FUNGAL GENETICS STOCK CENTER

CATALOGUE OF STRAINS

11th Edition

2006

Supplement to Fungal Genetics Newsletter No. 53

Kevin McCluskey, Ph.D. Curator
Michael Plamann, Ph.D. Director

School of Biological Sciences
University of Missouri, Kansas City
5007 Rockhill Road
Kansas City, MO 64110

816-235-6485

FAX 816-235-6561

WWW.FGSC.NET

Supported by National Science Foundation Grant DBI 0235887

This catalogue contains lists of materials held by the Fungal Genetics Stock Center. Major sections are devoted to Neurospora, Aspergillus, and plant pathogens, but the following points are generally applicable. The catalog is reprinted biannually and updates are posted on the FGSC web-site and in the Fungal Genetics Newsletter.

Availability of Stocks: Most strains are available within a few days of ordering. Strains that have not been ordered in ten years or more are considered archival and are available on an as-is basis.
Fees are described on the FGSC web-site at http://www.fgsc.net/newship.html. These are reviewed annually by the FGSC advisory board and are subject to change. Strains are made available regardless of the ability to pay, but fee waivers must be requested at the time of order. Fees are not waived for commercial requests nor for molecular tools. All materials in the FGSC collection are considered to be in the public domain. While the FGSC makes every effort to assure the validity of each stock, no warranty is made as to the validity or usefulness of any materials. We assume an educated clientelle and act accordingly.

Deposit of Stocks: We solicit deposit of cloned fungal genes, gene libraries, and cultures on which genetic or biochemical information is published or in press. We invite suggestions of valuable stocks which should be included. A deposit sheet can be downloaded from the FGSC web site. Additions or corrections to linkage data, genetic background, references, etc. are welcomed. Additional information of many stocks can be provided upon specific request.

Shipment of Strains: Most strains are stored on anhydrous silica gel. In preparation for shipment, a few crystals of the stock culture are transferred to fresh agar slants, and when growth can be seen, the slants are sent via FedEx. In most cases, strains can be dispatched 2-3 days after receiving a request. Strains may be sent via Express courier if an additional fee is paid. Phone orders may be placed at 816-235-6485; the FAX number is 816-265-6561; We encourage the use of E-mail as this assures timely and accurate ordering. The FGSC e-mail address is questions@fgsc.net. The FGSC can be found on-line at www.fgsc.net and questions or orders can be posted directly there.

Acknowledgments: Thanks are due to the many investigators who have deposited stocks, as indicated by initials in the list. These and others have provided a valuable service by providing accessory information, correcting errors, and depositing improved strains to supplement or replace those originally listed. Special thanks go to Dr. David Perkins for his considerable help with the Neurospora sections and Dr. Etta Kafer for help with the Aspergillus section and for formulating the gene listing for *A. niger*. If you have ideas of how to better organize portions of this catalog with which you are familiar, please offer your suggestions.

FGSC on the Internet: The FGSC web-site is the best place to find information on stocks or other materials in the FGSC collection. The FGSC can be found at www.fgsc.net.

Nomenclature: The most recent description of Neurospora nomenclature was in 1999 (Fungal Genetics Newsletter 46:31-41). This is also published in the 2001 “Neurospora Compendium” by D. D. Perkins *et al.* and in Davis, R. H. 2000. “Neurospora..” Please do not use the FGSC number as a substitute for the genotype, allele or locus.

Format: The 11th edition of the FGSC catalog continues the format initiated in volume 9. Molecular materials are listed with the organism from which they are derived; cloning vectors are still listed in section A. Since it makes up the majority of the collection, Neurospora is listed at the front of the catalog. Another important change is that the catalog will be available online in pdf format.

FGSC Catalogue of Strains - Table of Contents

Part V. Aberration Stocks

Part VI. Testers and stocks for special purposes

Section C. *Aspergillus*

Molecular resources

Fungal Strains

Section D. Other fungi

Magnaporthe grisea

Section A. Cloning tools

Cloning Vectors

λpAn - replacement Cre-*lox* vector with automatic subcloning	Holt and May 1993. Gene 133:95-97
pSV50 - Cosmid vector based on Benomyl resistance	Vollmer & Yanofsky 1986. PNAS 83:4869
pMSN1 - Neurospora *qa-2*$^{+}$-pGEM vector	Nelson & Metzenberg 1992 Fungal Gene Newsl 39:59
pDE1, pDE2, pDE3 - *lacZ* fusion vectors:	Ebbole 1990 Fungal Genet. Newsl 37:35-37
pLH1, pLH3 - tn5 with genes for selection in fungi	Hamer and Gilger 1997, FGN 44:19-23
pZHK2- bi-functional transformation vector	Kück and Pöggeler, 2004, FGN 51:4-6

Plasmid vectors based on hygromycin or phleomycin resistance:

pMOcosX		Orbach 1994. Gene 150:159-162
pCSN43	pCSN44	Staben et al. 1989. Fungal Genet. Newsl. 36:79-81
pES200		
pCB1003,	pCB1004	Carroll et al. 1994. Fungal Genet. Newsl. 41:22
pCB1636	pCB1636	Sweigard et al. 1997. Fungal Genet. Newsl. 44:52-53
pCB1490	pCB1179	
pCB1535	pCB1538	
cosmid AN26		Taylor and Borgmann 1996 Fungal Genet. Newsl. 43:52
pMTR::Hyg		Schroeder et al 1995 Fungal Genet Newsl 42:65-68
pBC-hyg,	pBC-phleo	Silar, 1995 Fungal Genet Newsl 42:73
pSM565		Fungal Genetics and Biology 37:211-222, AY142483

Vectors based on phosphoinothricin (Ignite/Basta) resistance:

pBARGEM5-1	pBARKS1	Pall and Brunelli 1993. Fungal Genet. Newsl. 40:59
pBARGEM7-1		
pBARGEM7-2	pBARGPE1	
pBARGRG1	λBARGRG1	Pall and Brunelli 1994. Fungal Genet. Newsl. 41:63
λBARGEM7	λBARMTE1	
λBARGPE1	λ-IIBARGEM7	
pCB1517	pCB1635	Sweigard et al. 1997. Fungal Genet. Newsl. 44:52-53
pCB1546	pCB1524	
pCB1525	pCB1530	
pCB1531	pCB1534	
pCB1537		

Vectors for expression of cDNA

pMYX2, pMYX10		Campbell et al. 1994. Fungal Genet. Newsl 41:20-21
ANEp2	AMA pyrG	Storms et al. 2005, Plasmid 53:191-204
ANEp4	AMA pyrG	Storms et al. 2005, Plasmid 53:191-204
ANEp6	AMA pyrG	Storms et al. 2005, Plasmid 53:191-204
ANEp7	AMA pyrG	Storms et al. 2005, Plasmid 53:191-204
ANEp8	AMA pyrG	Storms et al. 2005, Plasmid 53:191-204
ANIp7	pyrG	Storms et al. 2005, Plasmid 53:191-204
ANIp8	pyrG	Storms et al. 2005, Plasmid 53:191-204
p434	tTA, hyg	Vogt et al. 2005, BMC Microbiol. 5:1*
p444	tTA, ble	Vogt et al. 2005, BMC Microbiol. 5:1*
p473	tTa	Vogt et al. 2005, BMC Microbiol. 5:1*
p474	tTa	Vogt et al. 2005, BMC Microbiol. 5:1*
p480	tTA, ble	Vogt et al. 2005, BMC Microbiol. 5:1*
p482	tTa	Vogt et al. 2005, BMC Microbiol. 5:1*
p500	tTA, hyg	Vogt et al. 2005, BMC Microbiol. 5:1*
p502	tTA, hyg	Vogt et al. 2005, BMC Microbiol. 5:1*
		*Not available to for-profit companies

Vectors based on Sulfonylurea resistance:

pCB1528	pCB1637	Sweigard et al. 1997. Fungal Genet. Newsl. 44:52-53
pCB1551	pCB1550	
pCB1532	pCB1533	
pCB1536	pCB1539	

Vectors with fluorescent tags

pMF272	GFP	M. Freitag, Fungal Genet Biol. 41:897-910.
pMF280	hH1-GFP	Freitag et al. Fungal Genet Biol. 2004, 41:897-910
pMF309	Bml-GFP	Freitag et al. Fungal Genet Biol. 2004, 41:897-910
pRF280	gpd::GFP::stuA; argB	Toews *et al.*, 2004, Curr Genet. 45:383-9.
pRF281	gpd::GFP::stuA; pyr4	Toews *et al*, 2004, Curr Genet. 45:383-9
pJH19	gpd::DsRedT4::stuA; argB	Toews *et al.*, 2004, Curr Genet. 45:383-9
pRS54	gpd::cit::GFP	Suelmann and Fischer, Cell Motil Cytoskeleton. 2000 45:42-50.
pSK700	gpd::cit::DsRedT4	Toews *et al.*, 2004 Curr Genet. 45:383-9
pPND1	alcA::mRFP1::KipB	Rischitor *et al.*, 2004
pMT-OvE	alcA::ccdB	Toews *et al*, 2004, Curr Genet. 45:383-9
pMT-3xHA	alcA::ccdB::3xHA	Toews *et al.*, 2004, Curr Genet. 45:383-9
pMT-sGFP	alcA::ccdB::sGFP	Toews *et al.*, 2004, Curr Genet. 45:383-9
pMT-BFP	alcA::ccdB::BFP	Toews *et al.*, 2004, Curr Genet. 45:383-9
pMT-mRFP1	alcA::ccdB::mRFP1	Toews *et al.*, 2004, Curr Genet. 45:383-9
pDV2	gpd::ccdB::sGFP	
pSK800	gpd::cit::mRFP1	Toews *et al.*, 2004, Curr Genet. 45:383-9
pMF331	RFP	Freitag and Selker, 2005, Fungal Genet. Newsl. 52:14-17
pMF332	RFP	Freitag and Selker, 2005, Fungal Genet. Newsl. 52:14-17
pMF334	RFP	Freitag and Selker, 2005, Fungal Genet. Newsl. 52:14-17
pFN03	GFP	Yang *et al.*, 2004. Eukaryotic Cell 3:1359-1362
pXDRFP4	RFP	Yang *et al.*, 2004. Eukaryotic Cell 3:1359-1362

Vectors for gene disruption in Magnaporthe

pCX62	hph	Xinhua Z., *et al.* 2004, Fungal Genet. Newsl. 51:17-18
pCX63	hph	
pYK11	bleoR	

Vectors for protein tagging

pAO81	*A. fumigatus* pyrG-S-tag	Yang *et al.*, 2004. Eukaryotic Cell 3:1359-1362

Saccharomyces/*E.coli* phagemid vector

pRS426	URA3	

Transconjugation vector

pPK2	hyg/T-DNA borders	Covert *et al.*, 2001, Mycol Res 105:259-264

Vectors for gene disruption and targetting in *A. fumiagtus*

pME2891	loxP-phleo^{r}	Krappmann *et al.*, 2005, Eukaryotic Cell,4:1298-1307
pME2892	*niaD*::cre	Krappmann *et al.*, 2005, Eukaryotic Cell,4:1298-1307

Vectors for gene disruption and targetting in *A. nidulans*

pTN1	Af *pyroA*	Nyak *et al.*, 2006, Genetics 172:1557-1566
pTN2	Af riboB	Nyak *et al.*, 2006, Genetics 172:1557-1566

Vectors for Nourseothricin selection

pD-Nat1	Nat	Kück and Hoff, 2006, Fungal Genet Newsl. 53:9-11
pG-Nat1	Nat	Kück and Hoff, 2006, Fungal Genet Newsl. 53:9-11

Cyclospoine based vectors

pCSR1::hph	*csr-1*	Fungal Genet. Biol., 2006, submitted
pCSR1	*csr-1*	Fungal Genet. Biol., 2006, submitted

Silencing

pSilent	hph	Fungal Genetics and Biology 42:275-283

GENE LIBRARIES

The FGSC maintains several gene libraries for *Neurospora crassa*, *Aspergillus nidulans* and several other fungi in the collection. More are being added and investigators are encouraged to consider depositing copies of gene libraries with the FGSC. The most up to date listing of gene libraries can be found at the FGSC web site.

The FGSC fee scheme is designed to allow us to cover the cost of preparing and delivering materials. Hence ordered cosmid libraries cost from $75 to $250 while cDNA libraries and lambda libraries are priced the same as a single strain (plus shipping charges, if applicable). Commercial organizations are requested to pay double for libraries. Certain cDNA libraries cannot be sent to commercial organizations.
Fees are current as of 2006 and may change without notice. The most current pricing will be listed at the FGSC web site.

Shipping:
Ordered libraries are only sent FedEx. Phage and cDNA libraries may be sent by mail or FedEx. Ordered libraries can be sent either frozen in dry ice or on agar solidified medium within the US and to certain addresses in Canada. Libraries sent outside the US will be sent on agar-solidified medium because of the time required.

Fees are described on the FGSC web-site and are subject to change.
For detailed listings of the gene libraries, please look at the sections for the individual fungi.

CLONED GENES

A limited selection of individual genes are available from the FGSC. Individual clones from cosmid and BAC libraries can also be supplied. Identified clones are listed following descriptions of the libraries on following pages. In all cases, shipments will be made in the form of *E. coli* cells containing the relevant plasmid. Fees are described on the FGSC Web-site **The fee cap applied to fungal strains does not apply to cloned genes**.

Neurospora crassa **plasmids**

Cloned gene	Plasmid name	Reference
acr-2	pAC203	Nakashima Biochim. Biophys. Acta 1307:187-192
al-1 (phytoene dehydrogenase	pTJS342	Schmidhauser et al. 1990. Mol. Cell Biol. 10:5064
al-2 (phytoene synthetase)	pTJS542	Schmidhauser et al. 1994. J. Biol. Chem. 269:12060
am (glutamate dehydrogenase)	pJR1	Kinsey & Rambosek 1984. Mol. Cell. Biol. 4:117
am (glutamate dehydrogenase)	pJR2	ibid.
arg-2 (CPS synthetase A)	pAB1	Orbach et al. 1990. J. Biol. Chem. 265:10981
asn (asparagine synthetase)	pASN	F. Nargang (unpubl)
atp-1 (Mitochondrial ATP synthetase)	pF1αG4	Bowman and Knock, 1992 Gene 114:157-163
atp-2 (Mitochondrial ATP synthetase)	pF1β10A3	ibid
Bml^r (β-tubulin)	pBT6	Orbach et al. 1986. Mol. Cell. Biol. 6:2452-2461
Bml^r (β-tubulin)	pSV50 (cosmid)	Vollmer & Yanofsky 1986. PNAS 83:4869
Bml-GFP	pMF309	
chs-2 (chitin synthase)	pAB22	Beth Din & Yarden 1994. Microbiology 140:2189
chs-2 (chitin synthase)	pAB23	ibid.
chs-4 (chitin synthetase type IV)	pAB6	Beth Din, et al Mol Gen Genet 250:214-222.
chs-4 (chitin synthetase type IV)	pNCCSDE3	Beth Din, et al Mol Gen Genet 250:214-222.
cit-1 (citrate synthetase)	cit-1cDNA	Ferea et al 1994 Mol Gen Genet 242: 105-110
cit-1 (citrate synthetase)	cit-1genomic	ibid
cot-1 (protein kinase)	pOY18	Yarden et al. 1992. EMBO J. 11:2159-2166
cpc-1 (regulatory)	pCPC1-2	Paluh et al. 1988. PNAS 85:3728-3732
cpc-1 (regulatory)	pMO31	ibid.
cys-3 (regulatory)	pCYS3	Paietta et al. 1987. Mol. Cell. Biol. 7:2506-2511
cys-9	pCS907	Nakashima Genetics 146:101-110
cys-14 (sulfate permease II)	pJSK1	Ketter and Marzluf 1988 Mol.Cell.Biol 8:1504-1508
cys-14 (sulfate permease II)	pJSK2	Ketter and Marzluf 1988 Mol.Cell.Biol 8:1504-1508
cyt-18 (tyrosyl tRNA synthetase)	pRALcyt18	Akins and Lambowitz 1987. Cell 50:331-345
cyt-20 (valyl tRNA synthetase)	pCyt20+	Kubelik et al. 1991. Mol. Cell. Biol. 11:4022-4035
cyt-21 (mitochon. ribosomal protein)	p297-4	Kuiper et al. 1988. J. Biol. Chem. 263:2840-2847
cyt-22 (mitochon. ribosomal protein)	pCYT22	Kubelik 1989. Ph.D. thesis
eas (*ccg-2*)	pLW1ΔK	Bell-Pedersen et al. 1992. Genes Develop. 6:2382
erg-3 (C-14 reductase)	pKGP86	Papavinasasundaram & Kasbekar 1994. J Genet 73:33-41
erg-3	pCHYG1	Praksah et al. Microbiology 145:1443-1451
erg-3	pCHYG2	Praksah et al. Microbiology 145:1443-1451
erg-3	pCHYG3	Praksah et al. Microbiology 145:1443-1451
frq (cirdadian periodicity)	pCRM101	McClung et al. 1989. Nature 339:558-562
gdh-1	pVG1	Kapoor. Biochem. Cell. Biol. 71:205-219
gdh-1	pVG2	Kapoor. Biochem. Cell. Biol. 71:205-219
GFP	pMF272	Freitag et al. Fungal Genet Biol. 41:897-910
gla-2 (glucoamylase)	pLMN1	Ebbole and Madi, 1995 FGN 43:23-24
ccg-1(=grg-1)	pGEM3/2D30	McNally & Free 1988. Curr Genet 14:545
het-c^{GR}	het-cGR	Glass Genetics 146:1299-1309
het-c^{PA}	het-cPA	Glass Genetics 146:1299-1309
het-c^{OR}	het-cOR	Glass Genetics 143:1589-1600
his-3 (histidinol dehydrogenase)	pNH60 (CY)	Legerton & Yanofsky 1985. Gene 39:129-140
his-3 (for targetting transformants)	pRAUW122	Aramayo and Metzenberg, 1995 FGN 43:9-13
his-3 (for targetting transformants)	pBM60	Margolin et al, 1996 FGN 44:34-35

