1 trp1 ura3 leu2 lys5 cyh2 ade3::GALHO
S. cerevisiae	90729	L.L. Sandell LS21	Genotype: matΔ his3 ade2 can1 trp1 ura3 lys5 cyh2 ade3::GALHO rad52::LEU2
S. cerevisiae	90730	L.L. Sandell LS22	Genotype: matΔ his3 ade2 can1 ura3 leu2 lys5 cyh2 ade3::GALHO rad9::TRP1

S. cerevisiae	90731	L.L. Sandell LS24	Genotype: matΔ his3 ade2 can1 ura3 lys5 cyh2 ade3::GALHO rad52::LEU2 rad9::TRP1
S. cerevisiae	90629	G.H. Braus RH1242	Genotype: MATa aro7 leu2. Transform. host (Curr. Genet. 23:201-204, 1993)
S. cerevisiae	90737	E. Jarosch GW7/gd-21.2	Genotype: Mata leu2-3 leu2-112 his3-1 ura3-52 trp1-289 mrs2::HIS3 [rho+ mit+] (J. Biol. Chem. 267:6963-6969, 1992)
S. cerevisiae	90923	R. Esteban RE458	Genotype: MATα ski2-2 L-BC, W, 20S RNA. Produces high amounts of cytoplasmic 20S RNA when transferred to 1% potassium acetate medium after growing in complete medium at 28C (Nucleic Acids Res. 20:2761-2766, 1992)
S. cerevisiae	90924	R. Esteban 37-4C	Genotype: MATa leu1 kar1-1 T, W, 23S RNA, 20S RNA. Standard to purify T and W dsRNA at 28C (Nucleic Acids Res. 20:2761-2766, 1992)
S. cerevisiae	90733	R.F. Gaber R888	Genotype: HOL1-1-101 URA3 hol1Δ1 (Mol. Cell. Biol. 10:643-652, 1990)
S. cerevisiae	90734	R.F. Gaber R757	Genotype: MATα his4-15 ura3-52 lys9 hol1. Transformation host (Mol. Cell. Biol. 10:643-652, 1990)
S. cerevisiae	90481	C.L. Peebles BUB-24C	Genotype: MATα FUN40::URA3 leu2-Δ1 ura3-52. Defect in FUN40, chromosome I marker (Mol. Cell. Biol. 12:3843-3856, 1992)
S. cerevisiae	90482	C.L. Peebles POC8-23d	Genotype: MATα ade2-1 leu2-Δ1 lys2 pta1-1 trp1-Δ101 ura3-52. Defect in pre-tRNA maturation, chromosome I marker (Mol. Cell. Biol. 12:3843-3856, 1992). Transformation host (ibid.)
S. cerevisiae	90784	J. Jacoby HD56-5A/tal1Δ	Genotype: MATα tal1::HIS3 ura3-52 leu2-3 leu2-112 his3-11 his3-15 MAL SUC GAL. Transformation host (Mol. Microbiol. 10:867-876, 1993)
S. cerevisiae	90785	J. Jacoby HD56-5A	Genotype: MATα ura3-52 leu2-3 leu2-112 his3-11 his3-15 MAL SUC GAL. Transformation host (Mol. Microbiol. 10:867-876, 1993)
S. cerevisiae	90834	F. Spencer YPH 925	Genotype: MATα ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ63 leu2Δ1 cyh2R kar1Δ15.
S. cerevisiae	90835	G. Simchen 2477	Genotype: MATα ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ1 leu2Δ1 can1R kar1Δ15.
S. cerevisiae	90836	G. Simchen 2479	Genotype: MATa ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ1 leu2Δ1 can1R kar1Δ15.
S. cerevisiae	90837	G. Simchen 2480	Genotype: MATa ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ63 leu2Δ1 cyh2R kar1Δ15.
S. cerevisiae	90786	E.A. Craig DS16	Genotype: MATa ade2-101 GAL2 his3-11 his3-15 leu2-3 leu2-112 lys2 trp1 ura3-52 ssa1::HIS3 ssa2::LEU2. Temperature-sensitive transformation host (Mol. Cell. Biol. 10:3262-3267, 1990)
S. cerevisiae	90826	D.I. Johnson DJTD2-16A	Genotype: MATa cdc42-1ts ura3 his4 leu2 trp1 gal2. Transformation host (J. Cell Biol. 111:143-152, 1990; Mol. Cell. Biol. 14:1075-1083, 1994)
S. cerevisiae	90827	C.F. Clarke FW103	Genotype: MATα leu2-3 leu2-112 his3Δ1 trp1-289 ura3-52 Δcoq3::LEU2.
S. cerevisiae	90920	J.M. Salmon F23	Alcoholic fermentation (Biotechnol. Lett. 16:89-94, 1994)
S. cerevisiae	90921	J.M. Salmon A54	Alcoholic fermentation
S. cerevisiae	90922	J.M. Salmon A53	Alcoholic fermentation
S. cerevisiae	90838	J.A. Jaehning YJJ464	Genotype: MATa leu2Δ1 his3Δ200 ura3-52. Transformation host (Mol. Cell. Biol. 14:1160-1170, 1994)
S. cerevisiae	90756	S. Hohmann YSH 6.36.-3B	Genotype: MATa leu2-3 leu2-112 ura3-52 trp1-92 GAL SUC mal. Haploid derivative of strain M5 (Curr. Genet. 23:281-289, 1993). Transformation host (Mol. Cell. Biol. 14:4135-4144, 1994)
S. cerevisiae	90840	F. Winston FY23	Genotype: MATa ura3-52 trp1Δ63 leu2Δ1 GAL2+ (Yeast 11:53-55, 1995). Transformation host (Mol. Cell. Biol. 14:4002-4010, 1994)
S. cerevisiae	90841	F. Winston FY67	Genotype: MATa trp1Δ63 GAL2+ (Yeast 11:53-55, 1995)
S. cerevisiae	90842	F. Winston FY69	Genotype: MATa leu2Δ1 GAL2+
S. cerevisiae	90843	F. Winston FY73	Genotype: MATα his3Δ200 ura3-52 GAL2+

S. cerevisiae	90844	F. Winston FY833	Genotype: MATa his3Δ200 ura3-52 leu2Δ1 lys2Δ202 trp1Δ63 GAL2+
S. cerevisiae	90845	F. Winston FY834	Genotype: MATα his3Δ200 ura3-52 leu2Δ1 lys2Δ202 trp1Δ63 GAL2+
S. cerevisiae	90885	F. Karst CM59	Genotype: 14str::TRP1 fen1-1. Accumulates ignosterol as cell sterol; fenpropimorph-resistant (Lipids 28:907-912, 1993)
S. cerevisiae	90886	F. Karst FD49	Resistant to sterol biosynthesis inhibitors (Lipids 28:907-912, 1993)
S. cerevisiae	90909	P.W. Doerner Z042	Genotype: MATα leu2-3 leu2-112 his3-11 his3-15 pad1-42. Transformation host (Gene (Amst.) 142:107-112, 1994)
S. cerevisiae	90910	P.W. Doerner PDY10	Genotype: MATa his4Δ34 leu2-3 leu2-112 pad1-42
S. cerevisiae	90911	P.W. Doerner PDY102	Genotype: MATα ura3- pad1-42
S. cerevisiae	90915	D.R. Appling CBY6	Genotype: MATa ser1 ura3-52 trp1 leu2 his4 ade3-30 ade3-65 ade3-144. Transformation host for cloning and sequencing of gene encoding NAD-dependent 5,10-methylenetetrahydrofolate dehydrogenase on chromosome XI (J. Biol. Chem. 268:153-160, 1993). Does not require adenine in spite of point mutations in ade3 gene (Biochem. 33:74-82, 1994)
S. cerevisiae	90916	D.R. Appling KSY7	Genotype: MATα ser1 ura3-52 ade3-130 (Biochem. 33:74-82, 1994)
S. cerevisiae	90917	D.R. Appling DAY3	Genotype: MATa ser1 ura3-52 trp1 leu2 ade3-130. Requires histidine as indirect result of ade3 deletion (Biochemistry 33:74-82, 1994). Transformation host (J. Biol. Chem. 268:153-160, 1993)
S. cerevisiae	90918	D.R. Appling DAY4	Genotype: MATa ser1 ura3-52 trp1 leu2 his4 (Biochemistry 33:74-82, 1994). Transformation host (J. Biol. Chem. 268:153-160, 1993)
S. cerevisiae	90839	E.J. Louis YP1	Genotype: MATa ura3-52 lys2-801 ade2-101 (Genetics 123:81-89, 1989). Sequence of right telomere of chromosome III (Yeast 10:271-274, 1994). Transformation host (ibid.)
S. cerevisiae	90932	E.J. Louis EJL360-1D	Genotype: MATa ura3-52 ade2-101 lys2-801 leu2Δx-r his4-r can1 (Genetics 123:81-95, 1989)
S. cerevisiae	90933	E.J. Louis EJL363-12B	Genotype: MATα ura3-52 ade2-101 lys2-r2 leu2Δx-r cyh2 trp1::LEU2
S. cerevisiae	90934	E.J. Louis ELT363-6D	Genotype: MATα ura3-52 ade2-101 lys2-rs leu2Δx-r cyh2 trp1-h
S. cerevisiae	90935	E.J. Louis EJL542-16B	Genotype: MATα ura3-52 ade2-101
S. cerevisiae	90971	E.J. Louis S288C-ura3-	Genotype: MATα ura3-.
S. cerevisiae	90972	E.J. Louis tS288C-109	pEL61 integrated at left telomere of chromosome IV.
S. cerevisiae	90973	E.J. Louis tS288C-133	pEL61 integrated at right telomere at chromosome IV.
S. cerevisiae	90974	E.J. Louis tS288C-83	pEL61 integrated at left telomere of chromosome XII.
S. cerevisiae	90975	E.J. Louis tS288C-42	pEL61 integrated at right telomere of chromosome XII.
S. cerevisiae	90976	E.J. Louis tS288C-101	pEL61 integrated at right telomere of chromosome XII.
S. cerevisiae	90977	E.J. Louis tS288C-91	pEL61 integrated at left telomere of chromosome XV.
S. cerevisiae	90978	E.J. Louis tS288C-209	pEL61 integrated at right telomere of chromosome XV.
S. cerevisiae	90979	E.J. Louis tS288C-164	pEL61 integrated at left telomere of chromosome VII.
S. cerevisiae	90980	E.J. Louis tS288C-183	pEL61 integrated at right telomere of chromosome VII.
S. cerevisiae	90981	E.J. Louis tS288C-73	pEL61 integrated at left telomere of chromosome XVI.
S. cerevisiae	90982	E.J. Louis tS288C-64	pEL61 integrated at right telomere of chromosome XVI.
S. cerevisiae	90983	E.J. Louis tS288C-282	pEL61 integrated at left telomere of chromosome II.
S. cerevisiae	90984	E.J. Louis tS288C-197	pEL61 integrated at left telomere of chromosome XIII.
S. cerevisiae	90985	E.J. Louis tS288C-146	pEL61 integrated at right telomere of chromosome XIII.
S. cerevisiae	90986	E.J. Louis tS288C-19	pEL61 integrated at right telomere of chromosome II.
S. cerevisiae	90987	E.J. Louis tS288C-106	pEL61 integrated at left telomere of chromosome XIV.
S. cerevisiae	90988	E.J. Louis tS288C-208	pEL61 integrated at right telomere of chromosome XIV.