***Neurospora crassa* plasmids, continued**

Cloned gene	**Plasmid name**	**Reference**
his-3 (for targetting transformants)	pBM61	Margolin et al, 1996 FGN 44:34-35
his-3	pJHAM002	Curr Genet 43:17-23
his-3	pJHAM003	
his-3	pJHAM004	
his-3	pJHAM005	
his-3	pJHAM007	
VR telomere, *his-6*	pVRTEL1	Schechtman 1987. Mol. Cell. Biol. 7:3168-3177
hH1-GFP	pMF280	
histones (H3, H4)	pNcH3H4	Woudt et al. 1983. Nucl. Acids Res. 11:5347-5360
Hsp30	pHSP30	Plesofsky and Brambl 1990 JBC 265:15432-15440
hsp-80	pH807	Kapoor. Biochem Cell Biol 70:1365-1367
hsps-1	pG6D	Kapoor. J. Bacteriol. 177:212-221
ilv-2	pHS503	Sista and Bowman 1992 Gene 120: 115-118
ilv-3	pILV31	Jarai et al., Mol. Gen. Genet. 224:383-388
inl (inositol synthase)	pINL-1-724593 (AL)	Akins & Lambowitz 1985. Mol. Cell. Biol. 5:2272
inl	pOKE01	R.L. Metzenberg (unpubl)
inl	pRATT19	
inl mat-a^{1}	pRATT25d	
leu-1	pLEU11	Jarai et al., Mol. Gen. Genet. 224:383-388
leu-1	pLEU12	Jarai et al., Mol. Gen. Genet. 224:383-388
lux	pLUC6 delta BS	FGB 38:327-332
lys-4 (saccharopine cleaving)	pSL4	R.L. Metzenberg (unpubl)
mat-a	pRATT05	
met-7	pMET7	Crawford et al. 1992. Gene 111:265-266
met-10	pMET10	R.L. Metzenberg (unpubl)
mtA-1	pmtAG-2	Glass et al. 1990. PNAS 87:4912-4916
mta-1	pCSN4	Staben & Yanofsky 1990 PNAS 87:4917
mtr (neutral amino transport)	pCVN2.9	Koo & Stuart 1991. Genome 34:644-651
mtr (neutral amino transport)	pN846	Koo & Stuart 1991. Genome 34:644-651
ncd-2	pBNCD-2	Kurihara. Flavins and Flavoproteins, 1996 251-260
nic-1	pNIC-1	Akins & Lambowitz 1985. Mol. Cell. Biol. 5:2272
nit-2 (regulatory)	pNIT2	Fu and Marzluf 1987. Mol. Cell. Biol. 7:1691
nit-3 (nitrate reductase)	pNIT3	Okamoto et al 1991 Mol Gen Genet 227:213-223
nit-4 (regulatory)	pNIT4B	Fu et al 1989 J. Bact. 171:4067-4070
NiR (regulated by nit-4)	pniR-1.11	Colandene and Garrett 1996 FGN 44:11-12
nmr (regulatory)	pNMR	Fu et al. 1988 Mol Gen Genet 214:74-79
pan-2	pOKE102	R.L. Metzenberg (unpubl)
pep-4 (Proteinase A, genomic)	pep-4genomic	
pep-4 (Proteinase A, cDNA)	pep-4cDNA	
pho-2 (alkaline phosphatase)	pPL3	Grotelueschen et al. 1994. Gene 144:147-148
pho-4 (phosphate permease)	pBJ004	Mann et al. 1988 Mol. Cell. Biol. 8:1376-1379
pho-5 (phosphate permease)	pWV01	Versaw 1995 Gene 153:135-139
pma-1 (H^+-ATPase)	pKH14	Hager et al. 1986 PNAS 83:7693
pph-1 (type 2A phosphoprotein phosphatase)	pphCos1	Yatzkan and Yarden 1995 Curr Genet 28:458-466
pph-1 (type 2A phosphoprotein phosphatase)	pEY24	Yatzkan and Yarden 1995 Curr Genet 28:458-466
ppt-1 (serine/threonine protein phosphatase)	pEY43	Yatzkan and Yarden 1997 BBA 1353:18-22
preg	pPREG2.3[cDNA]	Kang and Metzenberg 1993 Genetics 133:193-202
pyr-4 (orotidine 5'-monophosphate decarboxylase)	pFB6	Buxton & Radford 1983 MGG 190:403
qa-2 (catab. dehydroquinase), qa-x	pMSK338	Geever et al. 1989 J. Mol. Biol. 207:15-34
qa-2, qa-4 (dehydroshikimate dehydrase)	pMSK374	Geever et al. 1989 J. Mol. Biol. 207:15-34
qa-3 (shikimate dehydrog.), qa-y	pMSK381	Geever et al. 1989 J. Mol. Biol. 207:15-34
qa-y (quinic acid permease), qa-1S	pMSK363	Geever et al. 1989 J. Mol. Biol. 207:15-34
qa-1F (regulatory)	pQA1F	Geever et al. 1989 J. Mol. Biol. 207:15-34
Nc-ras2	pTY6	Murayama. Mol. Gen. Genet. 254:427-432
Nc-ras2	pTY7	Murayama. Mol. Gen. Genet. 254:427-432
rco-3	pLMN1	Ebbole and Madi 1995 FGN 43:23-24

***Neurospora crassa* plasmids, continued**

rgb-1	pEY15	Yarden. Mol Microbiol. 31:197-209
sod-1 (superoxide dismutase)	pCN101	Chary et al. 1990 JBC 265:18961-18967
spe-1 (ornithine decarboxylase)	pGS1	Williams et al. 1992 Mol. Cell Biol. 12:347-359
spe-2	pSPE2	
spe-2	pSP6-spe-2	
spe-3	pTC102	Nakashima J. Biol Rhythm 13:452-460
Tad	pTAD3.2	
T (tyrosinase)	pTYR103	Kothe et al. 1993 Fungal Genet. Newsl. 40:43-45
thi-4	pDC107(17:4B)	Nakashima. Curr Genet 30:62-67
trp-1 (anthranilate synthetase)	pNC2	Schechtman & Yanofsky 1983 J Mol Appl Genet 2:83
trp-*trp-3* (tryptophan synthetase)	pDB1	Burns and Yanofsky 1989. JBC 264:3840
un-3 (valyl tRNA synthetase)	pUN3	Kubelik et al. 1991. Mol. Cell. Biol. 11:4022-4035
un-18	pTS182	Nakashima. Mol. Gen. Genet. 259:264-271
ribosomal protein	p1717	Tarawneh, K. et al. 1990 Nucl Acids Res 18:7445
vma-1 (genomic vacuolar ATPase)	pvma-1g	Bowman et al. 1988 JBC 263:13994-14001
vma-1 (cDNA)	pRB34	Bowman et al. 1988 JBC 263:13994-14001
vma-2 (genomic)	pBB4	Bowman et al. 1988 JBC 263:14002-17007
vma-2 (genomic)	pMW1	Bowman et al. 1988 JBC 263:14002-14007
vma-2 (cDNA)	pRB30	Bowman et al. 1988 JBC 263:14002-17007
vma-3 (genomic)	pHS214	Sista et al. 1994 Mol Gen Genet 243:82-90
vma-3, *ilv-2* ((genomic)	pHS171	Sista et al. 1994 Mol Gen Genet 243:82-90
vma-4 (genomic)	pAS4A	
vma-4 (cDNA)	pAS30	
vma-6 (genomic)	pvma-6g	
vma-6 (cDNA)	pvma-6c	
vph-1 (genomic)	pRB103A	
vph-1 (cDNA)	pRBS	
VR telomere, POGO	pNC36	Schechtman 1987 Mol. Cell. Biol. 7:3168-3177

Plasmids containing *Neurospora crassa* mtDNA

Plasmid	Description
pEco2	Eco2 fragment containing ND2, ND3, ND4 and part of ND5 in pBR322
pEco4	Eco4 fragment in pBR322
pEco6	Eco6 fragment in pBS$^+$
pHP2	PstI-5a subfragment of EcoRI-1 containing 19S rRNA sequence in pBR322
pRH70	HindIII-7c fragment containing the coI gene in pBR322
pBX17	XbaI/BamH1 subfragment of BamHI-3 containing only 19S rRNA sequences
pHPR4a	large rRNA 5' exon probe in pBR322
pND3	KpnI/XbaI fragment behind T7 promoter in pBS$^+$
pUCB2 - pUCB11	EcoRI fragments of mtDNA in pBR325

Neurospora Genomic libraries

pLorist6xh

This library, along with the pMOcosX library was mapped on the genome of *Neurospora crassa*. Individual clones are available.

Lambda-J1 Library

A Neurospora library constructed from strain 74-OR23-1A (FGSC # 987) by Marc Orbach in the lambda-J1 vector using a partial Sau3A digest is distributed as a phage suspension. The library is described in MCB 6:2452-2461.

Lambda-BARGEM7 Library

Random fragments ranging in size from 2 to 10 kb from a partial Tsp509I digest are inserted into the EcoRI polylinker of pBARGEM7 contained in a lambda gt7 derivative (Pall and Brunelli 1994 Fungal Genetics Newsletter 41:63-65). Inserts are automatically excised as plasmid when an appropriate *E. coli* strain is infected.

pcosAX cosmid Library

DNA from strain ORSa (FGSC # 2490) was partially digested with Sau3A and ligated into the vector pcosAX. 24,000 primary colonies were pooled and amplified. This library, constructed by R. Aramayo, is distributed frozen as a suspension of *E. coli* cells.

Orbach/Sachs pMOcosX cosmid Library

The vector pMOcosX has dominant selectable markers for fungi (hygromycin resistance) and *E. coli* (ampicillin resistance). To prepare the library, pMOcosX was digested with XbaI and the ends treated with phosphatase. The vector was then digested with XhoI and the ends partially filled in with dCTP and dTTP using klenow. 74-OR23-1VA (FGSC #2489) DNA was partially digested with MboI and the ends partially filled in with dATP and dGTP using klenow. The vector and genomic DNAs were ligated. The ligated DNA was divided into two parts. One part was packaged using Stratagene gold II extracts and the other part was packaged using Stratagene XL II extracts. The packaged material was plated on host strain DH5aMCR. 2400 colonies were picked from each packaged DNA set to 25 microtiter plates so that the entire library consists of 50 microtiter plates.
A list of identified cosmids in the library is available online. The pMOcosX library was used by the Broad Institute in their sequencing of the Neurospora genome and individual clones are also available.

pSV50 cosmid library

The pSV50 cosmid vector confers resistance to benomyl in Neurospora and Ampicillin in *E. coli*. The pSV50 library (Vollmer and Yanofsky 1986 PNAS 83:4869-4873), which consists of 32 microtiter plates was constructed from strain 74-OR23-1A (FGSC # 2489). Genomic DNA was partially digested with Sau3A1 and size fractionated on sucrose density gradients. DNA in the 35- 45 Kb range was ligated into BglII digested, dephosphorylated vector and packaged and transfected into *E. coli* DH1. The ordered library is made up of 3072 clones (out of >300,000).
A list of identified clones in the library is available at the FGSC web-site.

The Neurospora minimal library

Cosmid clones from the pLorist6xh library were picked to a reduced set of 33 plates which provide good coverage of the genome. Additional clones from the pMOcosX and MIPS BAC library will be used to provide additional coverage.

Neurospora YAC library

A yeast artificial chromosome library of *N. crassa* 74-OR23-1A (FGSC # 987) sequences, constructed by Mike Centola, is available from FGSC. It consists of 2204 clones (24 microtiter plates) with an average insert size of 170 kb (range of clones tested is 140 kb - 244 kb). The total size of inserted DNA represents 9 genomic equivalents. This library has not been replicated for over 10 years and is only available as long as the current sets are viable. It is offered on an as-is basis.

Neurospora cDNA libraries

cDNA libraries constructed by Matthew Sachs

Two cDNA libraries, which represent mRNA from the *Neurospora crassa* wild type strain, 74-OR23-1VA, were constructed in Lambda Zap version I+ (Short, Fernandez, Sorge and Huse. 1988 Nucl. Acids Res. 16:7583-7600) as described (Orbach, Sachs and Yanofsky. 1990 J. Biol.Chem. 265:10981-10987). cDNA libraries were prepared from macroconidia incubated in 1X Vogel's minimal medium with 2% sucrose for 0.5, 1, and 2 hours (combined to obtain the germinating library) and 6 hours (mycelial library). The libraries are supplied as lambda phage suspension. The germinating conidia library is no longer available.

Nitrogen induced cDNA libraries constructed by R.H. Garrett

One library (NO_3- induced) was made from poly(A)+ RNA isolated from *Neurospora crassa* mycelia grown on Vogel's minimal made with 3% sucrose and 20 mM glutamine, then induced for nitrate assimilation by transfer to a medium containing 20 mM nitrate as the sole N-source. The other library (glutamine-grown) was made from poly(A)+ RNA isolated from mycelia grown as above, then transferred to a medium containing 20 mM glutamine as the sole N-source. cDNA in each library was prepared from poly(A)+ RNA using a Pharmacia cDNA kit, ligated on *Eco*RI adapters, and cloned into lambda ZAP version II+ Both libraries are >98% recombinant phage as judged by blue/white selection and by individual plaque isolation.

Libraries in yeast/E. coli -lambda vectors designed for cre/lox-mediated plasmid excision and direct complementation in yeast and E. coli (M. Pall)

Two libraries are available with common features. Both vectors contain the yeast 2 micron origin, a modified pBR322 origin, ampicillin resistance and a polylinker similar to the KS/SK polylinker. The AD5-NC vector has TRP1 for selection in yeast and the ADH2 promoter, while PGE15-NC has URA3 for selection in yeast and the PGK promoter. See Brunelli and Pall 1993. Yeast 9:1309-1318.

Neurospora Genome Project cDNA libraries

Four different cDNA libraries, corresponding to three stages of the life cycle, constructed by Dr. S. Kang are available.
These libraries are described in Fungal Genetics and Biology (1997) 21:348-363.
The four are:

C-1 Conidial Library (74A conidia grown in Vogels 2% sucrose minimal medium with shaking for 4.5 hrs).
M-1 Mycelial Library (74A conidia grown in Vogels 2% sucrose minimal medium with shaking for 24 hrs).
P-1 Perethecial Library (FGSC 4347 was grown on crossing plates and fertilized with 74A. Perethecia were collected after 5 days).
W Mycelial (74 A conidia grown in Westergaard's and 1% sucrose for 36 hrs without shaking).

They are all made in the Uni-ZAP XR vector (Stratagene®). These libraries may not be distributed to commercial organizations.

Neurospora Genome Project 2-hybrid cDNA libraries

Three 2-hybrid libraries were prepared using cDNAs correponding to the three different tissues used above: C-1, M-1, P-1.
The libraries were constructed in the HybriZap™ Two-hybrid Vector kit (Stratagene).

Neurospora EST clone banks and Unigene sets

The FGSC no longer has the bulk of the Neurospora EST sets.
We have non-redundant sets of cDNA clones from the New Mexico and Dartmouth groups. Please contact the FGSC for details.
Many clones are represented in this set, but they are only available on an as-is basis.

Fee List

Please consult the FGSC web-site for current fees.

PART I. Single Mutant Stocks

(listed alphabetically by gene symbol)

In addition to point mutants, chromosome rearrangements that are inseparable from a mutant phenotype that is allelic with a known gene are listed in Part I; these may be non-revertible or useful in other ways. For loci where no single-mutant stock is available, the simplest multiple mutant is listed here. Some single mutant strains are necessarily or most conveniently carried in heterokaryons, usually with the helper strain a^{m1} *ad-3B cyh*-1 (ref. 187). Heterokaryons of mutants such as *uvs-4*, require the presence of a second forcing marker. Such heterokaryons are also listed with single mutants. A full list of strains with characterized chromosome aberrations is found in part V. Stocks in RL background probably contain *scot*, which affects growth at 34 °C and above. Symbols used, including 'genetic backgound,' are described at the end of part VIII.

Mutant strains from the Neurospora Functional Genomics Program are available as individual stocks or arrayed sets. Mutants with a defined gene symbol are included below and at the end of the single mutant section

		FGSC number mating type			Genetic back-ground		
Locus	Allele	A	a	Linkage Group		Muta-gen	Obtained from
ACCELERATED GROWTH GALACTOSE see *agg*							
am α-BINDING PROTEIN							
aab-1 trp-1			9597	IIIR IIIR			JAK
aab-1 trp-1			9598	IIIR IIIR			JAK
ACETYLAMINOFLUORENE							
aaf	no#(t)	632	633		M	S	PT
ABNORMAL see [*abn*] -- Part IV							
ACETATE							
ace-1	Y2492	107	205	IIR	SL	M	DDP
ace-2	37812	6014	6015	IIIR	SL	UV	DDP
ace-2	KG511		3469	IIIR	E	UV	HK
ace-2	KG526		3470	IIIR	E	UV	HK
ace-3	KG536	6629	3471	IR	M/E	UV	DDP/HK
ace-4	KG508	8212	3472	IVL	E	UV	FGSC/HK
ace-4	KG523		3473	IVL	E	UV	HK
ace-5	KG512	7557	3474	VR	E	UV	DDP/HK
ace-5	KG513		3475	VR	E	UV	HK
ace-6 see *suc*							
ace-7	KG539	8213	3476	IR	M	UV	FGSC/HK
ace-7	KG571		3476	IR		UV	HK
ace-8	KG570		4448	VIIC	E	UV	HK
ace-9	KG601	6952	6953	IIR	SL	UV	HK
ACONIDIAL							
acon-2	RS91(t)	3262	3263	IIIR	SL	EMS	DDP
acon-3	RS503	3286	5074	IVL	SL	EMS	DDP
ACETATE PERMEASE							
acp^i	FS800	3456	3457	--	SL	UV	AGD
ACRIFLAVINE RESISTANT							
acr-1	KH1(r)	876	875	IL	SL	S	KSH
acr-2	1001(r)	1060		IIIL	M	UV	HBH
acr-2	1002(r)	1059		IIIL	M	UV	HBH
acr-2	KH2(r)	878	877	IIIL	SL	S	KSH
acr-2	KH5(r)	4043	4044	IIIC	SL7	S	EK

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
acr-2	RC3(r)	2585		IIIL	SL	DS	DDP
acr-3	KH14(r)	1209	1215	IL	SL4	UV	DNP
acr-4;*shg*	KH16(r);KH160	2322		IL;IIIR	M	S	KSH
acr-5	JLC74	5077	5078	IIR	M	S	DDP
acr-5;*mo*(*KH161*)	KH27(r);KH161	2323	2324	IIR;--	M	G	KSH
acr-6 shg	KH19(r) KH160	2325	2326	IIIR R	M	S	KSH
acr-7	P1676(r)	2314	3841	IIIL	M	S	DDP
ACTIN							
act-1	33-29 2		9522				MP/JAK
act-1	33-29 5		9523				MP/JAK
act-1	33-29 4	9525					MP/JAK
act-1	33-29 3	9524					MP/JAK
ACETATE NON-UTILIZER							
acu-1	JI48		4080	V	SL6	NG	EK
acu-1 inl	JI48 R233	1731		VR R	M	NG	RBF
acu-3	JI38	1732		VR	SL	NG	RBF
acu-5	JI18	4032	4033	II(R)	SL7	UV	EK
acu-6	JI31	1734		VIL	SL	NG	RBF
acu-7	JI36	1735	3264	IIIR	M	NG	RBF/DDP
acu-8	T37-3	7125	7126	IIR	SL	RIP	JRF
acu-9 am	T11-1 *am*$_{132}$	7326		VII	SL	RIP	IFC
acu-10	S10-3	8214	7327	--	SL	NG	FGSC/IFC
acu-11	S30-12	8215	7328	VII	SL	NG	FGSC/IFC
acu-12	S10-4	7329	8216	IIR	SL	NG	IFC
acu-13	S10-2	7330		IIR	SL	NG	IFC
acu-13	S10-8	7331		IIR	SL	NG	IFC
acu-13	S10-15		7332	IIR	SL	NG	IFC
acu-13	S30-2	7333		IIR	SL	NG	IFC
acu-13	S30-9		7334	IIR	SL	NG	IFC
acu-15 am	61 132	9018		V VR			IFC
acu-15 am	61 132	9019		V VR			IFC
acu-15 am	73 132	9020		V VR			IFC
acu-15	KO	11013	11014	V	SL	KO	GP
ADENINE							
ad-1	Y234M419	672		VIL	SL	UV	MEC
(Contains *T(I;VI)Y234M419*)							
ad-1	3254	2281	410	VIL	M	X	DDP
ad-2	20705	8081	397	IIIR	M	X	MBM
ad-2	27663	8082	516	IIIR	M	UV	RWB
ad-2	70004(t)	380	8077	IIIR	M	UV	MBM
ad-2	STL2	26	8075	IIIR	M	S	DDP
ad-2	Y175M256		673	IIIR	SL	X	MEC
ad-2;*al*(*Y234M468*)	Y175M256;Y234M468	956		IIIR;IR	SL	X	AMK
ad-2	Y83M32	674	8085	IIIR	SL	X	MEC
ad-2;*inl*	1-175-256;JH319	5042	5046	IIIR;VR	SL		FJD
ad-3A	1-68-13	5041		IR	SL	X	FJD
ad-3A	1-112-13	6655	6656	IR	SL	X	DDP
ad-3A	1-230-49		5485	IR	SL		FJD
ad-3A	2-17-52	886		IR	SL	NA	FJD
ad-3A	2-17-814	2458		IR	SL	NA	FJD
ad-3A	2-17-825	5038	5636	IR	SL	NA	FJD
ad-3A	2-31-2		5628	IR	SL		FJD
ad-3A	2-32-10		5637	IR	SL		FJD
ad-3A	2-33-3		5634	IR	SL		FJD

ADENINE, continued from previous page

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic background	Mutagen	Obtained from
ad-3A	2-33-22		5630	IR	SL		FJD
ad-3A	2-33-34		5629	IR	SL		FJD
ad-3A	5-5-23		5632	IR	SL		FJD
ad-3A	5-5-47		5631	IR	SL		FJD
ad-3A	5-5-52		5635	IR	SL		FJD
ad-3A	5-5-74		5633	IR	SL		FJD
ad-3A	38701	5519	5518	IR	M	UV	MBM
ad-3A	38709	5521	5522	IR	M	UV	MBM
ad-3A	68306	5044	5043	IR	SL	UV	FJD
ad-3A	68306		5452*	IR	SL		FJD
ad-3A	IS11-10	4764		IR	SL		FJD
ad-3A al-2;cot-1; pan-2	N23 Y112M38;C102(t); Y387-15.7	3331		IR R; IVR;VIR	M	4-NQO	TMO
ad-3A al-2 nic-2 un-3;*tol*	2-17-814 Y112M38 43002 55701(t);N83	3820†		IR R R L;IVR	M	NA	AJG
T(I;II:III)Y155M64 ad-3A	Y155M64	3037	3038	I;II;III			DDP
T(I→IV)Y112M15 ad-3A	Y112M15	2957		IR;IV			AJG
ad-3A	Y175M167		661	IR	SL	X	MEC
ad-3A^{IR}	12-5-194	5028		IR	SL	X	FJD
ad-3A^{IR}	12-7-215	5029		IR	SL	X	FJD
ad-3B	1-112-2	677		IR	SL	X	MEC
ad-3B	1-112-2		4937	IR	SL		FJD
ad-3B	1-112-9	5447	5446	IR	SL		FJD
ad-3B	1-152-68		5483	IR	SL		FJD
ad-3B	1-155-55		5484	IR	SL		FJD
ad-3B	1-230-83		4928	IR	SL		FJD
ad-3B	1-234-148		5461	IR	SL		FJD
ad-3B	2-11-5		5462	IR	SL		FJD
ad-3B	2-11-6		5463	IR	SL		FJD
ad-3B	2-11-163		5464	IR	SL		FJD
ad-3B	2-15-72		5465	IR	SL		FJD
ad-3B	2-15-123	5051		IR	SL	DEB	FJD
ad-3B	2-15-146		5638	IR	SL		FJD
ad-3B	2-17-34	4004	4005	IL	SL5	NA	EK
ad-3B	2-17-34	883	4927	IR	SL	NA	FJD
ad-3B	2-17-55	884		IR	SL	NA	FJD
ad-3B	2-17-128	885	4765	IR	SL	NA	FJD
ad-3B	2-17-137	3259	3846	IR	SL/SL2	NA	FJD/DDP
ad-3B	2-31-8		4926	IR	SL	2-AP	FJD
ad-3B	2-32-3		4766	IR	SL	2-AP	FJD
ad-3B	2-32-5		4767	IR	SL	2-AP	FJD
ad-3B	3-10-16		5472	IR	SL		FJD
ad-3B	3-10-67		5473	IR	SL		FJD
ad-3B	3-10-70		5474	IR	SL		FJD
ad-3B al-2	3-10-109 1-112-38		5475	IR	SL		FJD
ad-3B	3-10-112		5476	IR	SL		FJD
ad-3B	3-10-114		5477	IR	SL		FJD
ad-3B	3-10-132		5478	IR	SL		FJD
ad-3B al-2	3-10-153 1-112-38		5479	IR	SL		FJD
ad-3B al-2;pan-2	3-10-384 1-112-38;1-153-96	5052		IR IR;VIR	SL		FJD
ad-3B	3-10-384		5047	IR	SL		FJD
ad-3B	3-10-446		5481	IR	SL		FJD
ad-3B	3-10-500		5482	IR	SL		FJD
ad-3B	35203	5517	244	IR	SL	UV	FJD/DDP
ad-3B	45601	5523		IR	SL		FJD
ad-3B	5-4-1	5050		IR	SL	S	FJD
ad-3B	5-4-5	5045		IR	SL	UV	FJD

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
ADENINE, continued from previous page							
T(I→III)Y112M4i ad-3B	Y112M4i	2637	2638	IR;IIIR			DDP
ad-3	Y175M155		675	IR	SL	X	MEC
ad-4	44206(t)	4045	4046	IIIR	SL6	UV	EK
ad-4	44415(t)	1106	8130	IIIR	M	UV	MEC
ad-4	Y112M16(F2)	442		IIIR	SL	X	MEC
ad-4	Y112M160(F4)	437		IIIR	SL	X	MEC
ad-4	Y155M13(F10)	445		IIIR	SL	S	MEC
ad-4	Y155M39(F12)	440		IIIR	SL	X	MEC
ad-4	Y193M1(F23)	438		IIIR	SL	S	MEC
ad-4	Y226M8(F31)	441		IIIR	SL	UV	MEC
ad-4	Y230M18(F39)	439		IIIR	SL	S	MEC
ad-4	Y234M63(F48)	444	443	IIIR	SL	UV	MEC
ad-5	71104	8129	15	IL	SL	UV	DDP
ad-5	Y152M40	3458	8193	IL	SL?		DDP
ad-5	Y175M253	8127	3459	IL	SL	X	DDP
ad-6	28610ad	65	628	IVR	L	UV	DDP
ad-6	35301	361	8076	IVR	L	UV	MBM
ad-6	Y175M30	664	8083	IVR	SL	X	MEC
ad-6	Y175M221		663	IVR	SL	X	MEC
ad-6	Y175M221	8206		IVR	SL		FGSC
ad-7	Y112M23		8207	VR	SL		FGSC
ad-7;ylo-1	44411;Y50539y	89		VR;VIL	M	UV	DDP
ad-7	44411	8084	517	VR	M	UV	RWB
ad-7	P73B171(t)	2619	2620	VR	SL	EMS	DDP
ad-7	Y112M23	666		VR	SL	X	MEC
ad-7	Y175M265	8132	665	VR	SL	X	MEC
ad-8	1-152-7(E6)	452	453	VIL	SL	X	TI
ad-8	1-175-1495 (E19)	3492		VIL	SL	S	TI
ad-8	1-182-20 (E27)	3493		VIL	SL	X	TI
ad-8	1-193-22(E32)	450		VIL	SL	UV	TI
ad-8	1-226-4 (E43)	3497		VIL	SL	S	TI
ad-8	1-226-21 (E51)	3498		VIL	SL	UV	TI
ad-8	1-226-41 (E70)	3499		VIL	SL	UV	TI
ad-8	1-261-12 (E200)	3507		VIL	SL	NA	TI
ad-8	1-262-3 (E206)	3508		VIL	SL	BUDR/FUDR	TI
ad-9	Y154M37	1984	952	IR	SL/M	X	BCT/DDP
ad-9	Y175M148	8126	454	IR	SL	X	MEC

* Forms strong bisexual heterokaryons with OR74A derived mutants

† heterokaryon compatibility type c D E

ad-3A^{IR} = irreparable - see F.J. de Serres 1964 Genetics 50:21-30

NOTE: Many more *ad-3A, ad-3B,* and *ad-8* alleles are available. See Part VI.

ADHERENT							
adh	NM227	1530	1531	VIIL	E	UV	DDP

ADENINE SENSITIVE							
ads	T51M1(s)(t)	3509		IV	SL	X	TI
ads	T52M13(s)(t)	3512		IV	SL	S	TI
ads	T52M15(s)(t)	3513		IV	SL	S	TI
ads	T52M26(s)(t)	3514		IV	SL	S	TI
ads	T52M6(s)(t)	3510		IV	SL	S	TI
ads	T52M8(s)(t)	3511		IV	SL	S	TI

ARGINASE							
aga	UM906	1698	1699	VIIR	M	UV	RHD

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
AGEING OF CONIDIA							
age-2	1	6757	6758	VIR	SL2	S	KDM
age-3 (allelic *al-1*)		6759	6760				
ACCELERATED GROWTH GALACTOSE							
agg	L-5	3270	--	M	UV	WKB	
ALTERED GLUCOSE REPRESSION							
agr-1;cot-1	RDS8;C102(t)?	7021		--;IVR		UV	SJF
ALBINO							
al-1(= *age-3*)	32	6759	6760	IR	SL		KDM
al-1	80-96	901		IR	SL	X	AMK
al-1 (= *aur*)	34508	3622	3623	IR	SL4	UV	DDP
al-1	ALS4	1526	2085	IR	M	UV	ALS/DDP
al-1	ALS19	2147		IR	M	UV	RES
al-1	ALS22	2148		IR	M	UV	RES
al-1	ALS23	2149		IR	M	UV	RES
al-1	ALS25	2150		IR	SL	UV	RES
al-1	car10	903		IR	M	UV	AMK
al-1	E54R11	899		IR	M	UV	AMK
al-1	JH216	3713	3714	IR	SL4	M	DDP
al-1	JP45-2		3858	IR	SL	NG	MLS
al-1; *eas*	JP45-2;UCLA191	4657	4658	IR;IIR			MLS
al-1	RES-25-4	2156	2157	IR			RES
al-1	RWT-ylo	3855	3856	IR	SL2	UV	MLS
al-1	Y234M471	898		IR	M	UV	AMK
al-1	Y246M2	902		IR	M	UV	AMK
al-1	Y246M3	906		IR	M	UV	AMK
al-1; *eas*	80-96;UCLA191	4665	4666	IR;IIR			MLS
al-1	al^{C}		800	IR	M	X	DDP
T(I;II)4637 al-1	4637	253	252	IR;IIR			DDP
al-2	15300	4014	3448	IR	SL7	X	EK/DDP
al-2	car1	900		IR	M	UV	AMK
al-2	car7	910		IR	M	UV	AMK
al-2	MN58p	2666	2667	IR	M	UV	DDP
al-2;cot-1;pan-2	Y112M38;C102;Y387-15.7	2583		IR;IVR;VIR	SL		FJD
al-2	Y234M469	914		IR	M	UV	AMK
al-2	Y254M165	904		IR	SL	UV	AMK
al-2	Y256M204	896		IR	M	UV	AMK
al-2	Y256M220		911 IR	M	UV	AMK	
al-2	Y256M221	913		IR	M	UV	AMK
al-2	Y256M222		907 IR	M	UV	AMK	
al-2	Y256M232	897		IR	M	UV	AMK
al-3	RP100	2082	4073	VR	SL/SL6	UV	RLP/EK
al-3;eas	P7775;UCLA191	4661	4662	VR;IIR			MLS
al-3^{ros}	Y234M470	3581	3582	VR	SL4	UV	DDP
al(85201)	85201		381 IR	M	M	MBM	
al(7-32)	7-32	912		IR	SL?	S	AMK
al(1500-008)	1500-008	1138		IR	M	EMS	PCH
al(1500-009)	1500-009	1139		IR	M	EMS	PCH
al(1500-010)	1500-010	1140		IR	M	EMS	PCH
al(1500-011)	1500-011	1141		IR	M	EMS	PCH
al(1500-012)	1500-012	1142		IR	M	EMS	PCH
al(1500-013)	1500-013	1143		IR	M	EMS	PCH
al(B102)	B102		799	IR	SL	UV	DDP
al(CN1)	CN1		1107		M	S	NFR
al(JH9698)	JH9698		801	IR	M		DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic background	Mutagen	Obtained from
		A	a				
ALBINO, continued from previous page							
al(RES6)	RES6	2152	2153	IR	M	UV	RES
al(RES100SUE)	RES100SUE	2154	2155	IR	M	UV	RES
al(Y256M231)	Y256M231	909		IR	M	UV	AMK
al(Y602)	Y602		797	IR	M	M	DDP
al(Y2170)	Y2170		796	IR	M	M	DDP
al(Y2171)	Y2171		795	IR	M	M	DDP
al(al^{M}*)*	al^{M}		798	IR	SL	UV	DDP
al(al^{S}*)*	al^{S}	827		IR	M	X	DDP
al(no#);*rib-1*	no#;C107		1225	IR;VIR			WSM
ALCOY see part VII							
alcoy		997	998				
alcoy;*csp-2*		3661	3434				
ALKALINE PHOSPHATASE see *pho*							
ALLANTOICASE DEFECTIVE							
alc-1	WRR1		2699	II	SL	UV	GAM
alc-1	WRR5		2700	II	SL	UV	GAM
ALLANTOINASE DEFECTIVE							
aln	U3		2701	VII	SL	UV	GAM
AMINATION DEFICIENT (NADP-specific glutamate dehydrogenase)							
am	32213(am$_{1}$)	521	1184	VR	M/SL6	UV	RWB/JRF
am	47305(am$_{2}$)	519	1185	VR	M/SL6	UV	RWB/JRF
am;al^{S}	47305(pr)(am$_{2a}$);al^{S}		782	VR;IR	M	UV→am$_{3}$	RWB
am	S2929(am$_{3}$)	522	523	VR	M	MC	RWB
am	S2929(am$_{3}$)		1186	VR	SL6	MC	JRF
am	S2929(partial revertant)(am$_{3a}$)		783	VR	M	UV→am$_{3}$	RWB
am	1381(am$_{4}$)	525	1187	VR	M/SL6	UV	RWB/JRF
am	B501(am$_{5}$)	4343	1188	VR	SL	UV	ELT/JRF
am	am$_{6}$		7095	VR	SL6	UV	JRF
am;al^{S}	K314(am$_{6}$);al^{S}		786	VR;IR	M		RWB
am	B410(am$_{7}$)		1189	VR	SL6	UV	JRF
am	am$_{8}$		788	VR	M	UV	RWB
am	am$_{8}$		7096	VR	SL6	UV	JRF
am;al^{S}	am$_{9}$;al^{S}		789	VR;IR	M	UV	RWB
am;al-2	am$_{10}$;15300		1679	VR;IR	M	UV	JRS
am	am$_{11}$		790	VR	M	UV	RWB
am	am$_{14}$		1190	VR	SL6	NA	JRF
am	am$_{15}$		1678	VR	SL6		JRS
am	am$_{16}$		1677	VR	SL6		JRF
am	am$_{17}$	1680	1684	VR	M	NA	TWS
am	am$_{19}$	1960	1961	VR	E4/E2	NA	DS
am	am$_{1}$	7097	7098	VR	SL	NA	JRF
am;al-2	RU1(am$_{21}$);15300	1737	1738	VR;IR	SL	UV	KJM
am	am$_{24}$		1853	VR	M	UV	TWS
am;rec-3	am$_{111}$;no#	5881		VR;IL	M	UV	JAK
am;rec-3	am$_{128}$;no#	5882		VR;IL	M	NA	JAK
am	am$_{132}$	5883	5884	VR	SL10	NA	JAK
am	am$_{120}$	9933	9932	VR			JAK
am	am$_{117}$		9934	VR			JAK
am;rec-3	UK23-44;no#	5874		VR;IL	M	DEO	JAK
am;rec-3	UK23-81;no#	5875		VR;IL	M	DEO	JAK
am;rec-3	UK23-82;no#	5876		VR;IL	M	DEO	JAK
am;rec-3	UK39-A4;no#	5877		VR;IL	M	DEO	JAK

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
AMINATION DEFICIENT, continued from previous page							
am;rec-3	UK48-2;no#	5878		VR;IL	M	DEO	JAK
am;rec-3	UK73-SG2;no#	5879		VR;IL	M	S	JAK
am;rec-3	UK73-40;no#	5880		VR;IL	M	DEO	JAK
Second site revertants							
am	am$_{21}$	7099	7100	VR	SL	UV	JRF
am	am$_{3a}$		7101	VR	SL	UV	JRF
am;arg-10	am$_{3a}$;B317		7102	VR	SL	UV	JRF
am	am$_{3a\text{-}1}$		7103	VR	SL	UV	JRF
am	am$_{3b}$		7104	VR	SL	UV	JRF
am	am$_{3b\text{-}1}$	7105		VR	SL	UV	JRF
am	am$_{3}$-18	7106		VR	SL	UV	JRF
am	am$_{6}$-L7		4389	VR	SL7	UV	JRF
am	am$_{6}$-R3		4386	VR	SL7	UV	JRF
am	am$_{6}$-R'13	4390		VR	SL7	UV	JRF
am	am$_{6}$-R14		4393	VR	SL7	UV	JRF
am	am$_{6}$-R15		4385	VR	SL7	UV	JRF
am	am$_{6}$-R27	4394		VR	SL7	UV	JRF
am	am$_{14}$R1	7107		VR	SL	NA	JRF
am	am$_{14}$-R5		4392	VR	SL7	UV	JRF
am	am$_{15}$R11		7108	VR	SL	A	JRF
am	am$_{15}$R15		7109	VR	SL	A	JRF
am	am$_{15}$R16		7110	VR	SL	A	JRF
am	am$_{19}$R24	7111		VR	SL	NA	JRF
am	am$_{19}$R24(1639-56)	7112		VR	SL	NA	JRF
am	am$_{19}$R24-1		7113	VR	SL	NA	JRF
am	am$_{19}$R24-2	7114		VR	SL	NA	JRF
am	am$_{17}$-RN35	4388		VR	SL7	UV	JRF
am	am$_{17}$-RU4		4387	VR	SL7	UV	JRF
Ectopic integrations							
am$_{132}$ *am*$^{+}$*T85 (204-5)*		7115			SL		JRF
am$_{132}$ *am*$^{+}$*T75 (214-1)*		7116			SL		JRF
am^{+} *am*$^{+}$*T75 (3)*			7117		SL		JRF
am^{+} *am*$^{+}$*T85 (2)*		7118			SL		JRF
am$_{132}$ *am*$^{+}$*T75 am*$^{+}$*T85 (4)*		7119			SL		JRF
Induced by RIP							
*am3** (=*am*$_{3SH}$)		7120			SL	RIP	JRF
am$_{S}$*-1*		7121			SL	RIP	JRF
am$_{S}$*-6*			7122		SL	RIP	JRF
am$_{H}$*-2*		7123			SL	RIP	JRF
am$_{H}$*-1*		7124			SL	RIP	JRF

The FGSC has received a collection of 121 strains carrying various *am* alleles from the collection of JRF. Please inquire if you are interested in these strains.