S. cerevisiae	90989	E.J. Louis tS288C-34	pEL61 integrated at left telomere of chromosome X.
S. cerevisiae	90990	E.J. Louis tS288C-168	pEL61 integrated at right telomere of chromosome X.
S. cerevisiae	90991	E.J. Louis tS288C-89	pEL61 integrated at left telomere of chromosome XI.
S. cerevisiae	90992	E.J. Louis tS288C-113	pEL61 integrated at right telomere of chromosome XI.
S. cerevisiae	90993	E.J. Louis tS288C-80	pEL61 integrated at left telomere of chromosome VIII.
S. cerevisiae	90994	E.J. Louis tS288C-72	pEL61 integrated at right telomere of chromosome VIII.
S. cerevisiae	90995	E.J. Louis tS288C-163	pEL61 integrated into left telomere of chromosome V.
S. cerevisiae	90996	E.J. Louis tS288C-88	pEL61 integrated into right telomere of chromosome V.
S. cerevisiae	90997	E.J. Louis tS288C-138	pEL61 integrated into left telomere of chromosome IX.
S. cerevisiae	90998	E.J. Louis tS288C-7	pEL61 integrated into right telomere of chromosome IX.
S. cerevisiae	90999	E.J. Louis tS288C-159	pEL61 integrated into left telomere of chromosome III.
S. cerevisiae	96000	E.J. Louis tS288C-36	pEL61 integrated into right telomere of chromosome III.
S. cerevisiae	96001	E.J. Louis tS288C-14	pEL61 integrated into left telomere of chromosome VI.
S. cerevisiae	96002	E.J. Louis tS288C-174	pEL61 integrated into right telomere of chromosome VI.
S. cerevisiae	96003	E.J. Louis tS288C-194	pEL61 integrated into left telomere of chromosome I.
S. cerevisiae	96004	E.J. Louis tS288C-1	pEL61 integrated into right telomere of chromosome I.
S. cerevisiae	96135	J. Colicelli PP5	Genotype: MATa leu2-3 leu2-112 ura3-52 his3-532 his4 cam pdel::URA3 pde2::HIS3. Phosphodiesterase-deficient and heat shock-sensitive transformation host (Proc. Natl. Acad. Sci. USA 90:11970-11974, 1993).
S. cerevisiae	96146	F. Doignon FD 310-1A	Genotype: MATα; flusilazole-resistant. Imidazole- and triazole-resistant transformation host (Plasmid 30:224-233, 1993)
S. cerevisiae	96147	F. Doignon FK erg16	Genotype: MATa erg16; lanosterol demethylase-deficient (Plasmid 30:224-233, 1993)
S. cerevisiae	90714	P. Sollitti JM1901	Genotype: MATα MAL1 his4 lys. AMP deaminase gene (J. Biol. Chem. 268: 4549-4555, 1993)
S. cerevisiae	90715	P. Hieter YPH636	Genotype: MATa ura3-52 lys2-801 ade2-101 his3Δ200 trp1Δ1 leu2Δ1 mck1::HIS3. Transformation host (Mol. Cell. Biol. 14:831-839, 1994)
S. cerevisiae	96093	J.C. Wang JCW 28	Genotype: Δtop1 top2-4; temperature-sensitive. DNA topoisomerase mutant.
S. cerevisiae	96094	J.C. Wang JCW 253	Genotype: Δtop3::TRP1 (slow growth). DNA topoisomerase mutant.
S. cerevisiae	96095	J.C. Wang JCW 263	Genotype: Δtop3::TRP1 top2-4; temperature-sensitive, growth slow at permissive temperatures below 26C. DNA topoisomerase mutant.
S. cerevisiae	96096	J.C. Wang JCW 26	Genotype: top2-4; temperature-sensitive. DNA topoisomerase mutant.
S. cerevisiae	96097	J.W. Wang JCW 27	Genotype: Δtop1. DNA topoisomerase mutant.
S. cerevisiae	96098	J.C. Wang CH1585	Genotype: MATa leu2Δ1 trpΔ63 ura3-52 his3-200.
S. cerevisiae	96039	M. Maiwald & R. Kappe HD 505/92	18S-rRNA sequence, EMBL J01353 (J. Med. Vet. Mycol. 32:115-122, 1994)
S. cerevisiae	76455	A. Tzagoloff N230	Genotype: MATα met6 atp13. Resp.-def. due to impaired expression of s.u. 9 of mitochondrial ATPase (FEBS Lett 278:234-238, 1991)
S. cerevisiae	76456	A. Tzagoloff C264	Genotype: MATα met6 atp12-1 [rho+]. Resp.-def. due to impaired mitochondrial ATPase assembly (J. Biol. Chem. 266:7517-7523, 1991)
S. cerevisiae	76457	A. Tzagoloff C164/L1/T1	Genotype: MATα leu2-3 leu2-112 cox11-1+ pG53/T1. Carries genomic library of COX11 in plasmid pG53/T1 (EMBO J. 9:2759-2764, 1990)
S. cerevisiae	76458	A. Tzagoloff B264/U4/T1	Genotype: MATa ura3-1 atp12-1 [rho+] pG57/T1. Carries genomic library of ATP12 in plasmid pG57/T1 (J. Biol. Chem. 266:7517-7523, 1991)

S. cerevisiae	76459	A. Tzagoloff W303∇MRP2	Genotype: MATα ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-1 MRP2::HIS3 [rho-]. Respiratory-deficient due to impaired mitochondrial ribosomal protein assembly (J. Biol. Chem. 262:3388-3397, 1987)
S. cerevisiae	76460	A. Tzagoloff aW303∇MSK1	Genotype: MATa ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-1 msk1::HIS3 rho-.
S. cerevisiae	76461	A.Tzagoloff aW303ΔCOX10	Genotype: MATa ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-1 cox10::HIS3 [rho+]. Respiratory-deficient due to impaired cytochrome oxidase assembly (J. Biol. Chem. 265:14220-14226, 1990)
S. cerevisiae	76462	A. Tzagoloff aW303ΔCOX11	Genotype: MATa ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-11 COX11::HIS3. Respiratory-deficient due to impaired cytochrome oxidase assembly (EMBO J. 9:2759-2764, 1990)
S. cerevisiae	76463	A. Tzagoloff C167/L1/T1	Genotype: MATα leu2-3 leu2-112 mrp2-1 [rho+]+ pG89/T1. Carries recombinant plasmid with wild-type MRP2 gene (J. Biol. Chem. 262:3388-3397, 1987)
S. cerevisiae	76464	A. Tzagoloff W303ΔATP13	Genotype: MATα ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-1 ATP13::HIS3. Respiratory-deficient due to impaired mitochondrial ATPase assembly (FEBS Lett. 278:234-238, 1991)
S. cerevisiae	76465	A. Tzagoloff W303ΔATP12	Genotype:MATα ade2-1 his3-11 his3-15 leu2-3 leu2-112 trp1-1 ura3-1 atp12::LEU2 [rho+]. Respiratory-deficient due to impaired mitochondrial ATPase assembly (J. Biol. Chem. 266:7517-7512, 1991)
S. cerevisiae	76466	A. Tzagoloff N230/U6/T1	Genotype: MATα ura3-1 atp13+ pG95/T1. Carries recombinant plasmid with wild-type ATP13 gene (FEBS Lett. 278:234-238, 1991)
S. cerevisiae	76467	A. Tzagoloff C145/L1/T6	Genotype: MATα leu2-3 leu2-112 msk1-1 [rho+]+ pG11/T6. Carries recombinant plasmid with w.t. MSK1 gene (J. Mol. Biol. 218:557-568, 1991)
S. cerevisiae	76468	A. Tzagoloff C145	Genotype: MATα met6 msk1-1 [rho+]. Resp.-def. due to impaired acylation of mitochondrial lys1-tRNA synthetase (J. Mol. Biol. 218:557-568, 1991)
S. cerevisiae	76469	A. Tzagoloff C164	Genotype: MATα met6 cox11-1. Respiratory-deficient (EMBO J. 9:2759-2764, 1990)
S. cerevisiae	96297	K. Tamamoto UH1-GRGZ	Genotype: MATα hsp82::LEU2 hsc82::LEU2 ade2 ura3 trp1 his3. Transformation host for isolation of HSP90 mutants (Proc. Natl. Acad. Sci. USA 90:11424-11428, 1993)
S. cerevisiae	96342	H.-J. Schuller JS89.27-3	Genotype: MATa ura3 leu2 trp1 can1 MAL3 SUC3. Transformation host (Mol. Cell. Biol. 14:3613-3622, 1994; Curr. Genet. 23:375-381, 1993)
S. cerevisiae	90855	G.R. Fink CG934	Genotype: MATa/MATα ura3-52/ura3-52 (pCG38). Requires a selective medium lacking uracil to maintain the plasmid. Induction of pseudohyphal growth on medium 1905 (Mol. Cell. Biol. 14:2100-2112, 1994)
S. cerevisiae	90856	G.R. Fink CG936	Genotype: MATa/MATα ura3-52/ura3-52 (pRS202). Requires a selective medium lacking uracil to maintain the plasmid. Induction of pseudohyphal growth on medium 1905 (Mol. Cell. Biol. 14:2100-2112, 1994)
S. cerevisiae	96316	M.N. Hall MH339	Genotype: MATa/MATα trp1/trp1 his4/his4 leu2/leu2 ura3/ura3 rme1/rme1 HMLa/HMLa TRP1/TRP1 HIS4/HIS4 LEU2/LEU2. Transformation host (Mol. Cell. Biol. 14:6597-6606, 1994)
S. diastaticus	90944	J.P. Delgenes rho(o)	Co-fermentation of glucose and xylose mixture to ethanol (Appl. Microbiol. Biotechnol. 39:760-763, 1993)
S'copsis sp.	62895	J. Haanstad & D. Norris	Ambrosia beetle, *Xyloterinus politus,* Wisconsin.
Schiz. pombe	90767	H. Gutz SA21(h+s)	Stable plus mating type (Curr. Genet. 23:108-114, 1993)
Schiz. pombe	90335	M. McLeod FYC1	Genotype: h- (Alfa, C., et al. Experiments with fission yeast. New York: Cold Spring Harbor Laboratory Press; 1993)
Schiz. pombe	90341	M. McLeod FYC12	Genotype: h- ade6-M216 (Alfa, C., et al. Experiments with fission yeast. New York: Cold Spring Harbor Laboratory Press; 1993)

Schiz. pombe	90357	M. McLeod FYC39	Genotype: h90 cgs2-2 leu1-32 ade6-M216 (Alfa, C., et al. Experiments with fission yeast. New York: Cold Spring Harbor Laboratory Press; 1993)
Schiz. pombe	90359	M. McLeod FYC71	Genotype: h90 mei2::mei2 lacZ leu1-32 ade6-M216. (Alfa, C., et al. Experiments with fission yeast. New York: Cold Spring Harbor Laboratory Press; 1993)
Schiz. pombe	90361	M. McLeod FYC75	Genotype: h90 mei2::mei2 lacZ (Alfa, C., et al. Experiments with fission yeast. New York: Cold Spring Harbor Laboratory Press; 1993)
Schiz. pombe	96341	P. Russell PR166	Genotype: h- swo1-26 ura4-D18 leu1-32. Temperature-sensitive transformation host (Mol. Cell. Biol. 14:3742-3751, 1994)
Schiz. pombe	96078	D. Beach SP530	Genotype: h(-S) cdc25-22 leu1-32 (Mol. Cell. Biol. 14:768-776, 1994)
Schiz. pombe	96079	D. Beach SP826	Genotype: h(+N)/h(+N) ura4-D18/ura4-D18 leu1-32/leu1-32 ade6-210/ade6-216 (Mol. Cell. Biol. 14:768-776, 1994)
Schiz. pombe	96080	D. Beach SP976	Genotype: h(+N)/h(+N) leu1-32/leu1-32 ade6-704/ade6-704 (Mol. Cell. Biol. 14:768-776, 1994)
Schiz. pombe	96081	D. Beach SP1051	Genotype: h(+N) ura4 leu1-32 ade6-704 (Mol. Cell. Biol. 14:768-776, 1994)
Schiz. pombe	96082	D. Beach SP1190	Genotype: h(-S) ura4 leu1-32 ade6-704 (Mol. Cell. Biol. 14:768-776, 1994)
Schiz. pombe	96083	D. Beach SP1191	Genotype: h(-S) ura4 leu1-32 ade6-704
Schiz. pombe	96084	D. Beach SP1192	Genotype: h(+N) cig1::ura4 ura4 leu1-32 ade6-704
Schiz. pombe	96085	D. Beach SP1193	Genotype: h(+N) cig1::ura4 cig2::sup3-5 ura4 leu1-32 ade6-704
Schiz. pombe	96086	D. Beach SP1194	Genotype: h(-S) cdc13-117 ura4 leu1-32 ade6-704
Schiz. pombe	96087	D. Beach SP1195	Genotype: h(+N) cig1::ura4 cdc13-117 ura4 leu1-32 ade6-704
Schiz. pombe	96088	D. Beach SP1196	Genotype: h(-S) cig2::sup3-5 cdc13-117 ura4 leu1-32 ade6-704
Schiz. pombe	96089	D. Beach SP1197	Genotype: h(-S) cig1::ura4 cig2::sup3-5 cdc13-117 ura4 leu1-32 ade6-704
Schiz. pombe	96092	D. Beach SP1200	Genotype: h(-S) ura4 leu1-32 ade6-704 sup3-5
Schiz. pombe	96090	D. Beach SP1198	Genotype: h+ cig2::sup3-5 ura4 leu1-32 ade6-704
Schiz. pombe	96091	D. Beach SP1199	Genotype: h(+N) ura4 leu1-32 ade6-704 sup3-5
Y. lipolytica	74234	Pfizer Inc. FD 29318	(Patent Application)
Y. lipolytica	96028	R.E. Levin CL1	Produces extracellular protease (J. Appl. Bacteriol. 71:354-359, 1991)
Y. lipolytica	90811	H. Nguyen JM12	Genotype: leu2-35 lys5-12 ura3-18 XPR2B. Control of XPR2 gene expression (Mol. Cell. Biol. 14:327-338, 1994). Transformation host (ibid.)
Y. lipolytica	90812	H. Nguyen JM23	Genotype: leu2-35 lys5-12 ura3-18 xpr2::LYS5B. Control of XPR2 gene expression (Mol. Cell. Biol. 14:327-338, 1994). Transformation host (ibid.)
Y. lipolytica	90813	H. Nguyen JM12PF	Control of XPR2 gene expression (Mol. Cell. Biol. 14:327-338, 1994)
Y. lipolytica	90814	H. Nguyen JM23SB	Control of XPR2 gene expression (Mol. Cell. Biol. 14:327-338, 1994)
Yeast	74271	Pillsbury Co.	GAL+/lts #8 (Patent Application)
Yeast	74272	Pillsbury Co.	a/α GAL+ #33 (Patent Application)

Workshops offered by ATCC

- Fermentation Microbiology, July 25-28, 1995.
- 13th Annual ATCC Biotechnology Patent Forum, August 24-25, 1995.
- Microscopy/Photomicrography, September 20-22, 1995.
- Cytogenetic and fluorescence in situ hybridization techniques, September 25-27, 1995.
- Downstream processing, recovery and purification of proteins, October 18-20, 1995.
- Freezing & Freeze-Drying of Microorganisms, November 1-3, 1995.
- Recombinant DNA: Techniques and Applications, November 6-10, 1995.
- Polymerase Chain Reaction (PCR) Applications/Cycle DNA Sequencing, November 14-17, 1995.

For additional information, contact: ATCC, Workshop Coordinator, 12301 Parklawn Drive, Rockville Md U.S.A. 20852. Tel (301)231-5566. Fax: (301)816-4364.

II. Centraalbureau voor Schimmelcultures, Oosterstraat 1, P.O.Box 273, 3740 AG Baarn, The Netherlands. Communicated by J.M.J. Uijthof <Uijthof@cbsc.nl>.

The following papers have been published.

1. Atlas of Clinical Fungi. Eds. G.S. de Hoog & J. Guarro. 1995. Centraalbureau voor Schimmelcultures, Baarn, The Netherlands. 720 pp. ISBN 90-70351-26-9.