AMINO TRIAZOLE RESISTANT see *atr*

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
AMYCELIAL							
amyc	K422	305	306	IL	SL3		DDP
ANAEROBIOSIS (FACULTATIVE)							
an^{+}	2B-12-3		3442	--	SL	UV	KDM
an^{+}	2B-16-9	3443		--	SL	UV	KDM
an^{+}	5B-8-2		3445	--	SL	UV	KDM

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
ANNEXIN							
anx-14; eas	Δ-hygR	9927		IVR			PR
ARGINASE see *aga*							
ALTERNATE OXIDASE DEFICIENT							
aod-1 pan-1		9936		IV IV			FN
aod-1 nic-1 al-2			9937	I I I			FN
ARGININE							
In addition to the strains displayed here, a variety of arg mutants from the collection of R.H. Davis are available from the FGSC.							
arg-1	36703	1459		IL	M	UV	DDP
arg-1	46004	528	407	IL	M	UV	RWB
arg-1	B369	325	324	IL	SL5	G	DDP
arg-1	CD145	3585		IL	M	UV	RHD
arg-1	CR237(t)	2382		IL	M	NNG	WMT
arg-1	K166		747	IL	M	UV	DGC
arg-1	K209		748	IL	M	UV	DGC
arg-1	K287		774	IL	M	UV	DGC
arg-1	K337		749	IL	M	UV	DGC
arg-1	K351		750	IL	M	UV	DGC
arg-1	K401		751	IL	M	UV	DGC
arg-1	K406		1331	IL	M	UV	DGC
arg-1	SDS1		2381	IL	M	UV	WMT
arg-2	33442	4760	66	IVR	SL/M		RHD/DDP
arg-2	CD80	3586	4232	IVR	M	UV	RHD/DDP
T(I;IV)MEP24 arg-2	MEP24	3170	3171	IVR			DDP
arg-3	30300	1068	1069	IL	SL3	UV	DNP
arg-3	NM136	2663		IL	M	UV	DDP
T(I;IV;IV→V)MEP35 arg-3	MEP35	3844	3845	IL			DDP
arg-3	CD-37	8402		IL	SL		RHD
arg-4	21502		90	VR	M	X	DDP
arg-4	21502		778	VR	M	X	DGC
arg-4	34105	91	84	VR	M	UV	DDP
arg-4	34105		779	VR	M	UV	DGC
arg-5	27947	4034	4035	IIR	SL6	X	EK
arg-5	CD6	3589	3590	IIR	M	UV	RHD
arg-5	K124		741	IIR	M	UV	DGC
arg-5	K128		752	IIR	M	UV	DGC
arg-6	29997	266		IR	M	UV	DDP
arg-6	29997		4015	IR	SL7	UV	EK
arg-6	C116	929		IR	M	S	MBM
arg-6	C122	549		IR	M	UV	DDP
arg-6	CD25	3591		IR	M	UV	RHD
arg-6	CD29	3592		IR	M	UV	RHD
arg-6	CD63	3593		IR	M	UV	RHD
arg-6	HY176(t)		1240	IR	M	UV	JH
arg-6	HY227(t)		1242	IR	M	UV	JH
arg-6	K131		773	IR	M	UV	DGC
arg-6	K142		693	IR	M	UV	DGC
arg-6	K169		753	IR	M	UV	DGC
arg-6	K190		754	IR	M	UV	DGC
arg-6	K374		755	IR	M	UV	DGC
arg-6	K395		742	IR	M	UV	DGC
arg-6	VP102	8259	8260	IR	M		DDP
arg-7	CD51		3594	VR	M	UV	RHD

		FGSC number mating type			Genetic back-	Muta-	Obtained
Locus	Allele	A	a	Linkage group	ground	gen	from
arg-8 see *pro-3*							
arg-9 see *pro-4*							
arg-10	B317	4091	4092	VIIR	SL9	UV	EK
arg-10	HY93(t)		1241	VIIR	M	UV	JH
arg-10	K112		743	VIIR	M	UV	DGC
arg-10	K323		745	VIIR	M	UV	DGC
arg-10	K402		772	VIIR	M	UV	DGC
arg-10	K405		756	VIIR	M	UV	DGC
arg-11	30820	145	136	VIIR	SL3	X	DDP
arg-11	44601	1532	3616	VIIR	SL3/SL4	UV	DDP
arg-12	CD3	3595		IIR	M	UV	RHD
arg-12	UM3	978		IIR	M	UV	RHD
arg-12	UM107	979	1527	IIR	M/SL2	UV	RHD/DDP
arg-12	37301s	893		IIR	L	UV	RHD
arg-13	CD7	3596	3597	IR	M	UV	RHD
arg-13	RU3	3157		IR	SL2	UV	DDP
arg-13	RU12	4018	4019	IR	SL7	UV	EK
ARGININE, continued from previous page							
arg-13	RU20	1726		IR	M	UV	KJM
arg-14	CD197	3598	3599	IVR	M	UV	RHD
T(IV→VII;I;II;IV)							
S1229 arg-14 pe	S1229	2946	268	IVR			EGB/DDP
AROMATIC AMINO ACIDS							
aro-1	311-1027	6142		IIR	SL	UV	MEC
aro-1	311-1075	6143		IIR	SL	UV	MEC
aro-1	311-1134	6144		IIR	SL	NG	MEC
aro-1	311-1183		6145	IIR	SL	NG	MEC
aro-1	Y306M80	1742	3617	IIR	SL	EMS	MEC/DDP
aro-1	Y7655	3629	3630	IIR	M	M	DDP
aro-1	Y7655		1695	IIR	L	M	SRG
aro-2	311-1084	6146		IIR	SL	UV	MEC
aro-2	311-1234	6148		IIR	SL	NG	MEC
aro-2	311-1277	6147		IIR	SL	NG	MEC
aro-2	Y306M81	1743		IIR	SL	EMS	MEC
aro-3	306-47	6167	6168	IIR	SL	EMS	MEC
aro-3	C163	1293	53	IIR	M	UV	DDP
aro-3;inl	R2017;89601	1103		IIR;VR	M	UV	MEC
aro-3;inl	R2202;89601	1098		IIR;VR			MEC
aro-3;inl	R2203;89601	1099		IIR;VR			MEC
aro-3;inl	R2205;89601	1100		IIR;VR			MEC
aro-3;inl	R2209;89601	1101		IIR;VR	M	UV	MEC
aro-3;inl	R2212;89601	1102		IIR;VR	M	UV	MEC
aro-3;inl	R2333;89601	1104		IIR;VR	M	UV	MEC
aro-3	Y306M87	1744		IIR	SL	EMS	MEC
aro-4	311-1044	6149		IIR	SL	UV	MEC
aro-4	311-1050	6150		IIR	SL	UV	MEC
aro-4	311-1057	6151		IIR	SL	UV	MEC
aro-4	311-1201	6152		IIR	SL	UV	MEC
aro-4	R2204	162	171	IIR	M	UV	DDP
aro-4;inl	R2219;89601	1105		IIR;VR	M	UV	MEC
aro-4	Y306M49	1745		IIR	SL	NG	MEC
aro-5	Y306M56	1863		IIR	SL	EMS	MEC
aro-5	311-1146	6153		IIR	SL	NG	MEC
aro-5	311-1154	6154		IIR	SL	NG	MEC
aro-5	311-1185	6155		IIR	SL	NG	MEC
aro-5	311-1224	6156		IIR	SL	NG	MEC
aro-6	DH1	1712	1713	VI	SL	UV	DMH

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
AROMATIC AMINO ACIDS, continued from previous page							
aro-7	DH7	1714	1715	IC	SL	UV	DMH
aro-8	DH8	1716	1717	IR	SL	UV	DMH
aro-9;inl;qa-2	M6-11;89601;M246	3952		IIR;VR;VIIR		MEC	
aro-9	Y325M6	3938	3939	IIR	M		DDP
aro(p)	Y306M54	1862	1854	IIR	SL	EMS	MEC
aro(p)(A-C)	311-1131	6157		IIR	SL	NG	MEC
aro(p)(A-C)	311-1163	6158		IIR	SL	NG	MEC
aro(p)(A-C)	311-63		6172	IIR	SL	UV	MEC
aro(p)(A)	311-58		6180	IIR	SL	UV	MEC
aro(p)(A)	311-1063	6182		IIR	SL	NG	MEC
aro(p)(B)	311-14	6163	6162	IIR	SL	UV	MEC
aro(p)(B)	311-1036	6176		IIR	SL	NG	MEC
aro(p)(B)	311-1136	6185		IIR	SL	NG	MEC
aro(p)(C)	311-1052	6175		IIR	SL	UV	MEC
aro(p)(C)	311-1148	6178		IIR	SL	UV?	MEC
aro(p)(D)	311-75	6169	6170	IIR	SL	UV	MEC
aro(p)(D)	311-1094	6177		IIR	SL	NG?	MEC
aro(p)(D)	311-1113	6183		IIR	SL	NG	MEC
aro(p)(D)	311-1116		6186	IIR	SL	UV	MEC
aro(p)(D)	311-1199	6159		IIR	SL	NG?	MEC
aro(p)(E)	311-34	6165	6166	IIR	SL	UV	MEC
aro(p)(E)	311-54	6171	6172	IIR	SL	UV	MEC
aro(p)(E or F)	311-1150	6184		IIR	SL	NG	MEC
aro(p)(F)	311-25	6164	6179	IIR	SL	UV	MEC
T(II;III)C161 aro	C161	2106	2107	IIR;III			DDP
ARYL SULFATASE DEFECTIVE							
ars	101		1864	VIIR	SL	UV	RLM
ars	101-PR1		1871	VIIR	SL	UV→101	RLM
ars	103		1865	VIIR	SL	UV	RLM
ars	108		1866	VIIR	SL	UV	RLM
ars	111		1868	VIIR	SL	UV	RLM
ars	113		1869	VIIR	SL	UV	RLM
ars	301		1867	VIIR	SL	UV	RLM
ars	312		1870	VIIR	SL	UV	RLM
*ars**	343		2052	VIIR			RLM
*ars**	UFC-220	1909		VIIR			RLM
* - originated in *N. tetrasperma*							
ABNORMAL ASCUS MORPHOLOGY							
asc(JL155)	JL155	7511	7512		M		NBR
asc(JL164)	JL164	7514	7515		M		NBR
asc(JL174)	JL174	2222	7516		M		NBR
asc(JL179)	JL179	7517	7518		M		NBR
asc(JL209)	JL209	2225	7519		M		NBR
asc(JL219	JL219	7520	7521		M		NBR
asc(JL223)	JL223	7522	7523		M		NBR
asc(JL235)	JL235	7524	7525		M		NBR
asc(JL239)	JL239	7526	7527		M		NBR
asc(JL266)	JL266	430	7530		M		NBR
ASCOSPORE ABORTION (same locus as *lys-5*)							
asco	37402	4096	4095	VIL	SL6	UV	EK

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
ASCUS DEVELOPMENT							
asd-1	A1	7570	--		SL	RIP	MAN
asd-1	A2		7571	--	SL	RIP	MAN
asd-2	N7		7572	VIIL	SL	TR	MAN
asd-2	N18	7573		VIIL	SL	TR	MAN
ASCOSPORE MATURATION							
mep-1 his-3+::Asm-1;mtr;pan-2;Asm ::mtr+		8298			OR		RLM
mep-1 his-3+::Asm-1; mtr ;pan-2;Asm ::mtr+		8300	8299		OR		RLM
mep-1 his-3+::Asm-1;mtr ;pan-2;Asm ::mtr+		8302	8301		OR		RLM
mep-1 his-3+::Asm-1;mtr ;pan-2;Asm ::mtr+			8303		OR		RLM
ASPARAGINE							
asn	C123	111	114	VR	M	UV	DDP
asn	S1007	3620	3621	VR	M	X	DDP
asn	T51M147	2351		VR	M	X	DDP
asn	T51M158(t)		3602	VR	SL	UV	DDP
ASPARTIC ACID							
asp	44303	3873	3874	V	M	UV	DDP
ATTENUATED							
at	D307	1666		VC	M	UV	DDP
at	D315	1667		VC	M	UV	DDP
at	M111	1664	1884	VC	M	S	DDP
at	NM221(t)	1665		VC	M	UV	DDP
AMINO TRIAZOLE RESISTANT							
atr-1	RC2	2296	2299	IL	SL	DS	DDP
AURESCENT see *al-1*, allele 34508							
AZAPURINE RESISTANT							
aza-3;his-2 ad-3A ad-3B nic-2;ad-2;inl		3182		III		UV	GRH
BALLOON							
bal	B56	105	337	IIL	SL3	UV	DDP
bal	C-1405	823		IIL	SL	P	DDP
(bal arg-5 + a^{m1} *ad-3B cyh-1)*	B56 27447		8251	IIL R	M		DDP
BANANA							
Ban	N452P63	2989		IL	M	S	DNP
Ban mei-3;inl	N452P63 N289;89601		2990	IL L;VR	M	S	DNP
BASIC AMINO ACID TRANSPORT							
bas^{a}*;his-3*	no#;K57	3271		II?;IR	E	UV	CWM
BAND							
bd	no#	1858	1859	IVR	SL3	S	MLS
BALD							
bld	NM213t	8252	1658	IVR	M		DDP
BENOMYL RESISTANT							
Bml	111(r)	2964		VIL	SL	UV	HDB
Bml	511(r)	2965	3460	VIL	SL	UV	HDB

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
BISCUIT see *pk*							
BUTTON							
bn	B40	3954		VIIC	SL4	UV	DDP
(bn A + *a*^{ml} *ad-3B cyh-1)*	B40 + 1 2-17-114 KH52(r)	4895		VII+I			DDP
bn	Y5296	4622	4577	VII	M	M	DDP
(bn A + a^{ml} *ad-3B cyh-1*)	Y5296	4446	4578	VII			DDP
BROWN ASCOSPORE							
bs	AR62	1780	1781	IR	SL	UV	DDP
CHROMATIN ASSEMBLY FACTOR							
his-3; *cac-1*^{rip1}			9012	IR,V			MF
CAFFEINE RESISTANT (see *cfs* for Caffeine sensitive)							
caf-1	KH101(r)	993	994	VL	SL	S	KSH
CALCIUM EXCHANGER							
cax-RIP, his-3	cax-10B-13		8629	VIL		RIP	BB
cax	10B-13-2		9360				BB
cax	10B-13-1	9361					BB
cax, nca-2		9363	9362				BB
cax, nca-3	6R	9364					BB
cax	KO	11249	11248		SL	KO	BB
CANAVANINE see *cnr*							
CARBOHYDRATE TRANSPORT							
car	I-20	2745		IVL	M	EMS	RH
CELLOBIOHYDROLASE							
cbh-1	FT3		7826	--	SL	RIP	AR
cbh-1	FT4	7823		--	SL	RIP	AR
cbh-1	FT7		7827	--	SL	RIP	AR
CLOCK CONTROLLED GENE (allelic with *grg-1*)							
his-3;bd;ccg-1	Y234M723;no#; Δccg-1	7487		IR;IVR;V	M	RIP	JCD
bd;ccg-1	no#; Δccg-1		7488	IVR;V	M	RIP	JCD
*ccg-2 (*see *eas*)							
IMPAIRED CHAIN ELONGATION OF FATTY ACIDS							
cel	EB2853(t)	5411	5412	IVR	M	S	EGB
cel	R2366o	6783	819	IVR	M	UV	FGSC/DDP
cel-2	mb-5	8293		IVR	OR	RIP	MT
cel-2	mb-17	8294		IVR	OR	RIP	MT
cel-2	mb-27	8295		IVR	OR	RIP	MT
cel-2	mb-19		8296	IVR	OR	RIP	MT
cel-2	mb-26		8297	IVR	OR	RIP	MT
cel-2	mb-27		8321	IVR	OR		RLM
CELLOBIASE/CELLULASE							
cell-1	T11(2-1)	4335			SL	UV	BME
cell-1	T11(2-3)	4336			SL	UV	BME
CAULIFLOWER *cfl* see *ro-3*							

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
CAFFEINE SENSITIVE							
cfs(OY305)	OY305(s)	3526	3527	I	SL8	UV	OCY
cfs(OY306)	OY306(s)	3528		IR	SL8	UV	OCY
cfs(OY306) al-2	OY306(s) 15300	3529		IR R	SL8	UV	OCY
cfs(OY307)	OY307(s)	3530	3531	I	SL8	UV	OCY
CHEESE							
che	H453G1	646		--			MJM
CHLORAMPHENICOL SENSITIVE see *cpl*							
CHOLINE							
chol-1	34486	2982	485	IVR	M	UV	DDP/RWB
chol-1	Y3261	8131	1116	IVR	M	M	ELT
chol-2	47904(t)	4093	4094	VIL	SL6	UV	EK
chol-2	47904(t)	8261	8262	VIL	M		DDP
chol-3	S2586	4645	4646	VR	SL3	EF	DDP
chol-4	S1089	4647	4648	IVR	SL2	X	DDP
CHROMATE RESISTANT see *cys-13*							
CHRONO							
bd;chr	no#;no#	4908		IVR;V	SL	NG	JFF
CHITIN SYNTHETASE							
chs-2	no #	8319		IV		RIP	OY
chs-4	no #	8244				RIP	OY
CLOCK							
cl	CL11	1166		VR	M	UV	AS
CLOCK AFFECTING GENE							
bd;cla-1	no#;no#		7504	IVR;VIIR	M	S	SB
CALCINEURIN B-1							
cnb-1; qa-2; aro-9; inv; al-2			10009				SF
CYANIDE INSENSITIVE							
cni-1;inl	1;89601	3232		--;VR	M	UV	DLE
CANAVANINE RESISTANT							
cnr^{R}	no#(r)	Use Oak Ridge wild types					
cnr^{S}	no#(s)	19	635	IR	SL3/M	O	DDP/PT
cnr^{S} *al-2*	no#(s) 15300	99	263	IR R	SL2/-	X/-	DDP
cog **see RECOMBINATION AFFECTORS**							
COIL							
coil-1	JI31	3648	3649	IVR	SL5	S	REB
coil-1?	P4120	3650		IVR			REB
COLONIAL							
col-1;pe;al-2	Y8743c;Y8743m;15300	536		IVR;IIR;IR	M	MC→col	ELT
col-1;pe	Y8743c;Y8743m		535	IVR;IIR	M	MC→col	ELT
col-1	Y8743c	8135	7020	IVR	M	MC	FGSC
col-2	Y5331	4560	4561	VII	SL4	MC	DDP
(*col-2* + a^{ml} *ad-3B cyh-1*)	Y5531 + 1 2-17-114 KH52(r)	4562	4563	VII+I			DDP

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
COLONIAL, continued from previous page							
col-3 (allelic *bn*)							
col-4	70007c	1177	1178	IVR	SL3	UV	DDP
col-4	B148	943	1442	IVR	SL	UV	DDP
col-4	D316	1615		IVR	M	UV	DDP
col-4	NM164	1307		IVR	M	UV	DDP
col-4	P4874	7403		IVR	SL3	S	DDP
col-5 (=*col-1*?)	B28	1656	1378	IVR	SL3/SL	UV	DDP/ELT
col-6 (see part VI)	S1302		1400	IVC	L	X→pe	ELT
col-7 (allelic *rg-1*)							
col-8	R2356	8128	1401	IVR	M	UV	ELT
col-9 inl	R2417 89601	8211	1385	VR R	M	UV	FGSC/ELT
col-10 (=pi?)							
col-12	R2440	1376	8210	I	M	UV	ELT/FGSC
col-13 (allelic *vel*)							
col-14 (allelic *sc*)							
col-15	R2531	3847	3848	IIIR	SL2	S	DDP
col-16	R2539	3461	3462	IIIR	M	UV	DDP
col-17	B5	1373	8133	VII	SL	UV	ELT
col-18	P4494	8283	8284	VIR	M		DDP
(col-18 A + *a^{m1} ad-3B cyh-1)*	P4494	8280	8279	VIR	M		DDP
col(B235r)	B235r	1652		IIIR	M	UV	DDP
col(D5)	D5		1633	IR	M	UV	DDP
col(D302)	D302		1653	IIIC	M	UV	DDP
col(P2615)	P2615	1643		I	M	S	DDP
COMPACT							
com	B54	106	179	IIIR	SL3	UV	DDP
CONIDIATION							
con-6	6RIP		9508	II			DJE
con-10 con-13	10RIP 13RIP		9507	IVR IVR			DJE
con-11	11RIP		9512	VIR			DJE
COBALT AND NICKEL RESISTANT							
cor	Co^R	7289	7290	IIIR	SL	S	PMM
COLONIAL TEMPERATURE SENSITIVE							
cot-1	C102(t)	4065	4066	IVR	SL6	UV	EK
($cot\text{-}1^{ir}$ *+ *a^{M1} ad-3B cyh*-1)	P4121+ helper	7658	7659	IVR	SL2	Spont	DDP
cot-2	R1006(t)	1513	2263	VR	SL2/M	UV	DDP
cot-3	R2006(t)	1517	1516	IVR	SL2	UV	DDP
cot-4	R2101(t)	3600	3601	VR	SL2	UV	DDP
cot-5	R2479(t)	3560	3561	IIL	M	UV	DDP
* ir = irreparable							
CROSS-PATHWAY CONTROL							
cpc-1	CD-15	4264		VIL	SL2	UV	RHD
cpc-1;$arg\text{-}12^S$	CD-15;37301s	4262	4263	VIL;IIR	SL	S	RHD
cpc-1	j-2	4431	4432	VIL	SL	UV	IB
T(VI→I)IBj-5 cpc-1	j-5	4433	4434	VIL	SL	UV	IB
cpc-1	j-9	4435	4436	VIL	SL	UV	IB
cpc-1	MN1	4379	4380	VI	SL2	UV	DDP
T(IV;VI)MN9 cpc-1	MN9	6700	6699	VIL	SL2		IB
cpc-2	U142	6918	6919	VII	SL	UV	IB
cpc-3::hph; cyh-2	no #; KH53*(r)*	8405	8406	V	SL7	D	ES
cpc-1 cpc-2		9004					MS

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
CROSS-PATHWAY CONTROL, continued from previous page							
cpc-2			9005				MS
cpc-2 cyh-2			9006				MS
cpc-2 cpc-3 cyh-2		9007					MS
cpc-3 cyh-2		9008					MS
cpc-2 cyh-2			9009				MS
cpc-1 cpc-3 cyh-2			9010				MS
△cpc-1		9011					MS
CYCLIC PHOSPHODIESTERASE							
cpd-1		8969	8970				DDP
cpd-2			8971				DDP
cpd-1	KH1190		9573				KH
cpd-1	KH119		9570				KH
cpd-1	KH166		9572				KH
cpd-1	KH166	9571					KH
cpd-2			8971				DDP
cpd-2	KH214		9574				KH
cpd-2	KH253		9577				KH
cpd-2	KH247	9576*					KH
cpd-2	KH231	9575*					KH
cpd-3 pho-2	KH345		9579				KH
cpd-3 pho-2	KH302		9578				KH
cpd-3 pho-2	KH359		9580				KH
cpd-4	KH417		9585				KH
cpd-4	KH45		9584				KH
cpd-4	KH424		9586				KH
cpd-4	KH44		9583				KH
cpd-4	KH42		9582				KH
cpd-4	KH413		9581				KH
*mating type ambiguous							
CYCLIC AMP-DEPENDENT PROTEIN KINASE							
cpk	no#	5138	5139	IIIR	SL	S	TM
CHLORAMPHENICOL SENSITIVE							
cpl-1	ANTAS6(s)	3739	2459	VIL	SL4/SL3	UV	DDP/JHC
CARPET							
cpt	P564	292	104	IIR	M	S	DDP
CRISP							
cr-1	B74	826	4345	IR	M	UV	DDP/ELT
cr-1	B122	804		IR	SL	UV	DDP
cr-1	B123	4008	4009	IR	SL9	UV	EK
cr-1	C-Ex-11-67		814	IR	M	P	DDP
cr-1	L	20		IR	SL3	S	DDP
cr-1	L151		5068	IR	SL		DDP
cr-1	R2360	4344	806	IR	M	UV	ELT/DDP
cr-2	AR5	1632		IR	M	UV	DDP
cr-2	R2445	3515	3516	IR	SL	UV	DDP
cr-3	R2509	3449	2329	IR	SL2/M	DDP	
cr-4	RLP558	5858	5859	IV	SL		DDP
cr(RLP805)	RLP805	6652	6653	IR	SL2		FGSC
cr(RLP808)	RLP808	5971		IR	SL2		FGSC
cr(RLP815)	RLP815	6701	6702	IR	SL2		FGSC
cr(RLP816)	RLP816	6669	6670	IR	SL2		FGSC
cr(RLP914)	RLP914	6671	6672	IR	SL2		FGSC

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
CRISP, , continued from previous page							
cr(RLP957)	RLP957	6141		IR	SL2		FGSC
cr?	B180	825		IR	M	UV	DDP
CYTOPLASMIC RIBOSOME BIOSYNTHESIS							
crib-1	PJ30201(t)	3300		IVR	M	NG	PJR
crib(PJ31562)	PJ31562	4283		IVR	M	NG	PJR
CUSHION							
csh	STL8	4518	4519	IR	SL2	S	DDP
(csh a +	STL8 +						
a^{m1} ad-3B cyh-1)	1 2-17-114 KH52(r)		4575	IR+IL R R			DDP
CONIDIAL SEPARATION							
csp-1	UCLA37	2554		IL	SL4	EMS	CPS
csp-2	FS590	2521	2522	VII	SL4	UV	CPS
csp-2	FS591	2523	2524	VII	SL4	UV	CPS
csp-2	UCLA101	4085	4086	VII	SL6	S	EK
csp-2;nic-2	UCLA102;43002	3871		VII;IR	SL4	S	CPS
csp-2 nic-3	UCLA102 Y31881	3872		VII L	SL4	S	CPS
CYCLOSPORIN RESISTANCE							
csr-1	B12	6920	6921	IR	SL	UV	IB
csr-1	B32	6922	6923	IR	SL	UV	IB
csr-1	B60	6924	6925	IR	SL	S	IB
CUMULUS							
cum	P5241	3877	3878	IIIL			DDP
CUT							
cut	LLM1	2385	2386	IVL	M	S	DDP
T(I;IV)HK53 cut	HK53	2272	2068	IC;IVL			DAS/DDP
CROSSWALL							
(*cwl-1 +*	R2441 +						
a^{ml} ad-3B cyh-1)	1 2-17-114 KH52(r)	5951		IIR			DDP
(*cwl-2 +*	P1998 +						
a^{ml} ad-3B cyh-1)	1 2-17-114 KH52(r)	6875	6876	IIR	SL2		DDP
CURLY							
cy	C170c	3859	3860	IL	M		DDP
CYTOCHROME a							
cya-3;nic-1 al-2	cya-3-16;3416 15300		7594	VIL;IR R	SL	NG	FEN
cya-5	cya-5-34		7596	IVR?	SL	NG	FEN
cya-8	P9178	4522	4523	VIIL	S		DDP
(cya-8 +	P9178 +						
a^{ml} ad-3B cyh-1)	1 2-17-114 KH52(r)	4524	4525	VIIL+IL R R		DDP	
cya-9	299-1(t)		3551	IVR			THP
CYTOCHROME b							
cyb-1;nic-1 al-2;pan-2	*cyb-1-1*;3416 15300;B3		7593	VR;IR R;VIR	SL	NG	FEN
cyb-3	A10-301-8(t)	3651	3652	IIL	SL	UV	DDP
CYTOCHROME c							
cyc-1 (= *cyt-12*)	12	4505	4506	IIR	SL	UV	DDP
cyc-1	RK3-21		3558	IIR;VIL	SL	UV	THP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
CYCLOHEXIMIDE RESISTANT							
cyh-1	54(r)	2576		IR	SL	UV	WK
cyh-1	1003(r)	1056		IR	SL	UV	HBH
cyh-1	KH52(r)	4012	4013	IR	SL8	S	EK
cyh-2	KH53(r)	4071	4072	VR	SL7	S	EK
CYSTEINE						363	
cys-1 ylo-1	84605 Y30539y	1092	2086	VIL L	M	X	NEM/DDP
cys-1	84605		323	VIL	M	X	NHH
cys-2	38401	2109	2110	VIL	M	UV	DGC
cys-2	80702	125		VIL	M	N	DDP
cys-2 ylo-1	80702 Y30539y		489	VIL L	M	N	BDM
cys-3;inl	29T(t);89601		3761	IIL;VR	M	UV	DRS
cys-3	NM27(t)	2292	1272	IIL	M/E	UV	DDP/NEM
cys-3	P22	1089	1090	IIL	E	UV	NEM
cys-3	P22	4028	4029	IIL	SL7	UV	EK
cys-3	REV 65 ts	9547		II			GAM
cys-4	K7	4067	4068	IVR	SL6	UV	EK
cys-4	NM252(t)		1273	IVR	M	UV	NEM
cys-4	P1		193	IVR	M	UV	NEM
cys-5	35001	977		IL	M	UV	NEM
cys-5	NM44		1274	IL	E	UV	NEM
cys-9	T156	1094	2160	IR	E2/M		NEM/DDP
cys-10	39816	4053	4054	IVL	SL6	UV	EK
cys-11	85518	887	2373	IL	M/SL5	M	NNH/RLM
cys-11	NM86		1276	IL	M	UV	NEM
cys-12	NM268(t)	1275	2383	IR	E/M	UV	NEM/DDP
cys-13	w4	2075	2076	IR	SL	UV	GAM
cys-13;cys-14	p1;p2		1839	IR;IV	SL	UV	GAM
cys-14	p2		2077	IV	O		GAM
cys-15 (oxD)	1	1872	888	IVR	M	UV	NHH/DDP
cys(71310)	71310	1091	972	VI	M	UV	NEM
CYTOCHROME							
cyt-1	C115	4292	3488	IL	SL2	S	DDP
cyt-1 al-2	C115 15300	7938	7939	IL IR	M		HB
cyt-2	C117	339	1981	VIL			MBM
cyt-2 pan-2	cyt-2-1 Y153M66		7364	VIL VIR			FEN
cyt-4	7	3919	3920	IR	SL		DDP
CYTOCHROME, continued from previous page							
cyt-7	20	7578	7579	VIIL	SL	UV	DDP
cyt-9	17		3925	V	M		DDP
cyt-12 see *cyc-1*							
cyt-18 al-2	299-9 no#		5062	IR R	SL	UV	AL
cyt-19;pan-2	1701;B3		5063	IVR;VIR	SL	NG?	AL
cyt-20(289-56)	1	4278	3541	IL	SL		AL/THP
cyt-21	297-24(t)		4279	--			AL
cyt-22	289-4(t)		3539	IIIL	SL2	UV	THP
D-AMINO ACID OXIDASE DEFICIENT see *oxD*							
het-d, het-D see Part VII							
DAPPLE							
da	R2375	1077	1078	IIL	M	UV	DDP
da (formerly *ro-9*)	R2526	2167	2168	IIL	SL2	S	DDP

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back- ground	Muta- gen	Obtained from
DEFECTIVE IN METHYLATION-2							
dim-2, arg-10	HMF1, B3A	8593	8592	VIIR,VIIR	OR		EUS
his-3; dim-2::hph	1-234-723; EK1		8594	IR, VIIR	M		EUS
DELICATE							
del	B137	7425	2069	VIR	SL2	UV	DDP
DEOXYGLUCOSE RESISTANT							
dgr-1	BE52	4326	4325	VL	SL	UV	BME
dgr-1	BEX5		4332	VL	SL	UV	BME
dgr-1	BEX5		4331	VL	SL	UV	BME
dgr-1	KHY15		8285	VL			SF
dgr-2	L1	4327	4328	IL	SL	UV	BME
dgr-3 (allelic *sor-4*)							
dgr-4	KHY7		8287	IR			SF
DIPLOID ASCOSPORES							
Dip-1		9537	9536	IIIR			RLM
DINGY							
dn	38502d	64	3308	IVR	SL3	UV	DDP
DOILY							
do	DS5-51	2261	2262	VIIL	SL2	UV	DDP
DOT							
dot	P789	1211	1218	IR	SL3	S	DNP
DOWNY							
dow	D308	1654		IIIR	M	UV	DDP
dow	P616	4051	4052	IIIR	SL8	S	EK
dow	P3053d	8263	8264	IIIR	M		DDP
DRIFT							
dr	P1163	1673	3869	VIIR	M	S	DDP
het-e, het-E see part VII							
EASILY WETTABLE (allelic with *ccg-2*)							
eas;bd	ccg-2;no#	7489		IIR;IVR	M	RIP	JCD
eas	JD105	7582	7583	IIR	SL2	RIP	DDP
T(IL;IIR)KH5-9 eas	KH5-9	7143	7144	IIR	M		DDP
See also section K,part VII (special teaching strains) and, for UCLA191 strains, part V.C.							
EDEINE RESISTANT							
edr-1	18(r)	2578		VI	SL	NG	WK
edr-2	29(r)	2579	2580	VI	SL	NG	WK
ENHANCER OF *am*							
en(am)-1	no#	3961	3962	VR	SL2		JRF
en(am)-1	no#		3963	VR	SL2		JRF
en(am)-2	ABT367-24		3930	IIR	M	UV	RHG
en(am)-2;am	C24;32213	1624		IIR;VR	M	UV	MS
en(am)-2 pe;am	C24 Y8743m;32213		1625	IIR R;VR	M	UV	MS
ENHANCER OF *pdx* PIGMENT							
En(pdx) al(G2)	K30 G2		649	IL R			MJM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ERGOSTEROL DEFICIENT							
erg-1	UV1		2721	VR	SL	UV	MG
erg-1;pan-2	UV1;Y153M66	2722		VR;VIR	M	UV	MG
erg-2	NAN25		2723	VR	SL	NA	MG
erg-2;pan-2	NAN25;Y153M66	2724		VR;VIR	M	NA	MG
erg-3	UV41	3439	2725	IIIR	M	UV	DDP/MG
erg-4	UVC53(t)	3653	3654	IR	SL	NA	DDP
erg(RES208) al-3	RES208(r) RP100		3155	VR R	SL	UV	RES
ENHANCER OF SPERMIDINE REQUIREMENT							
esr-1;aga	BMH566;UM906	7923		VR;VIIR		UV	RHD
esr-2;aga	BMH422;UM906	7922		I;VIIR		UV	RHD
esr-3;aga	BMH36;UM906	7921		--;VIIR		UV	RHD
esr(BMH8);aga	BMH8;UM906	7920		I;VIIR		UV	RHD
ETHIONINE RESISTANT							
eth-1	no#(r)(t)	1212	1220	IL	SL3	UV	DNP
EXOAMYLASE							
exo-1	SF26		2256	I	SL		HGG
EXTRANUCLEAR [*exn*] see Part IV							
FAST-MODIFIER OF [*poky*]							
f see *su([mi-1])-f*							
FLUORODEOXYURIDINE RESISTANT							
fdu-2; *his-2 ad-3A ad-3B* *nic-2;ad-2;inl*	GH14-6(r); C94 Y112M13 35203 43002;Y175M256;JH319	2542		IVR; IR R R R;IIR;VR	M	S	GRH
FEMALE FERTILITY							
ff-1 (glp-3)	JC744	3831	3832	IIR	SL5	S	DDP
ff-1 fl	JC744 P	7545	7546	IIR R	SL		SC
ff-1 (glp-3)	T30		2318	IIR	M	S	HCC
ff-1;his-3;hlp-1	T30;K458;B538	2320		IIR;IR;VIIR	M	UV	HCC
ff-3;ty-3(T22)	no#;135-333(T22)	2962		IR;IIIR	M	UV	JFF
ff(AB-I4);ad-2	STL2;AB-I4	3094		--;IIIR	M	UV	TEJ
ff(AB-J7);ad-2	STL2;AB-J7	3095		--;IIIR	M	UV	TEJ
ff(AB-K1);ad-2	STL2;AB-K	3096		--;IIIR	M	UV	TEJ
ff(AB-P5);ad-2	STL2;AB-P5	3097		--;IIIR	M	UV	TEJ
ff(AB-P6);ad-2	STL2;AB-P6	3098		--;IIIR	M	UV	TEJ
ff(AB-P11);ad-	AB-P11;STL2	3099		--;IIIR	M	UV	TEJ
ff(AB-R3);ad-2	STL2;AB-R3	3100		--;IIIR	M	UV	TEJ
ff(AB-R7);ad-2	STL2;AB-R7	3101		--;IIIR	M	UV	TEJ
ff(AB-R8);ad-2	STL2;AB-R8	3102		--;IIIR	M	UV	TEJ
ff(AB-T1);ad-2	STL2;AB-T1	3103		--;IIIR	M	UV	TEJ
ff(AB-T5);ad-2	STL2;AB-T5	3104		--;IIIR	M	UV	TEJ
ff(AB-T9);ad-2	STL2;AB-T9	3105		--;IIIR	M	UV	TEJ
ff(AB-T10);ad-2	AB-T10;STL2	3106		--;IIIR	M	UV	TEJ
ff(PB-I8);pyr-3	PB-I8;KS43	3074		--;IVR	SL	UV	TEJ
ff(PB-J3);pyr-3	PB-J3;KS43	3075		--;IVR	SL	UV	TEJ
ff(PB-J4);pyr-3	PB-J4;KS43	3076		--;IVR	SL	UV	TEJ
ff(PB-M4);pyr-3	PB-M4;KS43	3077		--;IVR	SL	UV	TEJ
ff(PB-M7);pyr-3	PB-M7;KS43	3078		--;IVR	SL	UV	TEJ
ff(PB-M8);pyr-3	PB-M8;KS43	3079		--;IVR	SL	UV	TEJ
ff(PB-N1);pyr-3	PB-N1;KS43	3080		--;IVR	SL	UV	TEJ
ff(PB-N4);pyr-3	PB-N4;KS43	3081		--;IVR	SL	UV	TEJ