The atlas treats over 135 pathogenic and 190 opportunistic fungi, including species causing animal mycoses. Recently discovered opportunists are devoted two full pages per species. These are described and illustrated with detailed line drawings and light and electron microscopic photographs. Reference to main taxonomic and clinical literature is made. The book contains extended keys to such emerging groups of fungi as black yeasts, the coelomycetes, and to all clinically relevant species of *Aspergillus, Fusarium, Penicillium* and many other genera. The chapter on yeasts is 35 pages long and handles about 30 pathogenic or opportunistic species.

2. G.S de Hoog, T. Matsumoto, T. Matsuda & J.M.J. Uijthof. 1994. *Exophiala jeanselmei* var. *lecanii-corni,* an aetiologic agent of human phaeohyphomycosis, with report of a case. J. Med. Vet. Myc. **32**:373-380.
3. G.S. de Hoog, L. Sigler, W.A. Untereiner, K.J. Kwon-Chung, E.Guého & J.M.J. Uijthof. 1994. Changing taxonomic concepts and their impact on nomenclatural stability. J. Med. Vet. Myc. **32** (Supp. 1):113-122.
4. G.S. de Hoog & N.A. Yurlova. 1994. Conidiogenesis, nutritional physiology and taxonomy of *Aureobasidium* and *Hormonema.* Antonie van Leeuwenhoek **65**:41-54.
5. J.M.J. Uijthof, G.S. de Hoog, A.W.A.M. de Cock, K. Takeo & K. Nishimura. 1994. Pathogenicity of strains of the black yeast *Exophiala (Wangiella) dermatitidis:* an evaluation based on polymerase chain reaction. Mycoses **37**:235-242.
6. J.M.J. Uijthof, A.W.A.M. de Cock, G.S. de Hoog, W.G.V. Quint & A. van Belkum. 1994. Polymerase chain reaction-mediated genotyping of *Hortaea werneckii,* causative agent of tinea nigra. Mycoses **37**:307-312.

The following papers are in press:

7. G. Haase, L. Sonntag, Y. van de Peer, J.M.J. Uijthof, A. Podbielski & B. Melzer-Krick. 1995. Phylogenetic analysis of ten black yeast species using nuclear small subunit rRNA gene sequences. Antonie van Leeuwenhoek.
8. G.S. de Hoog, A.H.G. Gerrits van den Ende, J.M.J. Uijthof & W.A. Untereiner. 1995. Nutritional physiology of type isolates of currently accepted species of *Exophiala* and *Phaeococcomyces.* Antonie van Leeuwenhoek.
9. K. Takeo, G.S. de Hoog, M. Miyaji & K. Nishimura. 1995. Conidial surface ultrastructure of human-pathogenic and saprobic *Cladosporium* species. Antonie van Leeuwenhoek.
10. J.M.J. Uijthof & G.S. de Hoog. 1995. PCR-ribotyping of type isolates of currently accepted *Exophiala* and *Phaeococcomyces* species. Antonie van Leeuwenhoek.
11. N.A. Yurlova, I.V. Mokrousov & G.S. de Hoog. 1995. Intraspecific variability and exopolysaccharide production in *Aureobasidium pullulans.* Antonie van Leeuwenhoek.
12. F. Masclaux, E. Guého, G.S. de Hoog & R. Christen. 1995. Phylogenetic relationships of human pathogenic *Cladosporium (Xylohypha)* species inferred from partial LS rRNS sequences. J.Med. Vet. Mycol.
13. G.S. de Hoog, K. Takeo, E. Göttlich, K. Nishimura & M. Miyaji. 1995. A human isolate of *Exophiala (Wangiella) dermatitidis* forming a catenate synanamorph that links the genera *Exophiala* and *Cladophialophora.* J.Med. Vet. Mycol.

14. G.S. de Hoog, E. Guého, F. Masclaux, A.H.G. Gerrits van den Ende, K.J. Kwon-Chung & M.R. McGinnis. 1995. Nutritional physiology and taxonomy of human-pathogenic *Cladosporium-Xylohypha* species. J. Med. Vet. Mycol.

15. K. Tintelnot, P. von Hunnius, G.S. de Hoog, A. Polak-Wyss, E. Guého & F. Masclaux. 1995. Systemic mycosis caused by a new *Cladophialophora* species. J. Med. Vet. Mycol.

16. U. Wollenzien, G.S. de Hoog, W.E. Krumbein and C. Urzi. 1995. On the isolation, cultivation and taxonomy of microcolonial fungi occurring on and in marble and other calcareous rocks. Sci.Total. Environm.

III. Department of Applied Microbiology and Food Science, University of Saskatchewan, Saskatoon, Canada S7N 0W0. Communicated by W.M. (Mike) Ingledew <ingledew@agric.usask.ca>.

The following papers have been published since our last report.

1. W.M. Ingledew, D.W. Hysert. 1994. Brewing Technology. In: Encyclopedia of Agricultural Science **1**:315-326.

The brewing of beer, long regarded as an art, has become an industry based on multidisciplinary sciences including food science, microbiology, engineering, chemistry, and aspects of commerce which ensure the longevity and profits of the enterprise. This review of brewing will focus on the scientific basis of brewing technology from the malting process through the production of wort, fermentation, aging and packaging (see Fig. 1 for a process flow diagram). The essential ingredients (water, malted barley, hops and yeast) and brewing adjuncts will also be described. Although the approach will of necessity be from an industrial viewpoint, the importance of the basic sciences and engineering will be obvious.

2. K.C. Thomas, W.M. Ingledew. 1994. Lysine inhibition of *Saccharomyces cerevisiae:* role of repressible L-lysine ε-aminotransferase. World J. Microbiol. Biotechnol. **10**:572-575.

Lysine added to grain mashes under nitrogen-limiting conditions (most industrial fermentations) inhibited growth of *S. cerevisiae.* This inhibition was relieved by raising the assimilable nitrogen content. Lysine induced inhibition is not mediated through accumulation of α-oxoadipic acid, an intermediate of lysine metabolism which accumulates by a back up of intermediates in de novo synthesis. Lysine degradation is regulated by the synthesis of L-lysine ε-aminotransferase, an enzyme that catalyzes the first step in one of three possible routes of lysine degradation (not previously reported in *S. cerevisiae*). Synthesis is repressed under nitrogen limiting conditions, but derepressed when excess assimilable nitrogen is available. Derepression results in degradation of lysine and decreases inhibitory effects on growth. The toxic compound appears to be lysine itself.

3. A.M. Jones, W.M. Ingledew. 1994. Fuel alcohol production: Assessment of selected commercial proteases for very high gravity wheat mash fermentation. Enz. Microb. Tech. **16**:683-687.

Seven commercial proteolytic enzymes were studied for use in very high gravity (VHG) fermentation. Wheat mashes containing 35 g dissolved solids per 100 ml were prepared and fermented at 20°C with active dry *Saccharomyces cerevisiae.* Proteases were assessed for their ability to hydrolyze soluble wheat proteins to free amino nitrogen, and to reduce the viscosity of very high gravity wheat mashes. It was found that the increased levels of yeast-assimilable nitrogen and reduced mash viscosity stimulated the rate of VHG fermentation. Ethanol yield was not appreciably affected, nor did the addition of proteolytic enzymes adversely affect saccharification by the glucoamylase enzyme. Therefore, under VHG conditions, utilization of proteases could eliminate the need for supplementing wheat mash with assimilable nitrogenous yeast foods. These data further contribute to the industrial assessment of VHG fermentation technology for the manufacture of fuel alcohol from wheat.

4. A.M. Jones, W.M. Ingledew. 1994. Fuel alcohol production: appraisal of nitrogenous yeast foods for very high gravity wheat mash fermentation. Proc. Biochem. **29**:483-488.

A scientific and economic appraisal of various nitrogen-containing yeast foods usable for very high gravity (VHG) fermentation technology was conducted. VHG wheat mashes containing 350 g dissolved solids per litre were prepared by enzymatic hydrolysis of milled wheat, and then fermented with active dry yeast (*Saccharomyces cerevisiae*). Although such wheat mashes were limiting in assimilable nitrogen, they fermented to completion within 9 days at 20°C. However, by adding assimilable forms of nitrogen, fermentation was accelerated. For example, in the presence of 1% (w/w) yeast extract, fermentation was completed in 4 days with a yield of 20.3% (v/v) ethanol. Unfortunately, yeast extract at the required level is too costly for routine use in the fuel alcohol industry. The testing of other nutrient supplements revealed that urea, ammonium ion, and Fermaid K compared favourably to yeast extract in stimulating VHG fermentation of wheat mash. Of these, urea is the most economically attractive for the industrial production of fuel alcohol. These results are an important contribution to the industrial assessment of VHG fermentation technology.

5. A.M. Jones, K.C. Thomas, W.M. Ingledew. 1994. Ethanolic fermentation of blackstrap molasses and sugarcane juice using very high gravity technology. J. Agric. Food Chem. 42: 1242-1246.

The fermentability of blackstrap sugar cane molasses was examined under very high gravity (VHG) conditions. Molasses fermentations were carried out over the range of 10.4 to 47.6% (w/v) dissolved solids. As the concentration of dissolved solids increased, the percentage of sugar actually converted to ethanol decreased. The suitability of molasses as a carbohydrate adjunct for VHG ethanolic fermentation was also studied; molasses was used to raise the dissolved solids content of both clarified wheat mash base and sugar cane juice to VHG levels. Fermentation of such mashes was 90-93% efficient. In VHG wheat mashes prepared with molasses adjunct, yeast extract accelerated the rate of fermentation, but had little effect on the final ethanol concentration. Sugar cane juice was not limiting in assimilable nitrogen since yeast extract or urea failed to stimulate the rate of fermentation of cane juice/molasses worts, or increase the final ethanol concentration achieved. This is the first report of the application of VHG technology to fermentation substrates other than wheat, wort, and grape juice. It is concluded that VHG fermentation of saccharine substrates could lead to moderate increases in alcohol concentration as compared to those presently achieved in industry.

6. K.C. Thomas, S.H. Hynes, W.M. Ingledew. 1994. Effects of particulate materials and osmoprotectants in very-high-gravity ethanolic fermentations. Appl. Environ. Microbiol. 60: 1519-1524.

The effects of osmoprotectants (such as glycine betaine and proline) and particulate materials on the fermentation of very high concentrations of sugars by the brewing strain *Saccharomyces cerevisiae* (*uvarum*) NCYC 1324 were studied. The yeast fermented only 43% of the sugar in 10 days at 20°C from a minimal medium which initially contained 35% (w/v) glucose. Supplementing the medium with a mixture of glycine betaine, glycine and proline increased the amount of sugar fermented to 87%. With such supplementation the viability of the yeast cells was maintained above 80% throughout the fermentation while it dropped to less than 12% in the unsupplemented controls. Among single additives, glycine was more effective than proline or glycine betaine. It is suggested that glycine and proline, known to be poor nitrogen sources for growth, may serve directly or indirectly as osmoprotectants. Nutrients such as tryptone, yeast extract or a mixture of purine and pyrimidine bases stimulated the rate of sugar uptake and ethanol production but did not maintain the high level of cell viability observed with the mixture of glycine betaine, glycine and proline. Particulate materials such as wheat bran, wheat mash insolubles, alumina, and soy flour stimulated sugar uptake and fermentation to varying degrees.

The following theses have been completed.

7. M.S. Whiting. 1995. Detection of *Lactobacillus* and *Pediococcus* surface antigens using polyclonal and monoclonal antibodies. PhD Thesis. University of Saskatchewan.

8. C.A. Patterson. 1995. Utilization and transport of dipeptides by *Saccharomyces cerevisiae* NCYC 1324. PhD Thesis. University of Saskatchewan.

IV. State Scientific-Research Institute for Genetics and Selection of Industrial Microorganisms, I Dorozhnyi 1, Moscow 113545, Russia. Communicated by G.I. Naumov and E.S. Naumova.

We would like to thank Enrique Sancho (Dept. of Microbiology, University of Cordoba), Rhona Borts and Edward Louis (Oxford University, U.K.), Liisa Halkka, Hilkka Turakainen and Dennis Bamford (Dept. of Genetics, University of Helsinki) and Matti Korhola (ALKO/PRIMALCO, Helsinki) for the possibility to do yeast research in their labs in 1993-1995. Our address in September-December 1995 is: Departamento de Microbiologia, Escuela Tecnica Superior de Ingenieros Agronomos, Universidad de Cordoba, Apartado 3048, 14080 Cordoba, España. Fax (34 57) 218563.

The following papers have been published recently or will appear in the near future.

1. G.I. Naumov, E.S. Naumova & E.D. Sancho. 1994. Sibling species of the *Saccharomyces sensu stricto* complex in Spain. Microbiologia SEM **10**:403-412.

2. E. Naumova, G. Naumov & A. Panek. 1994. Polymorphism of trehalose accumulation in sibling species of *Saccharomyces sensu stricto.* Revista Brasiliera de Genetica **17**:133-138.

3. G.I. Naumov. 1994. A study on taxonomic and evolutionary genetics of yeasts (Minireview). Biotechnologia **7**:3-4 (in Russian).

4. G.I. Naumov, F. Calero, E.S. Naumova & E. Sancho. 1994. Genetic peculiarities of Spanish sherry yeast *Saccharomyces cerevisiae* from the region Montilla-Moriles. Biotechnologia **8**:11-13 (in Russian).

5. E.S. Naumova, C.A. Michels & G.I. Naumov. 1994. Identification of genes for maltose fermentation in *Saccharomyces paradoxus.* Biotechnologia **11-12**:3-5 (in Russian).

6. G.I. Naumov. 1995. Breeding of eucaryotic microorganisms (Minireview). Biotechnologia (in press, in Russian).
7. G.I. Naumov, E.S. Naumova & M. Korhola. 1995. Chromosomal polymorphism of *MEL* genes in some populations of *Saccharomyces cerevisiae.* FEMS Microbiology Letters **127**:41-45.
8. G.I.Naumov, E.S. Naumova, A.N. Hagler, L.C. Mendonça-Hagler & E.J. Louis. 1995. A new genetically isolated population of the *Saccharomyces sensu stricto* yeast from Brazil. Antonie van Leeuwenhoek (in press).
9. G.I. Naumov, E.S. Naumova & E.J. Louis. 1995. Genetic mapping of the α-galactosidase *MEL* gene family on right and left telomeres of *Saccharomyces cerevisiae.* Yeast **11**:481-483.
10. G.I. Naumov, E.S. Naumova & M. Korhola. 1995. Karyotypic relationships among species of *Saccharomyces sensu lato - S. castellii, S. dairensis, S. unisporus* and *S. servazzii*. System. Appl. Microbiology (in press).
11. G.I. Naumov, E.S. Naumova & M.N. Shchurov. 1995. Chromosomal polymorphism of the type species *Pichia membranaefaciens:* sibling species. Dokl. Akad. Nauk (in press, in Russian).
12. M. Korhola, H. Torkkeli, H. Turakainen, V. Joutsjoki, E. Parkkinen, E. Naumova & G. Naumov. 1995. Natural and constructed melibiose$^+$ yeasts. In: Control of Metabolic Flux: Metabolic Pathway Engineering in Yeasts. 7-12 April, 1995, Granada, Spain, P. 26.
13. G.I. Naumov, E.S. Naumova & E.J. Louis. 1995. Two new genetically isolated populations of the *Saccharomyces sensu* stricto complex from Japan. J. Gen. Appl. Microbiol. (submitted).
14. G.I. Naumov, E.S. Naumova, H. Turakainen & M. Korhola. 1995. Identification of α-galactosidase *MEL* genes in some populations of *Saccharomyces cerevisiae:* new *MEL11* gene. (the research has been mainly done at the Department of Genetics of Helsinki University; manuscript in preparation).

Using genetic hybridization analysis, molecular karyotyping and Southern hybridization with the *MEL1* probe comparative study of *MEL* genes in wine, clinical and alpechin populations of *S. cerevisiae* have been conducted. A new *MEL11* member of α-galactosidase gene family was found. The *MEL11* gene was mapped by tetrad analysis at the left end of chromosome 1.

V. Industrial Biotechnology, Novo Nordisk A/S, Novo Allé, DK-2880 Bagsvaerd, Denmark. Communicated by K. Oxenbøll.

1. K. Oxenbøll. 1994. *Aspergillus* enzymes and industrial uses. In: The Genus *Aspergillus,* Edited by K.A. Powell *et al*., Plenum Press, New York, pp., 147-154.

Conclusion. The advent of gene technology offers a dramatic expansion in the range of microbial sources for new industrial enzymes. Therefore microbiologists who carry out screening programmes need no longer limit themselves to microorganisms that are easy to handle in large scale culture. Although in the long term this means the importance of *Aspergillus* as a source for future industrial enzymes will diminish. There is, however, every reason to believe that *Aspergillus* will remain the single most dominant genus on the arena of industrial enzymes from fungi for many years to come.

VI. National Collection of Yeast Cultures, AFRC Institute of Food Research, Norwich Laboratory, Norwich Research Park, Colney, Norwich NR4 7UA, United Kingdom. Communicated by I.N. Roberts <ian.roberts@bbsrc.ac.uk>.

The following publications have appeared recently.

1. James, S.A., Collins, M.D., Roberts, I.N. 1994. Genetic interrelationship among species of the genus *Zygosaccharomyces* as revealed by small subunit rRNA gene sequences. Yeast **10**:871-881.
2. James, S.A., Collins, M.D., Roberts, I.N. 1994. The genetic relationship of *Lodderomyces elongisporus* to ascomycete yeast species as revealed by small-subunit rRNA gene sequences. Lett. Appl. Microbiol. **19**:308-311.

3. Pearson, B.M., Carter, A.T., Furze, J., Roberts, I.N. 1995. A novel approach for discovering retrotransposons: characterization of a long terminal repeat element in the spoilage yeast *Pichia membranaefaciens* and its use in strain identification. Int. J. Syst. Bacteriol. **45**:386-389.

4. Bond, C.J. 1995. Cryopreservation of yeast cultures. In Day, J.G. & McClellan, M.R. (Eds) Methods in Molecular Biology: Cryopreservation and Freeze-drying Protocols. Humana Press, New Jersey.

VII. Department of Microbiology and Molecular Genetics, Oklahoma State University, Stillwater OK 74078. Communicated by H.S. Vishniac.

The following paper was accepted recently.

1. H. S. Vishniac. In Press. Simulated in situ ability and survival of a representative soil yeast, *Cryptococcus albidus*. Microb. Ecol.

Cryptococcus albidus successfully competes with the native bacterial biota of a loamy sand, for natural substrates, when co-cultured in a loamy sand microcosm under certain droughty conditions. Success appears correlated with bacterial lag phases.

VIII. Institut Curie, Section de Biologie, Bât. 110, Centre Universitaire, 91405 Orsay Cédex, France. Communicated by H. Fukuhara.

Recent publication

1. M. Wesolowski-Louvel & H. Fukuhara. 1995. A map of the *Kluyveromyces lactis* genome. Yeast **11**:211-218.

(Excerpted by Editor). Figure 1 is a compilation of available data assembled in the form of a preliminary map which may serve as a working tool and as a basis of future refinement. Here, mapping results on 75 genes identified have been assembled. Gene distances were obtained by meiotic segregation using the original formula of Perkins (1949). Cloned genes were mapped to specific chromosomes by hybridization of gene probes provided by several laboratories. Some gene linkages and organizations are based on sequencing data. Unpublished data from many colleagues are also included. No contradictions have been found so far between genetic and physical mapping, although a few strain-dependent gene duplications and deletions are known.

IX. Molecular and Population Genetics Group, Research School of Biological Sciences, The Australian National University, P.O. Box 475, Canberra, ACT 2601, Australia. Communicated by G.D. Clark-Walker <DCW@rsbs-central.anu.edu.au>.

The following paper was accepted recently.

1. X.J. Chen & G.D. Clark-Walker. In press. Specific mutations in α and γ-subunits of F_1-ATPase affect mitochondrial genome integrity in the petite-negative yeast *Kluyveromyces lactis*. EMBO J.

We have shown previously that mutations in nuclear genes, termed *MGI,* for mitochondrial genome integrity, can convert the petite-negative yeast *Kluyveromyces lactis* into a petite-positive form with the ability to produce mitochondrial genome deletion mutants (Chen & Clark-Walker, 1993, Genetics **133**:517-525). Here we describe that two genes, *MGI2* and *MGI5,* encode the α and γ-subunits of mitochondrial F_1-ATPase. Specific mutations, Phe443 → Ser and Ala333 → Val in *MGI2,* and Thr275 → Ala in *MGI5,* confer on cells the ability to produce petite mutants spontaneously with deletions in mitochondrial DNA and the capacity to lose their mitochondrial genomes upon treatment with ethidium bromide. Structural integrity of the F_1 complex seems to be needed for expression of the Mgi^- phenotype as null mutations in *MGI2* and *MGI5* remove the ability to form mtDNA deletions. It is suggested that *mgi* mutations allow petites to survive because an aberrant F_1 complex prevents collapse of the mitochondrial inner membrane potential that normally occurs on loss of mtDNA-encoded F_o subunits.

X. Biochemisches Institut der Universität Freiburg, Hermann-Herder-Straβe 7, D-7800 Freiburg, Germany. Communicated by H. Holzer.

The following paper was accepted recently.

1. S. Nwaka, M. Kopp, & H. Holzer. 1995. Expression and function of the trehalase genes *NTH1* and *YBR0106* in *Saccharomyces cerevisiae*. J. Biol. Chem. (in press).

The biological function of the trehalose degrading yeast enzyme neutral trehalase consist of the control of concentration of trehalose, which is assumed to play a role in thermotolerance, in germination of spores, and in other life functions of yeast. Resequencing of the neutral trehalase gene *NTH1* resulted in the observation of two possible start codons (Kopp M., Nwaka S., and Holzer H. (1994) Gene 150, 403-404. We show here that only the most upstream start codon which initiates translation of the longest possible ORF is used for expression of *NTH1 in vivo*. A gene with 77% identity to *NTH1*, *YBR0106*, which was discovered during sequencing of chromosome II by Wolfe and Lohan 1994 (Yeast 10, S41-S46), is shown here to be expressed into mRNA. Experiments with a mutant disrupted in the *YBR0106* ORF showed in contrast to a *NTH1* deletion mutant no changes in trehalase activity and in trehalose concentration. However, similar to the *NTH1* gene a requirement of the intact *YBR0106* gene for thermotolerance i.e. heat shock protein function is demonstrated in experiments with the respective mutants. This is the only phenotypic feature found at present for *YBR0106* deficiency.

XI. Department of Food Microbiology and Toxicology and Department of Bacteriology, University of Wisconsin-Madison, Madison, Wisconsin 53706, U.S.A. Communicated by E.A. Johnson and W.A. Schroeder.

Recent publications.

1. W.A. Schroeder & E. A. Johnson. 1995. Singlet oxygen and peroxyl radicals regulate carotenoid biosynthesis in *Phaffia rhodozyma.* J. Biol. Chem. (Accepted for publication).

Carotenoids have recently received considerable interest because of their potential in delaying or preventing degenerative diseases such as arteriosclerosis, cancer, and aging. In this study we show that the active oxygen species singlet oxygen ($^1O_2$) and peroxyl radicals differently affect carotenoid composition and biosynthesis in the yeast *Phaffia rhodozyma.* Photochemical generation of $^1O_2$ with rose bengal or α-terthienyl induced carotenoid accumulation. In contrast, peroxyl radicals derived from t-butylhydroperoxide (tBOOH) or H_2O_2 decreased the content of astaxanthin and increased 3-carotene by 4-fold, suggesting end-product feedback regulation by astaxanthin. ^{14}C labelling of carotenoids during oxidative stress confirmed the possibility of end product regulation. Carotenoids were bleached by 8 mM tBOOH within 6 h when carotenogenesis was inhibited by thymol. When treated with peroxides, a previously unreported pigment in *P. rhodozyma* was formed. The carotenoid had a mass of 580 Da and a molecular formula of $C_{40}H_{52}O_3$. Chemical derivatizations combined with mass and absorbance spectroscopy tentatively identified the carotenoid as dehydroflexixanthin (3,1'-dihydroxy-2,3,3',4'-tetradehydro-1',2'-dihydro-3, ψ-carotene-4-one). This study provides the first report of induction of astaxanthin biosynthesis by $^1O_2$, probable feedback control by astaxanthin, and the oxidative degradation of astaxanthin to novel pigments in *P. rhodozyma.*

2. E.A. Johnson & W.A. Schroeder. 1995. Astaxanthin from the yeast *Phaffia rhodozyma*. Proceedings from Vancouver IMCF Meeting (In press).

The heterobasidiomycetous yeast *Phaffia rhodozyma* was discovered by Herman Phaff and collaborators in fundamental ecological studies of habitats of yeasts. The sole habitat of *P. rhodozyma* appears to be slime fluxes of deciduous trees at high elevations. *P. rhodozyma* is unusual among the pigmented yeasts, primarily for its ability to synthesize the carotenoid pigment astaxanthin and to carry out both respiratory and fermentative metabolism. The yeast is becoming increasingly important in industrial microbiology as a source of astaxanthin by fermentation, and several industrial companies are developing production processes. The market for astaxanthin is probably greater than $100 million dollars. Astaxanthin is used primarily as a pigment source in aquaculture. Continued explorations and screening of yeasts should lead to the discovery of novel biologically active substances with commercial value.

3. E.A. Johnson & W.A. Schroeder. 1995. Microbial Carotenoids. Adv. Biochem. Eng. Biotechnol. (In press).

Carotenoids occur universally in photosynthetic organisms but sporadically in nonphotosynthetic bacteria and eukaryotes. The primordial carotenogenic organisms were cyanobacteria and eubacteria that carried out anoxygenic photosynthesis. The phylogeny of carotenogenic organisms is evaluated to describe groups of organism which could serve as sources of carotenoids. Terrestrial plants, green algae, and red algae acquired stable endosymbionts (probably cyanobacteria) and have a predictable complement of carotenoids compared to other prokaryotes, algae, and higher fungi which have a more

diverse array of pigments. Although carotenoids are not synthesized by animals, they are becoming known for their important role in protecting against singlet oxygen and preventing chronic diseases in humans. The growth of aquaculture during the past decade as well as the biological roles of carotenoids in human disease will increase the demand for carotenoids. Microbial fermentations offer a promising method tor production of carotenoids.

4. W.A. Schroeder & E.A. Johnson. 1995. Carotenoids protect *Phaffia rhodozyma* against singlet oxygen damage. J. Ind. Microbiol. (In press).

The only known habitat of the astaxanthin-containing *Phaffia rhodozyma* is in slime fluxes of deciduous trees at high altitudes. In this habitat, the function of carotenoids in *P. rhodozyma* is probably to provide protection against photogenerated antifungal substances in the tree flux such as singlet oxygen ($^1O_2$). To investigate the role of carotenoids in *P. rhodozyma*, genetic selections were employed to determine if carotenogenic yeast strains of *P. rhodozyma* have enhanced ability to quench $^1O_2$. Singlet oxygen was generated in liquid culture by the interaction of visible light ($\lambda = 550$ nm) with the photosensitizer rose bengal or by the activation of α-terthienyl with ultraviolet light ($\lambda = 366$ nm). In each case the treatments selected for growth of pigmented strains of *P. rhodozyma.* Albino (carotenoid-less) or yellow (ß-carotene producing) strains grew less well in media containing $^1O_2$. Addition of the $^1O_2$ quencher sodium azide to the medium with α-terthienyl allowed growth of non-pigmented strains. Since the ecological niche of *P. rhodozyma* is highly specific, we investigated whether extracts of birch trees *(Betula),* the original source of *P. rhodozyma,* contained a compound that would select for pigmented populations of the yeast. When *P. rhodozyma* strains were exposed to ethyl acetate extracts of *Betula papyrifera* excited with 366 nm ultraviolet light, only pigmented cells were able to grow. These results suggest that carotenogenesis developed in *P. rhodozyma* in response to the presence of photoactivatable antifungal compounds produced by the host tree.