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
FEMALE FERTILITY, continued from previous page							
ff(PB-R3);pyr-3	PB-R3;KS43	3082		--;IVR	SL	UV	TEJ
ff(PB-S1);pyr-3	PB-S1;KS43	3083		--;IVR	SL	UV	TEJ
ff(PB-S4);pyr-3	PB-S4;KS43	3084		--;IVR	SL	UV	TEJ
ff(PB-S7);pyr-3	PB-S7;KS43	3085		--;IVR	SL	UV	TEJ
ff(PB-S8);pyr-3	PB-S8;KS43	3086		--;IVR	SL	UV	TEJ
ff(PB-S9);pyr-3	PB-S9;KS43	3087		--;IVR	SL	UV	TEJ
ff(PB-T1);pyr-3	PB-T1;KS43	3088		--;IVR	SL	UV	TEJ
ff(PB-T2);pyr-3	PB-T2;KS43	3089		--;IVR	SL	UV	TEJ
ff(PB-T3);pyr-3	PB-T3;KS43	3090		--;IVR	SL	UV	TEJ
FISSURE							
fi	M155-2	1303	1304	IVL	M	S	DDP
FLAME see *os-1*, *os-4*							
FLUFFY							
fl	blo	4960	4961	IIR	SL	S	HGK
fl	C-1835		818	IIR	O	S?	DDP
fl	L	7430	7431	IIR	M	S	DDP
fl	M155-5		807	IIR	M	S	DDP
fl	P4499		2033	IIR	M	S	DDP
fl	P961	1616		IIR	M	S	DDP
fl(OR)	P	4317	4347	IIR	SL5	S	DDP
fl(RL);scot	P	6682	6683	IIR	RL4	S	DDP
fl(WE)	P	6962	6963	IIR	M		DDP
fl^{Y}	Y234M474	4240	4241	II	SL	UV	DDP
fl::cpc-1P		9515		II			DJE
fl	RIP	9504		II		RIP	DJE
fl+RGSH6		9505		II			DJE
fl+RGSH6		9514		ectopic			DJE
fl	KO		11044	II	SL		GP
FLUFFYOID							
fld	P628	7022	7023	IVR	M	S	FGSC
FLUFFYISH							
fls	STL6	255		IR	M	UV	DDP
fls al-1	STL6 34508		60	IR R	M	UV	DDP
FEMALE AND MALE FERTILITY							
fmf-1;pyr-3	PB-J6;KS43	3108		IL;IVR	SL	UV	TEJ
fmf-1;tol pan-1	PB-J6;N83 5531	3109	3110	IL;IVR R	M	UV	TEJ
FEMALE STERILE see *fs*							
FORMATE							
for	C24	9	3850	VIIR	M	UV	DDP
for		8611		VIIR			DDP
FOUR-SPORED ASCUS see *Fsp*							
p-FLUOROPHENYLALANINE RESISTANT							
fpr-1	R2-69(r)	8134	1696	VR	M	S	JAK
fpr-3	no#	3875	3876	IIIR	SL3	UV	DDP
fpr-4;su(mtr)	no#;17-2	3000		VR;IC	M	UV	JAK
fpr-5;pan-1;al-2	no#(r);5531;15300	3001	3002	IR;IVR;IR	M	UV	JAK
fpr-6	UM-300	4275	4276	VIR	SL	S	RHD

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
FROST							
fr	B110	103	102	IL	M	UV	DDP
.fr;acr-2	P4445,KH5	8107	8108	IL;III	M		DDP
(*fr nit-2 A +* *a*^{m1} *ad-3B cyh-1*)	B110, nr7	7868		IL, L ILRR			DDP
FREQUENCY							
frq^{1}*;bd*	1; no#	2670	2671	VIIR;IVR	M	NG	JFF
frq^{2}*;bd*	2;no#	2672	2673	VIIR;IVR	M	NG	JFF
frq^{3}*;bd*	3;no#	2674	2675	VIIR;IVR	M	NG	JFF
frq^{4}*;bd*	4;no#	2958	2959	VIIR;IVR	M	NG	JFF
frq^{5} see *prd*-1							
frq^{6}*;bd*	6;no#	4897		VIIR;IVR	SL	NG	JFF
frq^{7}*;bd*	7;no#	4898	4899	VIIR;IVR	SL	NG	JFF
frq^{8}*;bd*	8;no#	4900	4901	VIIR;IVR	SL	NG	JFF
frq^{9}*;bd*	9;no#	7779	7780	VIIR;IVR	SL	UV	JJL
frq^{10}*;bd*	10;no#	7490		VIIR;IVR		D/D	JCD
frq	KO		11554	VII	SL	KO	GP
FEMALE STERILE							
fs-1;nic-3	19-2;Y31881	3235	3236	I or II;VIIL	M	S	OMM
fs-2;pan-2	10-4(t);Y153M96		3237	II?;VIR	M	S	OMM
fs-2;pan-2;nic-3	10-4(t);Y153M96;Y31881	3238		II(?);VIR;VIIL	M	S	OMM
fs-3;nic-3	52-2;Y31881	3239		IL;VIIL	M	S	OMM
fs-3;pan-2	52-2;Y1531796	3240		IL;VIR	M	S	OMM
fs-4;nic-3	2326;Y31881		3241	I;VIIL	M	S	OMM
fs-4;pan-2	2326;Y153M96	3242		I;VIR	M	S	OMM
fs-5;nic-3	5-5;Y31881		3243	I or II;VIIL	M	S	OMM
fs-6;pan-2	2351;Y153M96	3244		I or II;VIR	M	S	OMM
fs-n	44-1		3245	I	M	S	OMM
fs-n	44-3	3246		I	M	S	OMM
fs-n	44-4		3247	I	M	S	OMM
fs-n	44-8	3248		I	M	S	OMM
FOUR-SPORED ASCUS							
Fsp-1	ALS141	2991	2992	IIR	M	UV	DDP
Fsp-2	DL709	4534	4535	IR	SL3	NG	NBR
Fsp-1;Fsp-2	ALS141;DL709	5069	5070	IIR;IR	SL		NBR
GIANT SPORE see *gsp*							
GINGER (from *N. sitophila*: possible *os-1* allele)							
gin	637/3.4		647	I		S	MJM
GLUCOAMYLASE [also see *sor(T9)*]							
gla-1	N15-3		7824	--	SL	RIP	AR
gla-1	N17-2		7825	--	SL	RIP	AR
GLUCOSEPHOSPHATE ISOMERASE DEFECTIVE see *gpi*							
GOLDEN							
gld	70007g	557			M	S?	ELT
GLUTAMINE							
gln-l	R1015		1449	VR	M		ER
gln-1 inl	R1015;89601	1450		VR R	M	M	ER
gln-1b	no#	4536		VR	SL	NG	RHG

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
GLUTAMINE REGULATION							
gln^r	no#		4615			NG	RMD
GLYCEROL NON-UTILIZER							
glp-1 wc-2	234 234(w)	2742	2743	IR R	M	UV	HGK
glp-2;ylo-1	JC17;Y30539y	2968*		IIR;VIL	M	UV	JBC
glp-2;inl	JC1444;83201(t)	2969*		IIR;VR	M	UV	JBC
glp-3 see *ff-1*							
ad-1 glp-4	3254 G660		7216	VIL C	M	NG	DDP
* Heterokaryon compatibility type C d e							
OLIGOPEPTIDE TRANSPORT DEFECTIVE							
glt;tys(LW101)	D240(r);LW101(s)	2736		--;IL	M	UV→2735	GAM
glt;leu-2	D240(R);37501		2737	--;IVR	M	UV	GAM
β-GLUCOSIDASE DEFECTIVE							
gluc-1;cot-1	CM26(3-8);C102(t)		1224	--;IVR	M	UV	BME
gluc-2	CM62	1227		--	M	UV	BME
GLYCINE RESISTANT							
am;gly^r	am$_{132}$;gly^r		6717	VR;--	SL	UV	JM
GLUCOSEPHOSPHATE ISOMERASE DEFECTIVE							
gpi;sor(T9)	T21M3;T9M150(r)	3431		IV;IL	M	UV	TI
gpi;pp	T66M37g;T66M37p	3432		IV;--	M	NG	TI
GLYCOHYDROLASE DEFECTIVE see *nada*							
GRANULAR							
gran	B42	794	793	VR	SL	UV	DDP
GREY							
grey;cr-1;cot-1	KH165;L;C102(t)	2327		IVR;IR;IVR	M	G	KSH
grey;cr-1;cot-1;ylo-1	KH165;L;C102(t);Y30539y	2328		IVR;IR;	M	G	KSH
GIANT SPORE							
gsp	26-125	3425	3426	IL	SL	NNG	AMS
GUANINE							
gua-1	OY301	3524	3525	IL	SL	UV→3448	OCY
gua-2	UW0525		3830	VR	M	EMS→3448	WLG
GULLIVER (modifier of *cot-1*)							
gul-1;cot-1	CA1;C102(t)	1962	1963	VR;IVR	E2		DS
gul-1	G		803	VR	SL2		DDP
gul-1;cot-1	G;C102(t)	817		VR;IVR	M		DDP
gul-2;pe fl;cot-1;inl	264;Y8743m L;C102(t);37401		1173	--;IIR R IVR;VR		UV	HFT
gul-3;pe fl;pt cot-1	845;Y8743m L;NS1(t) C102(t)		1174	IV;IIR R; IVR R		UV	HFT
gul-4;pe fl;cot-1;inl	42;Y8743m L;C102(t);37401	1605		VII;IIR R;IVR;VR		UV	JLR
gul-5;cot-1	BAT26-2;C102(t)		2956	VI;IVR		UV	JLR
gul-6;cot-1	BAT-26-21;C102(t)		3559	--;IVR			JLR
HAIRY							
hair	8615		648			X	MJM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
HYPHAL ANASTAMOSIS							
ham-2		9059		VR			NLG
ham-2			9060	VR			NLG
pyr-4; ham-2		9061		IIL;VR		RIP	NLG
ham-2	KO	12091		V	SL	KO	GP
HETEROKARYON COMPATIBILITY ***het*** see Part VI							
HEXAGONAL							
hex-1	KT73		8612	IL		RIP	BB
HISTIDYLGLYCINE UPTAKE							
hgu	4		2734	V	SL	UV	GAM
HISTONE							
hH1; his-3		9017	9016				AR
his-3$^+$*::Pccg-1-hH1+ -sgfp*$^+$		9518					MHF
(*matA his-3+:: Pccg-1-sgfp+ + mat A his-3*)		9516					MHF
hH1	KO	12224			SL	KO	GP
HISTIDINE							
his-1	C84	3435	3436	VR	M	UV	DDP
his-1	C85	403		VR	M	UV	MBM
his-1	C91	401	402	VR	M	UV	MBM
his-1	K85		729	VR	E	UV	DGC
his-1	K90		728	VR	E	UV	DGC
his-1	K93		703	VR	E	UV	DGC
his-1	K141		704	VR	E	UV	DGC
his-1	K624		727	VR	E	UV	DGC
his-1	K626		730	VR	E	UV	DGC
his-1	K744		919	VR	E	UV	DGC
his-1	K745		705	VR	E	UV	DGC
his-1	Y155M302	681		VR	SL	X	MEC
his-1	Y175M650		680	VR	SL	X	MEC
his-2	C94	950		IR	SL2	UV	DDP
his-2	FS1150(t)	3741	3742	IR	SL5	UV	SW
his-2	K74		706	IR	E	UV	DGC
his-2	K80		707	IR	E	UV	DGC
his-2	K153		708	IR	E	UV	DGC
his-2	K154		731	IR	E	UV	DGC
his-2	K246		709	IR	E	UV	DGC
his-2	K267		710	IR	E	UV	DGC
his-2	K545		711	IR	E	UV	DGC
his-2	K567		738	IR	E	UV	DGC
his-2	K571		732	IR	E	UV	DGC
his-2	K595		713	IR	E	UV	DGC
his-2	K605		733	IR	E	UV	DGC
his-2	K614		714	IR	E	UV	DGC
his-2	T51M152(t)	4624	4625	IR	SL	X	DDP
his-2	Y152M14	22	21	IR	SL	X	DDP
his-2	Y152M43	668		IR	SL	X	MEC
his-2;mtr col-4	Y152M43;10(r) 70007c		1720	IR;IVR R			DRS
his-2	Y175M611		667	IR	SL	X	MEC
his-2;neu^r	no#;HS-24	3273		IR;IVR?	E	UV	CEM
his-3	C140	2278	2277	IR	M	UV	FGSC
his-3;pt	C1710;S4342		206	IR;VR			DDP
his-3	K26 see *rec*						
his-3	K57		1682	IR	E	UV	DGC

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic background	Mutagen	Obtained from
HISTIDINE, continued from previous page							
his-3	K70		1154	IR	E	UV	DGC
his-3	K232		734	IR	E	UV	DGC
his-3	K433		720	IR	E	UV	DGC
his-3	K446		719	IR	E	UV	DGC
his-3	K458		1157	IR	E	UV	DGC
his-3	K469		718	IR	E	UV	DGC
his-3	K477		1155	IR	E	UV	DGC
his-3	K480		717	IR	E	UV	DGC
his-3	K504 see *rec*						
his-3	K727		716	IR	E	UV	DGC
his-3	K874 see *rec*						
his-3	K959		1153	IR	E	UV	DGC
his-3	K1164		1158	IR	E	UV	DGC
his-3	K1314		1156	IR	E	UV	DGC
his-3	TM42		4438	IR	SL		DDP
his-3	TM429 see *rec*						
T(I;V9 his-3	TM429	2530	2531	IR;VIIC			DDP
his-3	Y152M111	455		IR	SL	X	MEC
his-3	Y155M261	462	7088	IR	SL	X	MEC/FGSC
his-3	Y175M614	4495	4496	IR	SL	S	DDP
his-3 nic-2	Y269M5 43002	1855		IR R	M	EMS	MEC
SEE PART VI FOR A FULL LIST OF YALE *his-3* ALLELES							
his-4	C141	2161	2162	IVR	M	UV	DDP
his-4	P143h(t)	989		IVR	M	UV	NEM
his-5	K50		721	IVR	E	UV	DGC
his-5	K52		722	IVR	E	UV	DGC
his-5	K71		776	IVR	E	UV	DGC
his-5	K265		723	IVR	E	UV	DGC
his-5	K512		735	IVR	E	UV	DGC
his-5	K513		736	IVR	E	UV	DGC
his-5	K516		724	IVR	E	UV	DGC
his-5	K529		725	IVR	E	UV	DGC
his-5	K746		737	IVR	E	UV	DGC
his-5	Y152M108	456	8191	IVR	SL	X	MEC
his-5	K52	8208		IVR	M		FGSC
his-5	K71	8209		IVR	M		FGSC
his-6	K34	4342	775	VR	?/E	UV	ELT/DGC
his-6	Y152M105	4078	4079	VR	SL8	X	EK
his-6	Y175M616		459	VR	SL	X	MEC
his-7	K577		726	IIIR	E	UV	DGC
his-7	Y152M31	7499	7500	IIIR	SL	X	DDP
HISTIDINOL PERMEABILITY							
hlp-1;ff-1;his-3	BS38;no#;K458	2320		VIIR;IIR;IR	M	UV	HCC
hlp-2;his-3	HC114;K458		2319	VIIR;IR	M	UV	HCC
HOMOSERINE							
hom	35709	946	8194	IR	M	UV	DDP
hom	51504	3234	282	IR	M/SL2	UV	GWC/DDP
HISTIDINE SENSITIVE							
hss-1	MN332	5785	5786	IVR	M	S	DDP

i* see ENHANCER OF *am *[en(am)-1]*

IMPAIRED CHAIN ELONGATION OF FATTY ACIDS see *cel*

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
INDOLE see *trp-1, -2, -4*							
INDURATED ASCUS							
Iasc	29-405		3424	VR	SL	S	AMS
ISOLEUCINE							
ile-1	46003	123	124	VII	M	UV	DDP
ile-1	N596	2766	2767	VII		S	DDP
ile-1	OY338	3750	3751	VII	M	UV	DDP
ile-1	UK71-26	5885		VII	M	S	JAK
ISOLEUCINE + VALINE							
ilv-1	16117	3955	3956	VR	SL3	X	DDP
ilv-1	T304		1038	VR	E	UV	RPW
ilv-1	T311		1039	VR	E	UV	RPW
ilv-1	T318		1041	VR	E	UV	RPW
ilv-1	T321		1043	VR	E	UV	RPW
ilv-1	T323		1044	VR	E	UV	RPW
ilv-1	T326		1046	VR	M	UV	RPW
ilv-1	T327		1047	VR	M	UV	RPW
ilv-1	T328		1048	VR	M	UV	RPW
ilv-1	T329		1049	VR	M	UV	RPW
ilv-1	T330		1050	VR	M	UV	RPW
ilv-1	T331		1051	VR	M	UV	RPW
ilv-1	T332		1052	VR	M	UV	RPW
ilv-2	39709		1144	VR	L	UV	MEC
ilv-2	46807	501		VR	M	X	RWB
ilv-2	T313(t)		1040	VR	E	UV	RPW
ilv-2	T319	3744	3745	VR	E	UV	DDP
ilv-2	T320		1042	VR	E	UV	RPW
ilv-2	T322		1063	VR	E	UV	RPW
ilv-2	T324		1064	VR	E	UV	RPW
ilv-2	T325		1045	VR	E	UV	RPW
ilv-2	Y3786	574		VR	L	M	ELT
ilv-3;lys-1	T344;33933	1053		IVR;VL	M	UV	RPW
ilv-3;lys-1	T346;33933	1054		IVR;VL	M	UV	RPW
ilv-3;lys-1	T364;33933	1055		IVR;VL	M	UV	RPW
ilv-3	Y7110	575	1164	IVR	L/M	M	ELT/DDP
ilv(47711)	47711	395		VR	M	UV	MBM
ilv(71103)	71103	816	815	VR	M	UV	DDP
ilv(?6201)	(?6201)	169	69	VR	M	UV	DDP
ilv(STL3)	STL3	2431	2437	VR	M	S	DDP
INOSITOL							
inl	31719		4269	VR	L	X	ELT
inl	37102	669	2144	VR	M	UV	MEC/FGSC
inl	37401	4074	4075	VR	SL6	UV	EK
inl	46316		2321	VR	L	UV	ELT
T(V;VI)46802 inl	46802	670	1199	VR;VIL	L	UV	MEC/DDP
inl	64001	658	2146	VR	M	UV	MJM/FGSC
inl	83201(t)	2257	2258	VR	SL5	M	DDP
inl	89601	497	498	VR	M	M	RWB
inl	JH319	925	926	VR	M	UV+M	FJD
inl	JH2626	871	4360	VR	O?	M	ELT
inl	JH5652		671	VR	M	M	MEC
inl	P1882	1302		VR	M	S	DDP
inl	P4723	2066		VR			DDP
inl acu-1	R233 JI48	1731		VR R			RBF