XII. Department of Food Science and Technology, University of California, Davis, CA 95616, U.S.A. Communicated by H.J. Phaff.

The following paper is in press.

1. M. Kopecká,[1] G.H. Fleet,[2] & H.J. Phaff. Ultrastructure of the cell wall of *Schizosaccharomyces pombe* following treatment with various glucanases. J. Struct. Biol.

[1]Department of Biology, Faculty of Medicine, Masaryk University, Brno, Czech Republic
[2]Department of Food Science and Technology, The University of New South Wales, P.0. Box 1, Kensington, New South Wales, Australia

The ultrastructure of isolated cell walls of *Schizosaccharomyces pombe* was studied by electron microscopy after treatment with the following purified enzymes: endo-ß-(1→3)-glucanase, endo-ß-(1→6)-glucanase and endo-α-(1→3)-glucanase produced by *Bacillus circulans;* exo-ß-(1→3)-glucanase and endo-ß-(1→3)glucanase produced by *Schizosaccharomyces japonicus* var. *versatilis.* The exo-ß-(1→3)-glucanase had no detectable effect on the walls, but amorphous wall material was removed by action of the endo-ß-(1→3)- and endo-3-(1→6)-glucanases of *B. circulans* to reveal a wall component consisting of densely interwoven microfibrils. The fibrils were hydrolyzed by treatment with the *Schiz. japonicus* endo-ß-(1→3)-glucanase followed by *B. circulans* endo-α-(1 →3)-glucanase - suggesting that they were composed of ß-(1→3)-linked glucan and α-(1→3)-linked glucan. The presence of a fibrillar component in untreated walls was evident after negative staining.

XIII. Department of Genetics, Institute of Molecular Biology, University of Copenhagen, Øster, Farimagsgade 2A, 1353 Copenhagen K, Denmark. Communicated by J. Piškur.

The following note was accepted recently.

1. J. Piškur, S. Smole Možina, J. Stenderup[1] & M.B. Pedersen[2]. Mitochondrial molecular marker, *ori/rep/tra,* for differentiation of yeast species. Appl. Environm. Microbiol.

[1]Statens Serumsinstitut, Artillerivej 5, 2300 Copenhagen S, Denmark.
[2]Carlsberg Research Laboratory, Gamle Carlsberg Vej 10, 2500 Copenhagen Valby, Denmark.

Yeasts exhibit various mechanisms for the inheritance of their mitochondrial genomes. Differences among these mechanisms are based on variations within nuclear as well as mitochondrial genetic elements. Here we report diagnostic differences in the presence of biologically active mitochondrial intergenic sequences, *ori/rep/tra,* among related yeasts in the genera *Saccharomyces, Arxiozyma, Debaryomyces, Kluyveromyces, Pachytichospora, Torulaspora* and *Zygosaccharomyces.* A molecular probe containing *ori/rep/tra* can be employed specifically for the differentiation and identification of isolates belonging to the species complex *Saccharomyces* sensu stricto.

XIV. Institut für Angewandte Mikrobiologie, Universität für Bodenkultur, Nuβdorfer Läende 11, A-1190 Vienna, Austria. Communicated by H. Prillinger and R. Messner.

Posters presented at the 50th anniversary of the Institute of Applied Microbiology in Vienna.

1. K. Lopandic, H. Prillinger, I. Marquarding,[1] H.C. Evans,[2] G. Hagedorn[3] & R. Bauer.[4] 1995. Comparative study of the cell wall carbohydrate composition of basidiomycetous yeasts.

[1]T.U. Braunschweig, Institut für Mikrobiologie, Postfach 3329, D-38023 Braunschweig.
[2]International Institute Biological Control, Silwood Park, Ascot, Berks, SL5 7TA U.K.
[3]Biologische Bundesanstalt für Land und Forstwirtschaft, Institut für Mikrobiologie, D-14191 Berlin.
[4]Eberhard-Karls-Universität Tübingen, Spezielle Botanik/Mykologie, Auf der Morgenstelle 1, D-72076 Tübingen.

Carbohydrate composition of purified cell walls were examined in more than 50 species assigned to the different genera of basidiomycetous affinity. Three carbohydrate patterns were detected, mannose-glucose-galactose-fucose (*Microbotryum*-type), glucose-mannose-xylose (*Tremella*-type), and glucose-mannose-galactose (*Ustilago*-type), respectively. The importance of the qualitative and quantitative neutral sugar composition of purified cell walls to clarify phylogenetic relationships with respect to the level of genera, families, and orders could be corroborated.

2. R. Messner, H. Prillinger, C.P. Kurtzman[1] & E. Slaviková[2]. *Saccharomyces* species assignment by long range ribotyping.

[1]National Center for Agricultural Utilization Research, Peoria Il 61604, USA.
[2]Slovak Academy of Sciences, Institute of Chemistry, CS-84238 Bratislava, Slovakia.

Type strains of 10 genotypically distinct *Saccharomyces* species are differentiated by ribosomal DNA restriction fragment analysis (ribotyping). The full length of the chromosomal ribosomal repeat was amplified in two parts, the 18S rDNA including both ITS regions (2600 bp) and the 25S rDNA (3300 bp). Restriction fragments generated by 9 enzymes from these two products yield characteristic patterns, by which unknown *Saccharomyces* isolates are assigned to the type strains. For convenient separation and detection only fragments longer than 200 bp were monitored. In contrast to molecular differentiation methods of highest resolution as RAPD-PCR or fingerprinting, the results from ribotyping are absolutely reproducible and thereby suitable for databases.

3. Prillinger, H., Messner, R., Breitenbach, M.,[1] Briza, P.,[1] Staudacher, E.,[2] Molnár, 0., Weigang, F.,[3] Lopandic, K., Ibi, M.,[4] Himmler, G. & Huss, S. *Phytopathogenic* filamentous *(Ashbya, Eremothecium)* and dimorphic fungi with needle-shaped ascospores as new members within the Saccharomycetaceae.

[1]Universität Salzburg, Inst. f. Genetik u. Allg. Mikrobiologie, Hellbrunnerstr. 34, A-5020, Salzburg.
[2]Universität für Bodenkultur, Inst. f. Chemie; Gregor Mendel Str, 33, A-1180 Wien.
[3]Hewlett Packard GmbH, Lieblgasse 1, A-1222 Wien.
[4]Codon Genetic Systems, Colloredogaβe 29/13, A- 1180 Wien.

Conclusions:

1. Phenotypic criteria like ascospore shape and ornamentation as well as the presence or absence of hyphae are in most cases unreliable for definition of families in the Endomycetales (compare Kurtzman & Robnett, 1994 for further examples).

2. Based on a similar cell wall carbohydrate composition, the presence of dityrosine in endospores, and a high degree of ribosomal DNA sequence similarity especially with respect to the ITSI and ITS2 regions we redefine the family Saccharomycetaceae Winter to include unicellular saprophytic fungi like the genera *Kluyveromyces* and *Saccharomyces,* as well as dimorphic or filamentous parasitic fungi like species of the genera *Ashbya, Eremothecium, Holleya,* and *Nematospora.*

3. Our data suggest that unicellular ascomycetous yeasts like *Kluyveromyces* and *Saccharomyces* have evolved from filamentous plant pathogens with ontogenetic saprophytic yeast stages. The lack of the respective parasitic filamentous forms can be explained by an extinction of the respective hosts.

4. Molecular characteristics like cell wall sugars or ribosomal DNA sequence Information are reliable tools to trace ascomycetous yeasts back to a polykaryotic coenocytic ("siphonal") ancestor (Prillinger, 1987).

4. Molnar, O., Messner, R., Prillinger, H., Stahl, U., Silberhumer, H., Wunderer, W. 1995. Genotypic identification of industrial *Saccharomyces cerevisiae* strains using random amplified polymorphic DNA analysis.

5. Prillinger, H., Messner, R., Bauer, R., Doerfler, C., Himmler, G., Ibl, M., Huss, S. 1995. Genotypische Identifizierung von neuartigen staerkebildenden Hefen aus heren Pilzen.

The following papers have been published or accepted recently.

6. R. Messner, H. Prillinger, M. Ibl & G. Himmler. 1995. Sequences of ribosomal genes and internal transcribed spacers move three plant parasitic fungi, *Eremothecium ashbyi, Ashbya gossypii,* and *Nematospora coryli,* towards *Saccharomyces cerevisiae.* J. Gen. Appl. Microbiol. **41**:31-42.

7. R. Messner, H. Prillinger. 1995. *Saccharomyces* species assignment by long range ribotyping. Antonie van Leeuwenhoek. In press.

Type strains of 10 genotypically distinct *Saccharomyces* species are differentiated by ribosomal DNA restriction fragment analysis (ribotyping). The full length of the chromosomal ribosomal repeat was amplified in two parts, the 18SrDNA including both ITS regions (2600 bp) and the 25SrDNA (3300 bp). Restriction fragments generated by 9 enzymes from these two products yield characteristic patterns, by which unknown *Saccharomyces* isolates are assigned to the type strains. For convenient separation and detection only fragments longer than 200 bp were monitored. In contrast to molecular differentiation methods of highest resolution as RAPD-PCR or fingerprinting, the results from ribotyping are absolutely reproducible and thereby suitable for databases. The phylogeny computed from the discrete character matrix for presence / absence of fragments by the PHYLIP program package is in complete accordance to the phylogeny derived from ribosomal RNA sequence analysis. By this the field of application of the long range ribotyping can be regarded basically as equal to DNA sequence analysis of the same locus. Because distant relationships are recognized, misidentified genera were detected upon the species assignment. This cannot be done by methods of higher resolution like RAPD-PCR or fingerprinting.

8. O. Molnar, R. Messner, H. Prillinger, U. Stahl[1], E. Slaviková[2]. 1995. Genotypic identification of *Saccharomyces* species using random amplified polymorphic DNA analysis. Syst. Appl. Microbiol. in press.

[1]T.U. Berlin, Mikrobiologie und Genetik, D-1000 Berlin 65.
[2]Slovak Academy of Sciences, Inst. of Chemistry; CS-842 38 Bratislava.

According to different molecular approaches the genus *Saccharomyces* was divided recently into 10 genotypically distinct species (*S. bayanus, S. castellii, S. cerevisiae, S. dairensis, S. exiguus, S. kluyveri, S. paradoxus, S. pastorianus, S. servazzii, S. unisporus*). This was corroborated by Random Amplified Polymorphic DNA - Polymerase Chain Reaction (RAPD-PCR) analysis in the present paper. Thirty-two strains including the type strains of 20 *Saccharomyces* species defined originally by phenotypic characteristics (e.g. *S. chevalieri, S. diastaticus, S. ellipsoideus*) clustered with the pattern of *S. cerevisiae,* fourteen (e.g. type strains of *S. globosus, S. heterogenicus, S. inusitatus*) with the pattern of *S. bayanus,* six including the type strains of *S. carlsbergensis* and *S. monacensis* with the pattern of *S. pastorianus* and two with the pattern of *S. paradoxus.* Two further strains isolated newly were identified to belong to *S. paradoxus.* In comparison with nuclear DNA/DNA hybridization or electrophoretic karyotyping, RAPD-PCR analysis turned out to be a simple and reliable method to separate *Saccharomyces* species at the genotypic level.In contrast to phenotypic characters genotypic identification using RAPD-PCR analysis guarantees species specificity if type strains are included in the investigation. The ten *Saccharomyces* species arising from RAPD-PCR analysis are differentiated from each other to the maximal extent with exception of the relationship between *S. bayanus* and *S. pastorianus.* In this case, the estimated similarity value of 45% is significantly higher than the background noise (0-20%), but less than the values within species (83 to 100%).

XV. Faculté des Sciences Pharmaceutiques et Biologiques, Université Henri Poincaré - NANCY 1, 5, rue Albert Lebrun - B.P. 403, 54001 Nancy Cedex, France. Communicated by R. Bonaly.

The following papers have been published or accepted recently.

1. H. Mukhtar, A. Hakkou & R. Bonaly. 1994. Study on the activity of *Kluyveromyces lactis* S-adenosylmethionine: Δ24-sterol methyl transferase in presence of polyenic antifungal agents. Mycopathol. **126**:75-83.

The S-adenosylmethionine:Δ24-sterol methyltransferase (24 SMT) primarily considered as a mitochondrial enzyme, was recently mainly detected in lipid particles of yeasts. It catalyses the methylation of zymosterol which is an essential reaction for the synthesis of ergosterol. We have investigated in cellular extracts of two *Kluyveromyces lactis* strains the action of polyenic antifungal agents on the activity of this enzyme. Low concentrations of amphotericin B, candicidin and pimaricin strongly stimulate this activity. While high concentrations inhibit it or have no effect. Whatever the doses used, nystatin and filipin had no significant influence on this activity. According to the molar ratio amphotericin B/total sterols of the enzyme preparation, the interference of amphotericin B on the 24 SMT activity may result of two mechanisms.

2. S. Zaamoun, X. Tran Thi, 0. Reisinger, J.P. Guiraud, A. Fontana, & R. Bonaly. 1995. Incidence of aeration and [rho°] mutation on the structure of the cell walls of *Saccharomyces cerevisiae* and *Saccharomyces diastaticus.* Mycol. Res. (in press).

3. A. Belrhiti, B. Naji & R. Bonaly. 1995. Membrane lipid and sterol distribution in *Saccharomyces bayanus* grown in the presence of vaseline oil, sunflower oil, mono and diglycerides. Proc. Biochem. (in press).

4. M. Bellal, S. Benallaoua, L. Elfoul & R. Bonaly. 1995. Différences structurales des peptidomannannes pariétaux chez *Kluyveromyces lactis,* entre souches floculante et non floculante. Can. J. Microbiol. (in press).

Two strains, flocculating and nonflocculating, of the yeast *Kluyveromyces lactis* were grown in a Sabouraud's liquid medium containing Ca 0.07 mM. Treatment by ethylenediamine of isolated cell walls yielded three fractions: A, B and C. Fraction A, soluble in ethylenediamine, contained phosphopeptidomannan-like hydrosoluble polymers; these constituted the external parietal layer of the wall. Phosphopeptidomannans have also been extracted from entire yeast cells autoclaved at 140°C in a citrate buffer at pH 7.0. The flocculating and nonflocculating states of yeasts showed structural and quantitative variations in phosphopeptidomannans. The walls of the flocculating yeast cells contained higher amounts of peripheral polymers, the molecular masses of which were greater than those of nonflocculating yeast cells. These are the results of a more complex structure, due to the presence of a greater number of ramifications containing three or four mannose units. Analysis of the acetolysis products revealed in fact the release essentially of phosphorylated mannotriose and mannotetraose units by the flocculating yeast phosphopeptidomannans, while polymers of the nonflocculating yeast were characterized by the presence of mannobiose units. When such polymers were submitted to a ß-elimination reaction, mannobiose and mannose units were liberated in such a ratio that mannobiose units appeared to be more numerous in flocculating yeast cells. A lectin extracted from the flocculating strain was incubated with erythrocytes activated by phosphopeptidomannans derived from flocculating and nonflocculating yeasts and showed clearly that the more agglutinated erythrocytes were those activated by polymers derived from the flocculating yeast. The C fraction, insoluble in ethylenediamine, corresponded to the wall rigid matrix. The study of its chemical composition revealed no significative difference between the flocculating and the nonflocculating strains.

XVI. Department of Biology, Carleton University, 587 Tory Building, 1125 Colonel By Drive, Ottawa, Ontario Canada K1S 5B6. Communicated by B.F. Johnson.

The following article was published.

1. H. Miyata,[1] M. Miyata,[2] & B.F. Johnson. 1995. Parametric analysis of length distributions of the fission yeast, *Schizosaccharomyces pombe,* in chemostat culture. J. Gen. Appl. Microbiol. **41**:63-73.
[1]Nagoya Economics University, Inuyama 484, Japan.
[2]Gifu Pharmaceutical University, Gifu 502, Japan.

Assuming that cells grow exponentially in length, the cycle of cells in chemostat cultures was analyzed parametrically by the age-size method (James, T. W. *et al.,* Exp. Cell Res., 94, 267-276, 1975), which fitted well to the raw data of the length distribution. For simulation, we used the cell length and coefficient of variation at division from empirical data. The cell length and coefficient of variation at birth, the specific growth rate in extension, and the proportion of growing cells were estimated for simulation. We found that the stop-grow point of a cycle depended on the culture conditions: cells grown at D = 0. 247 h^{-1} in the chemostat culture had the stop-grow point at 0.72 of the cycle, similar to cells growing exponentially in the batch culture. Cells grown at D = 0.126 h^{-1} and D = 0.062 h^{-1} in the chemostat cultures had the stop-grow points at 0.85 and 0.97 of the cycles, respectively. There was a sub-population of non-growing cells estimated.

XVII. Department of Molecular Genetics and Microbiology, Robert Wood Johnson Medical School, University of Medicine and Dentistry of New Jersey, 675 Hoes Lane, Room 705, Piscataway, New Jersey 08854-5635, U.S.A. Communicated by M.J. Leibowitz.

The following papers were recently published or accepted.

1. J.J Lu,[1] M.S. Bartlett,[1] M.M Shaw,[1] S.F. Queener,**2** J.W. Smith,[1] M. Ortiz-Rivera, M.J. Leibowitz & C.H. Lee.[1] 1994. Typing of *Pneumocystis carinii* strains that infect humans based on nucleotide sequence variations of internal transcribed spacers of rRNA genes. J. Clin. Microbiol. **32**:2904-2912.
[1]Department of Pathology and Laboratory Medicine and
[2]Department of Pharmacology and Toxicology, Indiana University School of Medicine, Indianapolis, Indiana 46202, U.S.A.

Small portions of the 18S and the 26S rRNA genes, the entire 5.8S rRNA gene, and internal transcribed spacers ITSI and ITS2 (located between the 18S and 5.8S rRNA genes and between the 5.8S and 26S rRNA genes, respectively) of *Pneumocystis carinii* that infect humans were cloned and sequenced. The nucleotide sequences of the 18S, 5.8S, and 26S rRNA genes determined in the study were approximately 90% homologous to those of *P. carinii* that infect rats, while the

sequences of ITSI and ITS2 of *P. carinii* from the two different hosts were only 60% homologous. The 18S, 5.8S, and 26S rRNA gene sequences of *P. carinii* from 15 patient specimens were determined and were found to be identical to each other, whereas the ITS sequences were found to be variable. With the observed sequence variation, it was possible to classify the ITSI sequences into two types and the ITS2 sequences into three types. *P. carinii* strains that had the same type of ITSI sequence could have a different type of ITS2 sequence. On the basis of the sequence types of the two ITS regions, *P. carinii* from the 15 patients were classified into four groups. *P. carinii* from three patient specimens were found to contain two different ITS sequence patterns. More surprisingly, one additional specimen was found to have one ITS sequence typical of *P. carinii* isolates that infect humans and another typical of *P. carinii* isolates that infect rats. The studies indicate that it is possible to type *P. carinii* strains on the basis of their ITS sequences and that more than one ITS sequence pattern may be demonstrated in *P. carinii* from one patient, suggesting that coinfection with more than one strain of *P. carinii* may occur in the same patient.

2. M. Ortiz-Rivera, Y. Liu, R. Felder & M.J. Leibowitz. 1995. Comparison of coding and spacer region sequences of chromosomal rRNA-coding genes of two sequevars of *Pneumocystis carinii.* J. Euk. Microbiol. **42**:44-49.

Two distinct sequevars, denoted PcI and Pc2, of the opportunistic pathogen *Pneumocystis carinii* have been previously identified based on the sequence of their 26S rRNA genes, the location of group I self-splicing introns and pulsed field electrophoretic patterns of chromosomal DNA. This study shows that the sequences of 16S and 5.8S rRNA genes also vary between these sequevars, and that greater variation was seen in the internal transcribed spacer regions. Polymerase chain reaction and restriction analysis can distinguish between these sequevars.

3. Y. Liu & M.J. Leibowitz. 1995. Bidirectional effectors of a group I intron ribozyme. Nucl. Ac. Res. (in press).

The group I self-splicing introns found in many organisms are competitively inhibited by L-arginine. We have found that L-arginine acts stereoselectively on the Pcl.LSU nuclear group I intron of *Pneumocystis carinii,* competitively inhibiting the first (cleavage) step of the splicing reaction and stimulating the second (ligation) step. Stimulation of the second step is most clearly demonstrated in reactions whose first step is blocked after 15 minutes by addition of pentamidine. The guanidine moiety of arginine is required for both effects. L-Canavanine is a more potent inhibitor than L-arginine yet it fails to stimulate. L-Arginine derivatized on its carboxyl group as an amide, ester or peptide is more potent than L-arginine as a stimulator and inhibitor, with di-arginine amide and tri-arginine being the most potent effectors tested. The most potent peptides tested are 10,000 times as effective as L-arginine in inhibiting ribozyme activity, and nearly 400 times as effective as stimulators. Arginine and some of its derivatives apparently bind to site(s) on the ribozyme to alter its conformation to one more active in the second step of splicing while competing with guanosine substrate in the first step. This phenomenon indicates that ribozymes, like protein enzymes, can be inhibited or stimulated by non-substrate low molecular weight compounds, which suggests that such compounds may be developed as pharmacological agents acting on RNA targets.

XVIII. Division of Life Science, Lawrence Berkeley Laboratory, Berkeley, California 94720, and Department of Molecular and Cellular Biology, University of California, Berkeley, California, 94720. Communicated by R.K. Mortimer and T. Török.

One of our ongoing projects in the last three years has been to study the genetic diversity of the indigenous wine yeast flora in spontaneous fermentations. The task has been challenging and educational. Here is a summary of important findings, further plans and a list of publications.

The paramount source for wine yeasts is the vineyard. With improved isolation procedure, more selective media, PCR-screening and/or CHEF electrophoresis we were able to isolate hundreds of wine yeast strains from grapes, grape juices, and from different stages of fermentation. The frequency of *Saccharomyces cerevisiae* on the grapes is very low, less than 0.1% of the yeast flora. Seasonal re-occurrence of strains may vary widely.

The isolated wine yeasts display a diverse collection of strains. Nevertheless, two genotypes seem to be widely spread in Europe and in California. "Genome renewal" helps selection of the best fit.

Electrophoretic karyotyping of monosporic cultures shows mostly Mendelian segregation of chromosome length polymorphism. Karyotype differences between monosporic clones of a given strain, or between strains of the same species are way greater than thought earlier. Electrophoretic karyotyping is a highly reproducible, sensitive tool, however, its importance in species identification should not be overestimated.

Further plans include closing the circle: Where do wine yeasts spend the rest of the year when they are not on the grapes. Also, the role of viticulture in influencing the indigenous yeast flora. Competition between members of that flora as a factor affecting the fermentation kinetics. Which chemical aroma and flavor changes are the results of fermentation, differences between natural and inoculated fermentations.

The following papers have been published:

1. Romano, P., Suzzi, G., Mortimer, R. & Polsinelli, M. 1995. Production of high levels of acetoin in *Saccharomyces cerevisiae* wine yeasts is a recessive trait. J. Appl. Bacteriol. **78**:169-174.
2. Mortimer, R., Romano, P., Suzzi, G. & Polsinelli, M. 1994. Genome renewal: a new phenomenon revealed from a genetic study of 43 strains of *Saccharomyces cerevisiae* derived from natural fermentations of grape musts. Yeast **10**:1543-1552.
3. Mortimer, R. 1994. Genetic analyses of *Saccharomyces* yeasts isolated from spontaneous fermentations of California grape musts. Amer. Vineyard **8**:12-19.
4. Mortimer, R. 1995. Genetic investigations of yeasts isolated from spontaneous fermentations of grape musts in California and Italy. Practical Winery and Vineyard, in press, May-June issue 1995.
5. Mortimer, R., Romano, P., Suzzi, G. & Polsinelli, M. 1995. Heterothallism, homothallism and genome renewal in wine yeasts. Abstract 176B, Conference on Yeast Genetics and Molecular Biology, Seattle, August 1994.
6. Romano, P., Suzzi, G., Mortimer, R. & Polsinelli, M. 1994. The occurrence of high acetoin production in *Saccharomyces cerevisiae* wine yeasts as a possible process of genome renewal. Abstract to be presented at the XVII International Conference on Yeast Genetics and Molecular Biology, Lisbon, June 10-1 7, 1995.
7. Mortimer, R., Török, T., Romano, P., Suzzi, G. & Polsinelli, M. 1995. *Saccharomyces cerevisiae* is present on the grapes and is introduced into the fermentation must at the time of crushing. Abstract to be presented at the XVII International Conference on Yeast Genetics and Molecular Biology, Lisbon, June 10-1 7, 1995.
8. Mortimer, R., Romano, P., Suzzi, G. & Polsinelli, M. 1995. Genome renewal: a natural selective mechanism by providing new phenotypes in *Saccharomyces cerevisiae.* Abstract to be presented at the Vth International Symposium on Oenology, Bordeaux, June 14-17, 1 995.

XIX. Planta Piloto de Procesos Industriales Microbiológicos (PROIMI), Avenida Belgrano y Pasaje Caseros, 4000 S.M. de Tucuman, Argentina. Communicated by J.F.T. Spencer.

Papers in preparation.

1. L.M. Santopietro Ducrey, J.F.T. Spencer, D.M. Spencer & F. Siñeriz. Effects of oxidative stress on production of carotenoid pigments (astaxanthin) by *Phaffia rhodozyma*.

The resistance to killing by $H_20_2 + Fe^{2+}$ solutions, which are generators of free radicals, by two mutants of *Phaffia rhodozyma,* was determined. One of these (Mutant 5-7) did not produce astaxanthin but produced ß-carotene, and the other (Mutant 3-4) produced neither astaxanthin nor ß-carotene, or other carotenoid pigments. The resistances were compared with a wild-type strain of *P. rhodozyma* which produced astaxanthin in normal yields. The resistance of mutant 5-7 was approximately the same as that of the wild-type, but mutant 3-4 was killed much more rapidly than either mutant 5-7 or the wild-type, and its numbers in mixed continuous cultures decreased greatly. Possession of either carotenoid pigment increased the resistance to killing by free radicals in the culture medium considerably.

2. L.M. Ducrey Santopietro, J.F.T. Spencer, D.M. Spencer, & F. Siñeriz. Formation of protoplasts from *Phaffia rhodozyma.*

The classic protocol used for making protoplasts from *Saccharomyces cerevisiae* yields spheroplasts when used for obtaining protoplasts from *Phaffia rhodozyma.* These can be used in intergeneric fusion. However, when the isolation of total DNA from them is attempted, the yield is very low. The same difficulty is encountered when attempting to prepare blocks for separation of chromosomes by pulsed field gel electrophoresis. The object of this investigation was to develop an efficient protocol for preparing and regeneration of protoplasts and spheroplasts from *Phaffia rhodozyma,* for use in studies of the genetics of this yeast species.

3. L.M. Ducrey Santopietro, J.F.T. Spencer, D.M. Spencer & F. Siñeriz. Effects of oxidative stress on production of carotenoid pigments (astaxanthin) by *Phaffia rhodozyma*.