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
INTENSE							
int	ALS8	1528	2462	IVR	SL	UV	DDP
INVERTASE DEFICIENT							
inv	no#	1856	1857	VR	SL	S	MLS
ISOLEUCINE see *ile*							
ISOLEUCINE + VALINE see *ilv*							
IT POKES ALONG							
ipa	BVS7	3883	3884	IL	M	S	EGB
ISOPROPYLMALATE PERMEABILITY ($^{+}$ = permeable; $^{-}$ = wild type)							
ipm-1^{+};*ipm-2*$^{+}$;*leu-4*	no#;no#;R59	3365		--;--;IL	M	UV	SRG
ipm-1^{+};*ipm-2*$^{+}$;*leu-4*	no#;no#;R59		7024	--;--;IL			SRG
ipm-1^{+};*ipm-2*$^{+}$;*leu-4*	no#;no#;R59		3366	--;--;IL	M	UV	SRG
ipm-1^{-} ;*ipm-2*$^{-}$;*leu-4*	no#;no#;R59		3369	--;--;IL	M		SRG
ipm-1^{+} *ipm-2*$^{+}$ *leu-4 leu-1*	R59 D221		7025				SRG
ipm-1^{+};*ipm-2*$^{+}$	no#;no#	3368		--;--	M	UV	SRG
ipm-1^{-} ;*ipm-2*$^{-}$	no#;no#	3367		--;--	M		SRG
KINESIN							
kin-1		9938	9937	IV R			SS
KYNURENINASE DEFECTIVE							
kyn-1;leu	RC71-3;no#		2512	VII;--	SL	NG	PJR
LACCASE							
lacc, nic-3	HR6; Y31881		8379	VII; L			HI
LACCASE HALO							
lah-1	H12-1	8372		IL			HI
LETHAL ASCOSPORE							
le-1	C-M3	746		IVR	M	P	JCM
le-1;pe fl	S4355;Y8743m L		1402	IVR;IIR R L		UV→pe	ELT
le-2;inl	R2411;89601	1395		VIIR;VR	M	UV	ELT
LEUCINE							
leu-1	33757	4047	4048	IIIR	SL6	UV	EK
leu-1	D221		4270	IIIR			ELT
leu-1;leu-2	D221;R86	7007	7008	IIIR;IVR	E	UV	SRG
leu-1;leu-4	D221;FLR92	1501		IIIR;IL	M	UV	SRG
leu-2	37501	4816	4817	IVR	M	UV	RMD
leu-2	D6		6964	IVR	E	UV	SRG
leu-2	D22	6970	6969	IVR	E	UV	SRG
Many more *leu-2* alleles from S.R. Gross are available. See part VI							
leu-3	47313	3740	539	IL	M	UV	SW/RWB
leu-3	66108		341	IL	M	UV	MBM
leu-3	R14		1321	IL	M	UV	SRG
leu-3	R120		1322	IL	M	UV	SRG
leu-3	R156	4002	4003	IL	SL8	UV	EK
leu-3	R203		1323	IL	M	UV	SRG
leu-3	R229		1324	IL	M	UV	SRG
leu-3 cyt-1	R156, C115	8109		IL	M		DDP
leu-3 cyt-1 a ^{m33}	R156, C115, ^{m33}		8110	IL	M		DDP
leu-4	D133		4235	IL	SL2		DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
LEUCINE, continued from previous page							
leu-4;leu-1	FLR92;D221	1501		IL;IIIR	M	UV	SRG
leu-4	R59		3369	IL	M		SRG
leu-4	R108		175	IL	M	UV	DDP
leu-4	R142		7010	IL	E	UV	SRG
leu-4	R163		7011	IL	E	UV	SRG
leu-4	R173		7012	IL	E	UV	SRG
leu-4	R359	4233	4234	IL	SL3		DDP
leu-4;inl	D47		7013	IL	E	UV	SRG
leu-4	D63		7014	IL	E	UV	SRG
leu-4	D133		7015	IL	E	UV	SRG
leu-4;inl	D179;89601	7016		IL	E	UV	SRG
leu-4	D185		7017	IL	E	UV	SRG
leu-4;inl	D210;89601	7018		IL	E	UV	SRG
leu-5	45208(t)	939	340	VR	M	UV	DDP/MBM
LIGHT INSENSITIVE							
lis-1;bd	JP50;no#	7540		IR;IVR	SL	UV	JP
bd;lis-2	no# ;JP45	7541		IVR;VI	SL	NA	JP
bd;lis-3	no# ;JP52		7542	IVR;VR	SL	UV	JP
L-AMINO ACID OXIDASE							
lox;pmn pmb;pmg	rd9;no# no#;no#	4246	4247	IIIR;IVR R;IIL			RMD
LUMP							
lp	P736	421	555	II	M	S	DDP
LYSINE							
lys-1	33933	4069	4070	VL	SL6	UV	EK
lys-1	66202	400		VL	M	UV	MBM
lys-2	37101	2163	2164	VR	SL2	UV	DDP
lys-2	39302		1127	VR	M	UV	MBM
lys-3	28815		974	IR	M	UV	DDP
lys-3	4545	4302	540	IR	M	X	DDP
lys-4	15069	144	108	IR	M	X	DDP
lys-4	ST39	5436	5437	IR	SL		FJD
lys-4	STL4	3183	941	IR	M	S	DDP
lys-5	37402	4096	4095	VIL	SL6	UV	EK
lys-5	DS6-85	4097	4098	VIL	SL7	UV	EK
lys-5	STL7	139		VIL	SL	UV	DDP
lys(60C)	60C(t)	7576	7577	I	M	UV	FGSC
MICROCONIDIAL (*m*) see *pe*							
MALIC DEHYDROGENASE DEFECTIVE							
ma-1	M20	1108			M	UV	KDM
ma-2	M24	1109			M	UV	KDM
METHIONINE, ADENINE, CYSTEINE							
mac	65108	3609	3610	IR	SL3	UV	DDP
MITOGEN ACTIVATED PROTEIN KINASE							
mak-2	△mak2	9353		VII	SL	RIP	DJE
MAT A/a **MATING TYPE**							
mat a^{m1} *ad-3B cyh-1*	1 2-17-114 KH52(r)	4564		IL R R	M	UV	AJG
mat a^{m2} *ad-3B cyh-1*	2 2-17-114 KH52(r)	4565		IL R R	M	UV	AJG
mat a^{m5} *ad-3B cyh-1*	5 2-17-114 KH52(r)	4566		IL R R	M	UV	AJG

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
MATING TYPE, continued from previous page							
mat a^{m7} ad-3B cyh-1	7 2-17-114 KH52(r)	6840		IL R R	M	UV	DDP
mat a^{m10} ad-3B cyh-1	10 2-17-114 KH52(r)	6841		IL R R	M	UV	DDP
mat a^{m12} ad-3B cyh-1	12 2-17-114 KH52(r)	6842		IL R R	M	UV	DDP
mat a^{m24} ad-3B cyh-1	24 2-17-114 KH52(r)	6843		IL R R	M	UV	DDP
mat a^{m26} ad-3B cyh-1	26 2-17-114 KH52(r)	4567		IL R R	M	UV	AJG
mat a^{m30}	30	7450		IL	M	UV	RLM
mat a^{m30} ad-3B	30 2-17-114	6844		IL R R	M	UV	DDP
mat a^{m33}	33	5382		IL	M	UV	AJG
mat a^{m33} ad-3B cyh-1	33 2-17-114 KH52(r)	4568		IL R R	M	UV	AJG
mat A^{m42} un-3 ad-3A	42 55701(t) 2-17-814	4569		IL L R	M	UV	AJG
nic-2 cyh-1	43002 KH52(r			R R			
mat A^{m44} un-3 ad-3A	44 55701(t) 2-17-814	4570		IL L R	M	UV	AJG
nic-2 cyh-1	43002 KH52(r)			R R			
mat A^{m54} un-3 ad-3A	54 55701(t) 2-17-814	4571		IL L R	M	UV	AJG
nic-2 cyh-1	43002 KH52(r)			R R			
mat A^{m56} un-3 ad-3A	56 55701(t) 2-17-814	4572		IL L R	M	UV	AJG
nic-2 cyh-1	43002 KH52(r)			R R			
mat A^{m64} un-3 ad-3A	64 55701(t) 2-17-814	4573		IL L R	M	UV	AJG
nic-2 cyh-1	43002 KH52(r)			R R			
lys-1; thi-4 ad-2			8292	VL; III III			RLM
mat A^{del}::ADE5^{SC}				I -			
mat ΔA::ADE5;inl			8322		OR		RLM
mat ΔA::ADE5;inl;ad-2			8323		OR		RLM
mat ΔA::ADE5 his-3; inl			8324		OR		RLM
mat ΔA::ADE5 his-3; thi-4 ad-2			8325		OR		RLM
mat ΔA::ADE5 his-3			8326		OR		RLM
mat ΔA::ADE5; Δam::mat-A		8327			OR		RLM
mat ΔA::ADE5; Δam::mat-A inl		8328			OR		RLM
mat ΔA::ADE5 his-3; Δam::mat-A		8329			OR		RLM
mat A-2^{m}		9070					NLG
mat A-2^{m} ad3B		9071					NLG
mat A-3^{m1} pyr-4		9073					NLG
(*A^{m99} un-3 + a^m1 ad-3B cyh-1*)		9474		IL, L			DDP
A^{m99} un-3 nic-2 ad-3B cyh-1		9475		IL			DDP
a^{m33} arg-3 ad-3A			8964				DDP
a^{m33} csp-1			8965				DDP
a^{m33} acr-3			8966				DDP
leu-3 a^{m33} cyt-1			8967				DDP
mat a^{m1} sen			9601				RM
MAT (see *rug*)							
MALE BARREN							
mb-1	V8455	3562	3563	VII	M	UV	DDP
mb-2	V8553	3564	3565	I	M	UV	DDP
mb-3	V5538	3566	3567	IR	M	UV	DDP
MICROCYCLE CONIDIATION							
mcb	no#		7094	VR	SL5	S	RM
mcb	no#		7453	VR	SL7		RM
mcb	no#		7454	VR	SL7		RM
mcm	no#	7089	7090	IIL	SL5	S	RM
mcm	no#	7455		IIL	SL9		RM
mcm	no#		7456	IIL	SL9		RM
MAD							
md	MW84		1296	VR	M		AS

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic background	Mutagen	Obtained from
MATERNAL INHERITANCE [*mi*] see Part IV							
METHYLAMMONIUM RESISTANT							
mea-1	no#	4537		IL	SL	UV	RHG
MEDUSA							
med	R2401	4341	1403	IV	M	S	ELT
MEIOTIC							
mei-1	no#	2919	2920	IVR	M	M	DDP
Mei-2	ALS181	2621		VR	M	UV	DAS
Mei-2	ALS181	6944	6945	VR	SL4	UV	ALS
Mei-2;rg-1 cr-1	ALS181;B53 B123		2622	VR;IC R	M	UV	DAS
Mei-2;nic-3	ALS181;Y31881		5889	VR;VIIL			EK
mei-3	CF-3	6187	6188	IL	SL3	S	DDP
mei-3	JL102		6189	I	M	UV	NBR
mei-3	N289	2764		IL	SL3	S	DNP
mei-3 sn cr-1 al-2; pan-1;al-3 inl	SC25 C136 B123 15300; 5531;RP100 83201(t)	3908		I IC R R; IVR;VR R	M	NG	NCM
*mei-3;sn (cr-1?) al-2;pan-1;al-3 inl**	SC29;C136 (B123?) 15300;5531;RP100 83201(t)	3909		--;IR; IVR;VR	M	NG	NCM
mei-3;tol	N289;N83		2765	IL;IVR	SL3	S	DNP
mei-3	KO	12434	12433	I	SL	KO	GP
mei-3^{pr1}	N289(pr)		2936	I	M	S	DNP
mei-4	N395		2762	IIIR	M	S	DNP
mei-4;arg-3	N395;30300	2763		IIIR;IL	M	S	DNP

* Abnormal *sn cr-1* phenotype; possibly changed by secondary mutation

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic background	Mutagen	Obtained from
MELON allelic with *do*(?)							
mel-1	C-L2B	185		VIIL	SL	P	DDP
mel-2 see *bal*							
6-METHYLPURINE RESISTANT							
mep	LP10(r)	6012	6013	IL	M	UV	DDP
mep(3)	3(r)	3568	7468	IL	M	UV	AMW/RLM
METHIONINE							
met-1	35599	317	922	IVR	M	UV	NHH
met-1	35599		3281	IVR	SL		NEM
met-1 het Cde	38706	3049	3050	IVR	M	UV	EGB
met-1	38706		559	IVR	M	UV	RWB
met-1	K59		3274	IVR	E	UV	NEM
met-1	NM65(t)		1277	IVR	E	UV	NEM
met-1	NM66(t)		1278	IVR	E	UV	NEM
met-1	NM298		3276	IVR	E	UV	NEM
met-2	48004	316		IVR	M	UV	NHH
met-2	H98	283	201	IVR	E3	X	NEM
met-2 het Cde	K5		3282	IVR	SL	UV	NEM
met-2	K23		200	IVR	E3	UV	NEM
met-2	K43	4061		IVR	SL5		EK
met-2	K44		199	IVR	M	UV	NEM
met-2	NM301(t)		1279	IVR	M	UV	NEM
met-2	P81		198	IVR	M	UV	NEM
met-2	P99		197	IVR	M	UV	NEM
met-2	P133		196	IVR	M	UV	NEM
met-2	P140		195	IVR	M	UV	NEM
met-2	P159	4062		IVR	SL5		EK
met-2	P169		194	IVR	M	UV	NEM

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
METHIONINE, continued from previous page							
met-3	36104	112	502	VR	M	UV	DDP/NEM
met-3 inl	92935 37401	2159		VR R	M	UV	GAM
met-4 see *cys-10*							
met-5	9666	3861	3862	IVR	M	X	DDP
met-5	86304	319		IVR	M	M	NHH
met-5	K22	3277	3283	IVR	E/SL	UV	DDP
met-5	K55		3278	IVR	E	UV	NEM
met-5	K62		3279	IVR	E	UV	NEM
met-5	NM307(t)		1280	IVR	M	UV	NEM
met-6	35809	1330	301	IR	M/E3	UV	DNP/NEM
met-6	S2706	4248	4249	IR	SL		DNP
met-7	4894	4087	4088	VIIC	SL7	X	EK
met-7	39103	777	4340	VIIR	M	UV	DGC/ELT
T(I;VII)K79 met-7	K79	2297	2298	I;VIIR			DDP
met-7 wc-1	NM56 P829		3928	VIIR R	E	UV	DDP
met-7 thi-3	NM251 18558		3915	VIIR R	E	UV	DDP
met-7 wc-1	NM251 P829	3914		VIIR R	E	UV	DDP
met-7	NM297(t)	1281		VIIR	E	UV	NEM
met-7 met-9 wc-1	NM331 NM43(t) P829	3607		VIIR R R			AR
met-8	P53	5090	98	IIIR	SL/E2	UV	DDP
met-9	C124	552	3280	VIIR	M	UV	DDP
met-9	NM43(t)		1282	VIIR	M	UV	NEM
met-10	PD1(t)	2937	2938	IR	SL2	UV?	DNP
met(26U);inl	26U(t);89601		3762	IVR;VR	M	UV	DRS
met(105W);inl	105W(t);89601		3764	IVR;VR	M	UV	DRS
met(119W);inl	119W(t);89601		3765	--;VR	M	UV	DRS
met(152C) inl	152C(t) 89601		3759	V(?) VR	M	UV	DRS
met(T27)	T27		969 --	E	UV	FJL	
met(T70)	T70	970		I or II	E	UV	FJL
met(T112)	T112	971		--	E	UV	FJL
MATING FACTOR a-1							
al-2; mfa-1 inl			8940	IR; VR VR			MAN
mfa-1 inl		8941		VR VR			MAN
MIGRATION OF TREHALASE see *tre*							
6-METHYLPURINE RESISTANT see *mep*							
4-METHYLTRYPTOPHAN RESISTANT see *mtr*							
5-METHYLTRYPTOPHAN SENSITIVE see *cpc*							
MORPHOLOGICAL							
mo-1	R2436	4361	4439	I	M	UV	ELT/DDP
mo-2	R2464	1394		VII	M	UV	ELT
mo-4	R2467	3912	3913	IIIR	SL3	UV	DDP
mo-5	R2487	4251	4252	IL	SL		DDP
mo(36703-4-20)	36703-4-20		1671	VI	M	UV	DDP
mo(AR501)	AR501	5932		II	SL2	A	DDP
mo(B8)	B8	1648		IIIR	SL	UV	DDP
mo(B107)	B107	1663		VR	SL3	UV	DDP
mo(D301)	D301		1640	IR			DDP
mo(D306)	D306		1659	IVR	M	UV	DDP
mo(D309)	D309	1647		II	M	UV	DDP
mo(D314)	D314		1660	IVR	M	UV	DDP
mo(D318)	D318	1668		V	M	UV	DDP
mo(KH161);acr-5	KH161;KH27(r)	2323	2324	--;IIR	M	G	KSH
mo(M126)	M126	1649		IIIR	M	S	DDP
mo(M184)	M184	4367	1634	IC	M/SL3	S	ELT/DDP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
MORPHOLOGICAL, continued from previous page							
mo(M193-1)	M193-1	1635		IC	SL3	S?	DDP
mo(NM119)	NM119		1657	IVR	M	UV	DDP
mo(NM201f)	NM201f	1676		II	M	UV	DDP
mo(NM203)	NM203		1636	I	E	UV	DDP
mo(NM211)	NM211	1650		IIIR	E	UV	DDP
mo(NM216s)	NM216s		1639	I	E	UV	DDP
mo(NM218)	NM218		1645	II	E	UV	DDP
mo(NM219)	NM219		1651	III	M	UV	DDP
mo(NM220)	NM220		1646	II	M	UV	DDP
mo(NM226)	NM226	1672		VIIC	M	UV	DDP
mo(NM359)	NM359	1661		IVR	M	UV	DDP
mo(P1135)	P1135	1670		VIL	S		DDP
mo(P1417)	P1417	1641		IR	M	S	DDP
mo(P1718)	see *sk* allele P1718						
mo(P1898)	P1898		1662	VR	M	S	DDP
mo(P3816)	P3816	7340	7341	IVR	SL	S	DDP
mo(R2374s)	R2374s	7026	7027	IIIR	M		DDP
mo(R2374)	R2374	7311	7312	IIIR			DDP
(mo(R2374) A + a^{ml} *ad-3B cyh-1)*	R2374(3828-3)	7309	7310				DDP
mo(VP103)	VP103	8309	8310	IR	OR		DDP
MODIFIER OF PERMEABILITY							
mod-5	no#		1603	VI	SL	UV	PSL
MODIFIER OF SCUMBO							
mod(sc) pan-1	KH251 5531	1162	1163	IVR R	M	S	KSH
MORPHOLOGICAL-ENVIRONMENT SENSITIVE							
moe-1	Y6821	4272		VIIR	L	MC	ELT
moe-2;inl	R2532;89601	1386		VIC;VR	M	UV	ELT
4-METHYLTRYPTOPHAN RESISTANT							
mtr	6(r)	3043	3288	IVR	M	UV	DDP
mtr col-4;su(mtr)	10(r) 70007c;21-2	1719		IVR R;IC	M		DRS
mtr col-4;his-2	10(r) 70007c;Y152M43		1720	IVR R;IR			DRS
mtr col-4;his-2	14(r) 70007;Y152M43		3016	IVR R;IR			DRS
mtr	15(r)	4057	4058		SL8		EK
mtr;su(mtr)	21(r);21-0	1718		IVR;IR	M		DRS
mtr;pdx-1;his-2	26(r);37803;Y142M43		2728	IVR R;IR			NGB
mtr;pdx-1;his-2	26-R1364*(s);37803;Y142M43		2731	IVR R;IR			NGB
mtr;pdx-1;his-2	26-R1373*(s);37803;Y142M43		2729	IVR R;IR			NGB
mtr;pdx-1;his-2	26-R2435*(s);Y142M43;37803		2730	IVR R;IR			NGB
mtr col-4;his-2	30(r) 70007;Y152M43		3017	IVR R;IR	M	UV	DRS
mtr;pdx-1;his-2	112(r);37803;Y152M43	3018		IVR R;IR	M	UV	DRS
mtr;pdx-1;his-2	119(r);37803;Y152M43	3020		IVR R;IR	M	UV	DRS
mtr;pdx-1;his-2	120(r);37803;Y152M43	3021		IVR R;IR	M	UV	DRS
mtr;pdx-1;his-2	121(r);37803;Y152M43	3022		IVR R;IR	M	UV	DRS
mtr(t-1)[†]	1560(r)/(t;r)	3023		IVR;IR;IVRM		UV	DRS
mtr(t-2)[†]	1561(r)/(t;r)	3024		IVR;IR;IVR	M	UV	DRS
mtr(t-3)[†]	1562(r)/(t;r)	3025		IVR;IR;IVR	M	UV	DRS
mtr(t-4)[†]	1563(r)/(t;r)	3026		IVR;IR;IVR	M	UV	DRS
mtr(t-5)[†]	1564(r)/(t;r)		3027	IVR;IR;IVR	M	UV	DRS
mtr(t-6)[†]	1565(r)/(t;r)	3028		IVR;IR;IVR	M	UV	DRS
mtr(t-7)[†]	1566(r)/(t;r)	3029		IVR;IR;IVR	M	UV	DRS
mtr(t-8)[†]	1567(r)/(t;r)	3030		IVR;IR;IVR	M	UV	DRS
mtr(t-9)[†]	1568(r)/(t;r)	3031		IVR;IR;IVR	M	UV	DRS