The resistance to killing of two mutants of *Phaffia rhodozyma,* by free radicals generated by $H_20_2 + Fe^{2+}$ solutions, was determined. One of these (Mutant 5-7) did not produce astaxanthin but produced ß-carotene, and the other (Mutant 3-4) did not produce astaxanthin, ß-carotene, or any other carotenoid pigments. The resistances were compared with a wild-type strain of *P. rhodozyma* which produced astaxanthin in normal yields. The resistance of mutant 5-7 was approximately the same as that of the wild-type, but mutant 3-4 was killed much more rapidly than either mutant 5-7 or the wild-type, and its numbers in mixed continuous cultures decreased greatly. Possession of either carotenoid pigment increased the resistance to killing by free radicals in the culture medium considerably.

The following two lectures were given at Oregon Graduate Institute, Beaverton, Oregon, upon invitation by Professor J.M. Cregg.

4. D.M. Spencer. Protoplast fusion as a method of genetic manipulation of industrial yeasts.

5. J.F.T. Spencer. Yeasts associated with pods and exudates of algarrobo trees (*Prosopis* spp.) and giant cacti in north-west Argentina.

Introductory lecture, at PROIMI, for course on PCR techniques given by Dr. Carlos Abate.

6. J.F.T. Spencer. Yeast genetics and molecular biology.

The following three lectures were given in a short course on yeasts, in the CFTRI (Central Food Technological Research Institute), Mysore, India.

7. D.M. Spencer. Protoplast fusion as a method of genetic manipulation of industrial yeasts.

8. J.F.T. Spencer. Biodiversity and the isolation of industrially useful yeasts from Nature.

9. J F.T. Spencer. The methylotrophic yeasts: their uses in biotechnology and their production by high cell density fermentation.

10. D.M. Spencer & J.F.T. Spencer. Genetic manipulation of yeasts and filamentous fungi for construction of industrially including selection, mutation, classical and rare mating, protoplast fusion, and transformation.

The genetic improvement of yeasts to obtain strains for industrial purposes can be done by strain selection, mutation of existing strains, rare mating, fusion of protoplasts, and by transformation of the strains with plasmids, including YACs (yeast artificial chromosomes). All of these methods except the first involve modification of the genomic DNA. All require a selection system to identify and isolate the strains desired. Mutation with a mutagenic agent (heat, drying, irradiation with UV or gamma radiation or chemical mutagens) may be used. Rare mating is used to obtain classical intraspecific hybrids between strains which mate poorly. Protoplast fusion between intact protoplasts or isolated nuclei of yeast strains, filamentous fungi or animal cells has been used successfully to obtain hybrids. Transformation uses plasmids of various kinds, including yeast artificial chromosomes (YACs) for construction of new strains for special purposes. In all of these methods, the design of the selection system is extremely important.

11. J.F.T. Spencer & D.M. Spencer. The importance of biodiversity in obtaining new microbial strains, valuable in modern biotechnology, as illustrated by the yeast microflora of algarrobo trees (*Prosopis* spp.) and giant cacti in northwest Argentina.

The role of biodiversity is important in the search for improved strains of yeasts and other microorganisms used in industry. One of the celebrated events in the search for important organisms and processes is the discovery by René Dubos of bacterial strains which degraded the capsular polysaccharide of *Pneumococcus,* and popular tradition is that the best of the early strains of *Penicillium* was isolated from a moldy cantaloupe obtained from a local market. To make best use of the method requires a knowledge of the habitat as well as of the properties of the desired organisms, and this is illustrated by the characteristics of the yeasts associated with the exudates from the leguminous trees (*Prosopis* spp.) and giant cactus native to north-west Argentina. The trees produce an exudate having a high content of sugar, tannins and alkaloids, which favors the growth of osmotolerant and methylotrophic yeasts. The latter are important in production of heterologous proteins of considerable commercial value. In giant cacti, the yeast population also includes species fermenting xylose. Other yeasts isolated from nature, producing potentially useful microbial products, include species of osmotolerant yeasts, (polyhydroxy alcohols, sophorosides, esters of long-chain fatty alcohols, and lipophilic species (*Yarrowia lipolytica*). Similarly, bacteria (*Bacillus* spp.) produce high yields of hydrolytic enzymes.

XX. École Nationale Supérieure Agronomique de Montpellier, Chaire de Microbiologie Industrielle et de Génétique des Microorganismes. Communicated by P. Galzy.

Recent publications.

1. Drider D., Janbon G., Chemardin P., Arnaud A. and Galzy P. 1994. Enzymatic hydrolysis of monoterpene glycosides of passion fruit and mango with a ß-glucosidase from yeast. Bioresource Technol. (GBR) **49**:243-246.
2. Gueguen Y., Chemardin P., Arnaud A. and Galzy P. 1995. Comparative study of extracellular and intracellular ß-glucosidases of a new strain of *Zygosaccharomyces bailii* isolated from fermenting agave juice. J. Appl. Bacteriol. (GBR) **78**:270-280.
3. Besançon X., Itomahenina R. and Galzy P. Isolation and partial characterization of an esterase from a *Debaryomyces hansenii* strain. Netherlands Milk and Dairy Journal (in press).
4. Venturin C., Boze H., Moulin G. and Galzy P. 1994. Glucose metabolism, enzymic analysis and product formation in chemostat culture of *Hanseniaspora uvarum* K5. Yeast **11**:327-336.
5. Venturin C., Zulaika J., Boze H., Moulin G. and Galzy P. 1995. Purification and properties of an alcohol dehydrogenase (HU ADHII) from *Hanseniaspora uvarum* K5. J. Appl. Bacteriol. In press.
6. Briand D., Dubreucq E. and Galzy P. 1995. Functioning and regioselectivity of the lipase of *Candida parapsilosis* (Ashford) Langeron and Talice in aqueous media. New interpretation of regioselectivity taking acyl migration into account. Eur. J. Biochem. **228**:169-175.

XXI. Department of Biology, Faculty of Medicine, Masaryk University, 66243 Brno, Czech Republic. Communicated by M. Kopecká <mkopecka@med.muni.cz>.

The following papers have recently been accepted for publication and they are now in the press.

1. Svoboda A., Bähler J. & Kohli J. Microtubule-driven nuclear movements and linear elements as meiosis-specific characteristics of the fission yeasts *Schizosaccharomyces versatilis* and *S. pombe.* Chromosoma (in the press).
2. Gabriel M. & Kopecká M. 1995. Disruption of the actin cytoskeleton in budding yeast results in formation of an aberrant cell wall. Microbiology (UK) 141 (April issue). For cover page of this issue our electron micrograph of freeze-etched yeast cell *Saccharomyces cerevisiae* was accepted.
3. Kopecká M. & Gabriel M. 1995. Actin cortical cytoskeleton and cell wall synthesis in regenerating protoplasts of the *Saccharomyces cerevisiae* actin mutant DBY 1693. Microbiology (UK) 141 (in the press).
4. Kopecká M., Fleet G.H. & Phaff H.J. : Ultrastructure of the cell wall of *Schizosaccharomyces pombe* following treatment with various glucanases. J. Struct. Biol. (Acad. Press Inc.) (in the press). See abstract under Prof. Phaff's communication.

The following dissertation has been presented.

5. Kopecká M. Yeast cell wall ultrastructure and molecular mechanisms of its assembly. Associate professor dissertation lecture. Scientific Council of the Faculty of Medicine, Masaryk University, Brno, November 1994.

XXII. Department of Plant Sciences, University of Western Ontario, London, Ontario N6A 5B7. Communicated by M.A. Lachance.

The following are in press.

1. Lachance, M.A., D.G. Gilbert[1] & W.T. Starmer.[1] 1994. Yeast communities associated with *Drosophila* species and related flies in an eastern oak-pine forest: a comparison with western communities. J. Industr. Microbiol. (special issue, in press).

[1]Department of Biology, Syracuse University, Syracuse, New York 13244.

Intestinal yeast mycobiota were studied in 14 species of *Drosophila* and in the drosophilid species *Chymomyza amoena,* captured at Pinery Provincial Park, Ontario. Over 56 yeast species, some undescribed, were isolated. These yeast communities were compared with those from two similar surveys conducted in western portions of North America. The community structures were influenced significantly by the habitat rather than phylogeny of the flies. Geographic separation was a factor affecting yeast taxa frequencies in the fly species, but it was largely overshadowed by ecological factors when the communities were described physiologically. The notion that habitats are filled by yeasts which add up to a suitable physiological potential, more or less independently of their taxonomic affinities, was thus confirmed.

2. Lachance, M.A. 1995. Yeast communities in a natural tequila fermentation. Antonie van Leeuwenhoek (special issue, in press).

Fresh and cooked agave, *Drosophila* spp., processing equipment, agave molasses, agave extract, and fermenting must at a traditional tequila distillery (Herradura, Amatitan, Jalisco, México) were studied to gain insight on the origin of yeasts involved in a natural tequila fermentations. Five yeast communities were identified. (1) Fresh agave contained a diverse mycobiota dominated by *Clavispora lusitaniae* and an endemic species, *Metschnikowia agaveae*. (2) *Drosophila* spp. from around or inside the distillery yielded typical fruit yeasts, in particular *Hanseniaspora* spp., *Pichia kluyveri,* and *Candida krusei*. (3) *Schizosaccharomyces pombe* prevailed in molasses. (4) Cooked agave and extract had a considerable diversity of species, but included *Saccharomyces cerevisiae*. (5) Fermenting juice underwent a gradual reduction in yeast heterogeneity. *Torulaspora delbrueckii, Kluyveromyces marxianus,* and *Hanseniaspora* spp. progressively ceded the way to *S. cerevisiae, Zygosaccharomyces bailii, Candida milleri,* and *Brettanomyces* spp. With the exception of *Pichia membranaefaciens*, which was shared by all communities, little overlap existed. That separation was even more manifest when species were divided into distinguishable biotypes based on morphology or physiology. It is concluded that crushing equipment and must holding tanks are the main source of significant inoculum for the fermentation process. *Drosophila* species appear to serve as internal vectors. Proximity to fruit trees probably contributes to maintaining a substantial *Drosophila* community, but the yeasts found in the distillery exhibit very little similarity to those found in adjacent vegetation. Interactions involving killer toxins had no apparent direct effects on the yeast community structure.

3. Lachance, M.A. 1995. Review of "Esser, K. & P.A. Lemke (Series Editors) The Mycota. A Comprehensive Treatise on Fungi as Experimental Systems for Basic and Applied Research. Vol. I. Wessels, J.G.H. & F. Meinhardt (Volume Editors) Growth, Differentiation and Sexuality. Springer-Verlag, Berlin, 433 pp." World J. Microbiol. (in press).

The following paper will be presented at the 7th International Symposium on Microbial Ecology, Santos, SP, Brazil in September.

4. Lachance, M.A. 1995. Ecology and evolution of yeasts in tropical cactus forests.

Cactus species that are subject to localized decay of their succulent tissue share a microbial community. This involves a succession of microbial species, beginning with bacteria that macerate the injured tissue, and culminating with the establishment of a characteristic yeast community. Various insects play an important role in the establishment of a specific microbiota from which they apparently benefit nutritionally, and in its spread across a cactus community. These include cactophilic drosophilids, neriids, and possibly moths. An overview of recent developments in our understanding of injured cactus as a microbial ecosystem is given. Major cactophilic yeasts belong to the genera *Pichia*, *Candida*, *Sporopachydermia*, and *Clavispora*. Among these, some species are found exclusively in cactus or even only in particular cactus species. These ecological specificity patterns are discussed, with an emphasis on the most recently described species. Cactophilic yeasts are interesting in evolutionary terms. Some species have readily identifiable relatives in non-cactus habitats (*Sporopachydermia, Clavispora,* certain *Pichia* species), and others do not (*Pichia amethionina* complex, *Candida sonorensis, Candida caseinolytica*). In some cases, the colonization of cacti by yeast has resulted in extensive genetic diversification (*Sporopachydermia cereana* complex). An account of current progress in this area is given.

XXIII*. Departamento de Microbiologia, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, C.P. 486, Belo Horizonte-MG, 31270-901, Brazil. Communicated by V.R. Linardi, P.B. Morais & C.A. Rosa <Carlrosa@oraculo.lcc.ufmg.br>.

The following papers have recently been published or are in press.

1. V.R. Linardi, C.M.M.C. Carvalho, & A.A.M. Dias. 1993. Instraspecific protoplast fusion of amylase-producing strains of *Candida fennica.* World J. Microbiol. Biotechnol. **9**:601-602.
2. V.R. Linardi, C.M.M.C. Andrade, M.M. Figueira, M.C. Andrade, & A.A.V. Souza. 1993. Characterization of the amylolytic system of *Candida strains.* Folia Microbiol. **38**:281-284.
3. M.C.A. Andrade, M.M. Figueira, & V.R. Linardi. 1995. Utilization of ammonia, generated from abiotic cyanide degradation, by *Rhodotorula rubra.* World J. Microbiol. Biotechnol. **11**: (In press).
4. P.B. Morais, C.A. Rosa, A.N. Hagler, & L.C. Mendonga-Hagler. 1994. Yeast communities of the cactus *Pilosocereus arrabidae* as resources for larval and adult stages of *Drosophila serido.* Antonie van Leeuwenhoek **66**:313-318.
5. C.A. Rosa, M.A. Resende, F.A.R. Barbosa, P.B. Morais, & S.P. Franzot. 1995. Yeast diversity in a mesothophic lake on the karstic plateau of Lagoa Santa, MG - Brazil. Hydrobiologia (In press).
6. P.B. Morais, C.A. Rosa, A.N. Hagler, & L.C. Mendonga-Hagler. 1995. Yeast communities as descriptors of habitat use by the *Drosophila fasciola* subgroup (*repleta* group) in Atlantic Rain Forests. Oecologia (In press).
7. P.B. Morais, M.A. Resende, C.A. Rosa, & F.A.R. Barbosa. 1995. Occurrence and diel distribution of yeasts in a paleokarstic lake of Southeastern Brazil. Rev. Microbiol. (In press).
8. R.S. Dias, E.A. Bambirra, M.E. Silva, & J.R. Nicoli.[1] 1995. Protective effect of *Saccharomyces boulardii* against the cholera toxin in rats. Brazilian J. Med. Biol. Res. **28**:323-325.
   [1]Corresponding author
9. S.P. Franzot[1] & J.S. Hamdam. 1995. Effect of amphotericin B on the lipids of five different strains of *Cryptococcus neoformans.* Mycopathologia (In press).
   [1]Corresponding author

The following communications have recently been presented.

10. J.C.T. Dias, N.C.M. Gomes, C.A Rosa, & V.R. Linardi. 1995. Yeast occurrence in a gold mining plant and screening for degradation of cyano-metals. Second Latin American Biodegradation and Biodeterioration Symposium, Gramado-RS, Brazil. 2-5 April, p. 38.
11. V.R. Linardi, J.C.T. Dias, C.A. Rosa, & N.C.M. Gomes. 1995. Degradation of nitriles by a *Candida famata* strain. Second Latin American Biodegradation and Biodeterioration Symposium, Gramado-RS, Brazil. 2-5 April, p. 13.

Forthcoming meetings

17th ISSY. Yeast Growth and Differentiation: Biotechnological, Biochemical, and Genetic Aspects. 27 August - 1st September 1995, Heriot-Watt University, Edinburgh, Scotland

The first announcement and call for papers is now available. Morning and afternoon sessions will consist of invited lectures and offered papers to be selected from those submitted. It is anticipated that individual sessions will be dedicated to product formation, aerobic growth and anaerobic growth, dimorphism & differentiation, cell wall metabolism and diversity of the physiology of growth in yeasts. Poster sessions will also be held. **Contact:**

Prof. D.R. Berry
Department of Bioscience and Biotechnology
University of Strathclyde
204 George Street, Glasgow G1 1XW
Scotland, U.K.

Tel. 041 552 4400 ext 2092
Fax. 041 552 6524

6th International Symposium on the Microbiology of Aerial Plant Surfaces, 11-15 September 1995, Island of Bendor, Bandol, France

Since 1970 scientists from diverse disciplines have met every five years to discuss issues related to the biology and ecology of microorganisms associated with aerial surfaces of plants. These symposia have helped advance our understanding of a habitat that harbors plant pathogens as well as microorganisms beneficial for plant health. Furthermore, this tremendously complex habitat harbors microorganisms that may influence global weather, that have an impact on food technology, and that may be noxious to animals or a part of their normal intestinal flora. The Symposium in 1995 will strive to bring together researchers in the areas of microbiology, plant pathology, physiology, biochemistry, ecology, micrometeorology, microscopy, statistics, food science and genetics. It will provide a forum to explore recent research on the nature of the environment at plant surfaces, biotic and abiotic factors that influence colonization of plant surfaces by microorganisms, the response of plants to microorganisms associated with their aerial surfaces, and the impact of these microorganisms on agricultural practices and food quality. The major topics will include: the physical and chemical environment of aerial plant surfaces; interactions between microbial epiphytes and plants; interactions among microorganisms in epiphytic communities; quantification and prediction of spatial and temporal dynamics of epiphytic microorganisms; the impact of epiphytic microorganisms on agricultural practices and food quality. The Symposium will be held on the magnificent Island of Bendor, in the Mediterranean Sea just off the coast of Bandol, France. This island is a 5-minute ferry ride from the city of Bandol and is equipped with an auditorium and several hotels with multiple conference rooms and diverse recreational facilities. The site, which is readily accessible through domestic and international means of transportation, was chosen for its ambiance. It will be extremely conducive to informal discussion among participants during leisure time. The date of the conference, 11 - 15 September 1995, was chosen to avoid the high tourist season on the French Riviera while maximizing the probability of excellent weather. **For additional information please contact:**

Cindy E. Morris
INRA - Station de Pathologie Végétale
B.P. 94
84143 Montfavet Cedex, France

Phone: (33)-90-31-63-84
Fax: (33)-90-31-63-35
E-mail: <cornic@jouy.inra.fr>
Telex: INRAAVI 432.870 F

Biotecnologia Habana '95. New Opportunities in Plant, Animal, and Industrial Biotechnology. Center of Genetic Engineering and Biotechnology (CIGB), Havana. November 12-17, 1995.

Three parallel events will take place, based on the following subjects: (1) Biotechnology applied to animal production and health. (2) Biotechnology applied to plant production. (3) Biotechnology applied to industry. Registration: USD$325 (private sector), USD$250 (academic and government), USD$150 (students). **Contact:**

Organization Committee, Biotecnologia Habana '95
Apartado Postal 6162, C.P. 10600
Havana, Cuba

Tel. (53-7) 218008, 216008, 218164, 216832.
E-mail: <biot95@ingen.cigb.edu.cu>

Beijerinck Centennial Symposium.
Microbial Physiology and Gene Regulation: Emerging Principles and Applications.
The Hague, The Netherlands, 10-14 December 1995.

The symposium will be held at The Hague, The Netherlands, 10-14 December 1995, and will include a visit to Delft. This Beijerinck Symposium celebrates 100 years of the Delft School of Microbiology, and honours Martinus Willem Beijerinck and his successors Albert Jan Kluyver and Cornelis Bernardus van Niel. The teachings of"The Delft School" have had a lasting influence on the study of microbial biochemistry, biodiversity and biotechnology. Beijerinck and his successors each addressed basic questions in microbial physiology: How does the intact organism interact with its abiotic and biotic environment? How can fundamental principles be brought to bear on applied problems? What is the place of micro-organisms in the natural world?

Modern tools of molecular biology bring us deeper understanding of these enduring problems and allow us to formulate new principles of metabolic control and microbial gene regulation. There are new opportunities for the application of microbes to human benefit such as optimization of primary and secondary metabolite production, yield improvement, agricultural productivity, understanding of virulence mechanisms, production of enzymes and heterologous proteins, and novel pathways for biodegradation. The biochemical virtuosity of micro-organisms from extreme environments can now be harnessed in novel ways; traditionally exploited fermentation systems can be engineered to higher productivity.

The Beijerinck Centennial will bring together an international group of scientists in a Symposium that addresses cutting-edge principles of microbial physiology and gene regulation as observed in important model and production organisms. It will highlight the microbial diversity that provides the raw materials for this research, and will honour the grand tradition of the Delft School, teaching that microbes can be the basis of whole new ways of thinking in biology, and whole new commercial processes within industry.

The Beijerinck Centennial will be organized jointly by the American Society for Microbiology, the Netherlands Biotechnological Society, and the Netherlands Society for Microbiology, under the auspices of the Netherlands Foundation for Biotechnology. **For further information please contact:**

Beijerinck Centennial, Symposium Office,
W.A. Scheffers,
Kluyver Laboratory of Biotechnology,
Julianalaan 67, 2628 BC Delft, The Netherlands.

Tel.: (31) 15782411
Fax: (31) 15 782355 or (31) 15133141.

10th International Biotechnology Symposium, August 25-30, 1996, Sydney, Australia

In recognition of biotechnology's growth and its impact on the country, the Australian Biotechnology Association is proud to be hosting the 10th International Biotechnology Symposium in Sydney between August 25-30, 1996. The Symposium will be held right in the heart of Sydney at the Sydney Convention and Exhibition Centre, Darling Harbour. Not only will it be a showcase for Australian biotechnology but also your opportunity to come and see the industry firsthand. Professor Peter Gray is Chairman of the Organising Committee. **To join the mailing list for the Symposium, contact:**

Australian Biotechnology Association,
PO Box 4, Gardenvale Victoria 3185,
Australia.

Telephone: 61 3 596 8879
Facsimile: 61 3 596 8874

ISY IX - Ninth International Symposium on Yeasts, Sydney, Australia, 25-30 August 1996

This is an invitation to attend the 9th International Symposium on Yeasts (ISY) to be held in Sydney on 25-30 August 1996. The ISY is held every four years as an activity of the International Commission on Yeasts (ICY) to foster interest in the science and technology of yeasts. This will be the first time that ISY has been held in Australia. As an added attraction, it will be held concurrently with the 10th International Biotechnology Symposium (IBS). The ISY and IBS will be held in the heart of Sydney at the spectacular harbourside Sydney Convention Centre. This large purpose-built facility is set in 50 hectares of parks, gardens, museums, shopping malls and amusement areas. It overlooks the harbour with spectacular views of the city. It is a five minute monorail ride to the city centre and within walking distance of several hotels. Sydney itself is the cosmopolitan centre of Australia and is one of the most beautiful cities in the world, with its deepwater harbour, Opera House and sandy beaches.

As in previous ISY, the scientific program will be arranged in a number of symposium topics as shown. Leading international researchers will be invited to present the latest advances within the symposia topics. Input into the content of the scientific program has already been obtained from the vast international network of councillors on the International Yeast Commission. In addition, key plenary lectures and poster presentation sessions will complement the symposium papers and there will be opportunity to attend sessions in the IBS program.

The Australian Biotechnology Association is honoured to be hosting the symposium. As with any scientific meeting, the success of this ISY will depend on its participants. We hope that you will be able to accept our invitation, and look forward to seeing you in Sydney 1996.

Symposium Topics

Symposium I: **Systematics and Taxonomy**. Current status. Classical and molecular approaches. Phylogeny. Basidiomycetes and yeast like organisms.

Symposium II: **Ecology and Biodiversity**. Extreme environments. Soil, Water, Plants, Animals.

Symposium III: **Biochemistry and Physiology**. Metabolism. Stress. Transport. Tolerance of extremes.

Symposium IV: **Molecular Biology and Genetics**. Genome project. Secretion. Expression. Regulation.

Symposium V: **Cell Cycle**. Morphogenesis. Cell interactions.

Symposium VI: **Ultrastructure**. Organelles. Membranes. Cell wall.

Symposium VII: **Yeasts as Pathogens and Allergens**. Epidemiology, Pathogenesis. Treatment. Drug resistance and sensitivity

Symposium VIII: **Biodegradation**. Xylose fermentation. Polysaccharide degradation. Metal accumulation.

Symposium IX: **Alcoholic Beverages**. Brewer's yeast. Wine yeast. Sake yeast. Distillers yeast.

Symposium X: **Food and Feed Processing**. Spoilage yeasts. Yeasts as sources of food additives (colours, flavours, vitamins).

Symposium XI: **Enumeration and Detection of Yeasts**. Rapid methods. ELISA. Molecular methods.

Symposium XII: **Fermented Foods**. Baker's yeast. Traditional fermented foods. Yeasts in dairy products

Symposium XIII: **Biocontrol and Probiotic Yeasts**. Biocontrol of food spoilage. Probiotic species in human and animal foods.

Symposium XIV: **Fermentation Technology**. Immobilised yeasts. Novel bioreactor systems

Symposium XV: **Training and Education in Yeast Biology and Technology**.

Scientific Organising Committee. Desmond Clark-Walker, Australian National University; Ian Dawes, University of New South Wales; David Ellis, Adelaide Childrens Hospital; Graham Fleet, University of New South Wales; Phillip Franks, Burns Philp, Food and Fermentation Division; Paul Henschke, Australian Wine Research Institute; Ian Jenson, Burns Philp, Food and Fermentation Division; Neville Pamment, University of Melbourne; Ken Watson, University of New England.

The First Circular on the 9th IYS Sydney has been sent out.

For further information contact:

9th ISY '96 Secretariat
GPO Box 128
Sydney NSW 2001
Australia

Tel: 61 2 262 2277
Fax: 61 2 262 2323
EMAIL: tourhosts@tourhosts.com.au

OR

Graham H Fleet
Department of Food Science & Technology,
The University of New South Wales,
Sydney, New South Wales 2052,
Australia

Telephone 61 2 385 5664
Fax: 61 2 385 5931

Brief News Items

Change of address: Gerold Barth

I have accepted a new position as Professor of general microbiology and Head of the newly founded Institute of Microbiology at the Technical University to Dresden, Germany. My new address is:

Prof. Dr. Gerold Barth
Technische Universität Dresden
Institut für Mikrobiologie
Mommsenstraße 13
01062 Dresden
Germany

YEAST Email list, version 7.10 - Yeast Research on the Internet

The most recently updated list of electronic mail addresses of yeast researchers (7.10) can be retrieved by anonymous FTP to **ncbi.nlm.nih.gov** in the **/repository/yeast** directory. The list can also be searched by using the gopher server at **gopher.gdb.org** in the following section:

--> 14. Searching For Biologists/
--> 12. E-mail Addresses of Yeast Researchers/

In this section you can also add or correct your email address.

E-mail Addresses of Yeast Researchers

1. About The Yeast E-mail Directory.
2. Browse E-mail Addresses of Yeast Researhers/
3. Search E-mail Addresses of Yeast Researchers <?>
4. Retrieve the entire Yeast E-mail Addresses Directory.

--> 5. Add (or Correct) Your Address to the Yeast E-mail Directory <TEL>

This gopher server is also reachable via the *Saccharomyces cerevisiae* World Wide Web server. The URL for this server is: **http://genome-www.stanford.edu**. The list is updated once a month at the **gopher.gdb.org** site (on about the first of each month).

The list is prepared by Francis Ouellette (**francis@ncbi.nlm.nih.gov**). The gopher application is prepared by Dan Jacobson (**danj@gdb.org**). The WWW application is managed by Mike Cherry (**cherry@genome.stanford.edu**). Users of this list are reminded that, as a courtesy to others on this list, this directory should not be used as a general mailing list, and that people can post to **YEAST/bionet.molbio.yeast** if they want to propagate information to a YEAST interested audience. If you have any questions about how to participate in the **YEAST/bionet.molbio.yeast** newsgroup, or if you have corrections, additions or comments, please contact Francis Ouellette (**francis@ncbi.nlm.nih.gov**).