		FGSC number mating type			Genetic back-		
Locus	Allele	A	a	Linkage group	ground	Mutagen	Obtained from
4-METHYLTRYPTOPHAN RESISTANT, continued from previous page							
mtr	flr271(s)[‡]	1317		IVR		Co-60	SRG
mtr	flr354(s)[‡]	1318		IVR		UV	SRG
mtr	flr380(s) [‡]	1319		IVR		UV	SRG
mtr(pmn)	Pm-22(r)	2274		IVR	M	UV	LW
mtr(pmn)	Pm-22(r)	4812	4813	IVR	SL		RMD
mtr pmb	Pm-22(r) can-37(r)		2276	IVR R		Co-60	SRG
mtr;pmg	Pm-22(r);no#	4808	4809	IVR;IIL	SL		RMD
mtr	SR33	7539	7538	IVR		S	RLM
mtr	SR62		7537	IVR		S	RLM

[*] Contains intragenic suppressor resulting in reversion; i.e. sensitivity to MT

[†] All contain *his-2 pdx*-1; all contain two altered sites in *mtr* - one conditional

[‡] trifluoroleucine sensitive

5-METHYLTRYPTOPHAN SENSITIVE see *cpc-1*

MUTAGEN SENSITIVE

mus-7	FK107	5142	5143	IIR	SL7	NG	EK
mus-7	FK116	6401	6402	IIR	SL2	4-NQO	EK
mus-8	FK108	5144	5145	IVR	SL7	NG	EK
mus-8	KO	12414	12413	IV	SL	KO	GP
mus-9	FK104	5146	5147	IR	SL7	NG	EK
mus-9	FK129	6403	6404	IR	SL4	4-NQO	EK
mus-10	FK110	5148	5149	VIIR	SL7	NG	EK
mus-11	FK111	5150	5151	VR	SL7	NG	EK
mus-11	FK117	6409	6410	VR	SL4	4-NQO	EK
mus-12 al-3 inl; pan-1	SC15 RP100 83201(t);5531	3906		VR R R; IVR	M	NG	NCM
mus-14;al-2;pan-1	SC3;15300;5531		3903	VIL;IR;IVR	M	NG	NCM
mus-15 al-2;cot-1; pan-2	SA7 Y112M38;C102(t); Y387-15.7	7296	7297	IC IR; IVR;V	SL	UV	HI
mus-16;al-2;pan-2	JMB15.2;Y112M38;Y387-15.7	6820	6821	V;IR;IVR	SL3	M	HI
mus-17	SA17	7298	7299	IVR	SL	UV	HI
mus-18;al-2;cot-1; pan-2	SA8B;Y112M38;C102(t); Y387-15.7a	7137	7138	VL;IR; IVR;VIR	SL3	UV	HI
mus-18	KO	12356	12357	V	SL	KO	GP
mus-19 al-2;pan-2	SA19 Y112M38;Y387-15.7	7300	7301	IR IR;VIR	SL	UV	HI
mus-20;al-2;cot-1; pan-2	SA2;Y112M38;C102(t); Y387-15.7	7302	7303	IIIR;IR; IVR;VIR	SL		HI
mus-21	FK120	6418	6419	IIIR	SL2	4-NQO	EK
mus-21	FK121	6414	6415	IIIR	SL6	4-NQO	EK
mus-21	FK127	6422	6423	IIIR	SL2	4-NQO	EK
mus-21	SC10	5890	5891	IIIR	M	NG	EK
may contain *T(II;III;VI)*							
mus-21	FK131	6459	6460	IIIR	SL2	UV	EK
mus-21	FK132	6463	6464	IIIR	SL2	UV	EK
mus-21	KO	11162	11163	III	SL	KO	GP
mus-22	SA22	7304	7305	IR	SL		HI
al-2; pan-2; mus-23	Y112M38, Y387-15.7,SA23	8341	8342	IR; VI;II	OR		HI
mus-24	SA24	8344	8343	II			HI
mus-24	C2-T120-38a		8930	II			HI
mus-25	FK123	6424	6425	VIIL	SL4	4-NQO	EK
mus-26;al-2; cot-1 pan-2	SA3B;Y112M38; Y387-15.7 C102(t)	6822	6823	IVR;IR; IVR;VIR	SL	S	HI
mus-26	KO	12058		IV	SL	KO	GP
mus-27	FK124	6428	6429	IIR	SL4	4-NQO	EK
mus-27	KO		12518	II	SL	KO	GP
mus-28	FK118	6434	6435	IIIR	SL4	4-NQO	EK

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
MUTAGEN SENSITIVE, continued from previous page							
mus-29	FK119	6438	6439	VIR	SL4	4-NQO	EK
mus-30	FK115	6444	6445	IVR	SL4	4-NQO	EK
mus-38	SA56	8352	8351	I	OR		HI
mus-39	FK133	6467	6468	VI	SL2	UV	EK
mus-51	Hyg^r	9595				GD	HI
mus-51 Δ::bar;his-3			9538			GD	RLM
mus-52	Hyg^r	9567	9568			GD	HI
mus-52 Δ::bar;his-3			9539			GD	RLM
mus(FK125)	FK125	6450	6451	--	SL4	UV	EK
mus(FK128)	FK128	6456	6457	--	SL4	UV	EK
mus(SC1);pan-1	SC1;5531	3902		--;IVR	M	NG	NCM
mus(SC13) al-2; pan-1	SC13 15300;5531		3905	IR R;IVR	M	NG	NCM
mus(SC17);al-3 inl;pan-1	SC17;RP100 83201(t);5531		3907	V;IR; IVR;VR	M	NG	NCM
NAD(P) GLYCOHYDROLASE DEFECTIVE							
nada	61	2687	2688	IVC	SL3	EMS	REN
nada	62(t)	2689	2690	IVC	SL3	EMS	REN
nada	64	2691	2692	IVC	SL3	EMS	REN
nada	65	2693	2694	IVC	SL3	EMS	REN
nada	100	2695	2696	IVC	SL3	EMS	REN
NEUTRAL AND ACIDIC AMINO ACID PERMEABILITY							
nap	no#	1604		V	SL2	UV	ESJ
CALCIUM P-TYPE ATPase							
nca-3	nca-3 6R		9357				BB
nca-2		8944					BB
nca-2		8945					BB
nca-2		8946					BB
nca-2	nca-2 11R	9358	9359	VI			BB
nca-2, nca-3		9365					BB
NATURAL DEATH							
(*nd al-2 a + lys-1 a*)			3572	IR	SL7	UV	KDM
(*nd al-2;lys-1 a + helper*)			3571	IR	SL7	UV	KDM
(*nd al-2;lys-1 a + helper*)			3570	IR	SL7	UV	KDM
(*nd al-2 nic-1 a + pan-2 a*)			6878	IR	SL	UV	BSR
NUCLEAR DIVISION CYCLE							
ndc-1 inl	1(t) 89601	7867	3441	VR R	M	UV	DDP/DRS
NEUTRAL AMINO ACID TRANSPORT							
neu^a*;his-3*	no#;K57	3272		--;IR	E	UV	CWM
neu^r*;his-2*	no#;HS-24	3273		IVR(?);IR	E	UV	CWM
NICOTINIC ACID							
nic-1 os-1 al-1	3416 B135 34508	3584		IR R R			DDP
nic-1	3416	8248	561	IR	M	X	RWB
nic-1	39113	765		IR	SL7	UV	PSL
nic-1	S1413	763	764	IR	SL7	X	PSL
T(I→V)S1325 nic-2	S1325	1558	1557	IR;VR		X	DDP
T(I→III)4540 nic-2	4540	766	767	IR;IIIR;IR			PSL
nic-2	39303		371	IR	M	UV	MBM
nic-2	43002	2527		IR	SL	UV	CPS

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
NICOTINIC ACID, continued from previous page							
nic-2	43002	4006	4007	IR	SL9	UV	EK
nic-2	Y31455	770	771	IR	SL7	M	PSL
nic-3	Y31881	2528		VIIL	SL	M	CPS
nic-3	Y31881	4081	4082	VIIL	SL7	M	EK
NITRATE NONUTILIZATION							
nit-1	34547	54	32	IR	M	UV	DDP
nit-2	I7	2698		IL	SL	UV	GAM
nit-2	K31	33		IL			DDP
nit-2 leu-3	KGP0220 R156	6024		IL L	M	UV	GAM
nit-2	nr37	983	982	IL	SL	UV	GS
nit-2	RIP4		9546	IL			GAM
nit-2	KO		11392	IL	SL	KO	GP
nit-3	KGP026	6028		IVR	M	UV	GAM
nit-3	KGP0213	6027		IVR	M	UV	GAM
nit-3	KGP1222	6026		IVR	M	UV	GAM
nit-3	KGP1211	6025		IVR	M	UV	GAM
nit-3	14789	3009	358	IVR	M	X	DDP
nit-3	RIP22	9545		IVR			GAM
nit-3	RIP15	9552		IVR			GAM
nit-4	no#	2993	2994	IVR	SL3		DDP
nit-5=4	nr15	985	984	IVR	SL	UV	GS
nit-4	KO	11007	11008	IV	SL	KO	GP
nit-6	OP4	3463	3464	VI	SL	NG	OCY
nit-7	V1M59	3933		IIIR	M	UV	RHG
nit-8	V1M44	4236	4237	IR	M	UV	DDP
nit-9A	V1M5	3935	8197	IVR	M	UV	RHG
nit-9B	V1M32	8196	3936	IVR	M	UV	RHG
nit-9C	V1M50	3937	8195	IVR	M	UV	RHG
nit(25376)	25376		653	IV	M	X	MJM
nit(JH2003)	JH2003	6011	2384	--	M		FGSC/DDP
nit-10	RIP-28	9548					GAM
nit-10	RIP-40	9549					GAM
NITROGEN METABOLITE REGULATION							
nmr-1	MS5	4609	4610	VR	SL	NG	RMD
nmr-1	V2M304	4611	4612	VR	SL	UV	RMD
nmr-1	RIPIIA	9544					GAM
NON REPRESSOR OF CONIDIATION							
nrc-1; qa-2; aro-9; inv; al-2			10007				SF
nrc-2; qa-2; aro-9; inv; al-2			10008				SF
NICOTINIC ACID OR TRYPTOPHAN							
nt	295	2438	2439	VIIR	M	NG	FHG
nt	39401	4348	563	VIIR	M	UV	ELT/RWB
nt	65001	4089	4090	VIIR	SL6	UV	EK
nt	A370	1736	1711	VIIR	M	UV	MA
nt	C86	4349	869	VIIR	M	UV	ELT
NUCLEASE DEFICIENT							
nuc-1	T28-M1 (Also A1)	1995	1994	IR	M	UV	TI
nuc-1^{C}	BC-152		3947	IR	UV		RLM
nuc-1	KO		11448	I	SL	KO	GP
nuc-2	T28-M2 (Also B1)	1996	1997	IIR	M	UV	TI
nuc-2 (pcon^{C}*)*	UW6	2534		IIR	M	UV	RLM
nuc-3	701	4909		IIR	SL	NG	NCM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
NUCLEASE DEFICIENT, continued from previous page							
nuc-3;pan-2	701;1-153-96		4910	IIR;VIR	SL	NG	NCM
nuc-4	51		4911	IIR	SL	NG	NCM
nuc-5;inl	276;83201(t)		4912	IIR;VR	SL	NG	NCM
nuc-6	936	4913		IIR	SL	NG	NCM
nuc-6;inl	936;83201(t)		4914	IIR;VR	SL	NG	NCM
nuc-7	24	4915		IIR	SL	NG	NCM
nuc-7;pan-2	24;1-153-96		4916	IIR;VR	SL	NG	NCM
NUCLEASE HALO							
nuh-1	FK001	4180	4181	IIIR	SL9	NG	EK
nuh-2	FK027	4182	4183	IIIR	SL7	NG	EK
nuh-3	FK003	4184	4185	VR	SL9	EMS	EK
nuh-5	FK005	4186	4187	IIR	SL9	EMS	EK
nuh-6	FK006	4188	4189	ICR	SL8	EMS	EK
nuh-7	FK017	4591	4592		SL6	NG	EK
nuh-8	FK018	4593	4594	IR	SL6	UV	EK
nuh-9	FK037	4595	4596	IIR	SL6	NG	EK
nuh-10	FK028	4597	4598	VIR	SL6	NG	EK
nuh	FK019	4599	4600		SL6	NG	EK
nuh	FK022	4601	4602		SL9	NG	EK
nuh	FK041	4603	4604		SL4	NG	EK
nuh	FK042	4605	4606		SL5	NG	EK
NYSTATIN RESISTANT see *erg*							
OAK							
oak	R2358	4579	4580	VR	M		DDP
OLIGOMYCIN RESISTANT							
oli	16-16	8739	8739	VIIR			RLM
oli;csp-1;bd	16-16;UCLA37;no#	3483		VIIR;IL;IVR	M		SB
oli;csp-1;bd	CD-5;UCLA37;no#	6706		VIIR;IL;IVR	M		SB
ORNITHINE see *arg-5, -6, -7*							
OSMOTIC							
os-1	AR2	1675		IR	M	S	DDP
os-1	B135	951	810	IR	SL	UV	DDP
os-1	E11200	47	34	IR	M		DDP
os-1	171-1		3901	--	RL		NCM
os-1	M16	812	813	IR	SL3	UV	DDP
os-1	M155-1	824		IR	M	S	DDP
os-1	NM204(t)	1637	2273	IR	E/M	UV	DDP
os-1	NM233t	4493	4494	IR	SL6	UV	DDP
os-1 al-2	P641 15300		866	IR R	M	S/os	DDP
os-1	P668		973	IR	M	S	DDP
os-1	P3282		1508	IR	M	S	DDP
os-1	P5990	2432		IR	SL	S	DDP
os-1	P6549		2584	IR	M	S	DDP
os-1 (=flm-1)	Y256M209	3624	3625	IR	SL	UV	DDP
os-1	KO	11696	11695	I	SL	KO	GP
os-2	ALS10	1509	1510	IVR	M	S	DDP
os-2	UCLA80	2238	2239	IVR	SL	EMS	CPS
os-2	KO	11436		IV	SL	KO	GP
os-4	NM201o	2429	2430	IL	M	UV	DDP
(os-4;pan-2 a + a^{m1} *ad-3B cyh-1)*	NM201o + 1 2-17-114 KH52(r)		5894	IL;VIR	SL		DDP

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
OSMOTIC, continued from previous page							
os-4 (=flm-2)	Y256M223	6040	6041	IL	SL	UV	DDP
(os-4 + a^{m1} *ad-3B cyh-1)*	Y256M223 + 1 2-17-114 KH52(r)	6042	6043	IL	SL		DDP
os-5	NM216o	1638	4576	IR	M	UV	DDP/FGSC
os-5	P5341	2310		IR	M	S	DDP
os-5	UCLA84		2243	IR	SL4	EMS	CPS
os-6	14-3		3896	--	RL		NCM
os-6	56-4	3898		--	RL		NCM
os-6	171-7		3900	--	RL		NCM
os(P3282)	P3282		1644	IR	M	S	DDP
ORNITHINE TRANSAMINASE DEFECTIVE							
ota	UM728	1700	1701	IIIR	SL3	UV	RHD
OVERACCUMULATOR OF CAROTENOIDS							
ovc	S20-16		4503	IVR	M	UV	RWH
D-AMINO ACID OXIDASE DEFICIENT							
oxD (cys-15)	1	1872	888	IVR	M	UV	DDP/NHH
oxD	8		889	IVR	M	UV	NHH
oxD	9	890		IVR	M	UV	NHH
oxD	11	891		IVR	M	UV	NHH
oxD	13		892	IVR	M	UV	NHH
p-AMINOBENZOIC ACID							
pab-1	830	496		VR	M	X	RWB
pab-1	1633	5953	3863	VR	M	X	DDP
pab-1	5359	564	4359	VR	M	UV	ELT
pab-1	21850	4358	8190	VR	L	X	ELT
pab-1	36111	363	8189	VR	M	UV	MBM
pab-1	38113	367	8249	VR	M	UV	MBM
pab-2	H193	4076	4077	VR	SL9	X	EK
PANTOTHENIC ACID							
pan-1	5531	4063	4064	IVR	SL7	X	EK
pan-1	S1246	5015	8192	IVR	SL		FGSC
pan-2	B2(Y153M66)	465	466	VIR	SL	X	MEC
pan-2	B3(Y153M96)	2248	2249	VIR	SL		OMM
pan-2	B5(Y154M64)	4103	4104	VIR	SL8	X	EK
pan-2	B36	4105	4106	VIR	SL8		EK
pan-2;al-2; *cot-1*	Y387-15.7;Y112M38; C102(t)	2583		VIR;IR; IVR	SL		FJD
Additional *pan-2* strains from Dr. M. Case are available. Please inquire if you are interested.							
PATCH							
pat	no#		981	IC	M		AS
PHOSPHATASE CONTROL see *nuc-2*							
PURINE DEGRADATION CONTROL							
pco-1	RIP 1		9550	IV			GAM
pco-1	RIP 7		9551	IV			GAM
PYRIDOXINE							
pdx-1	35405(t)	1408	1407	IVR	M	UV	AR
pdx-1	37803	4055	4056	IVR	SL7	UV	EK
pdx-1	39106(p)	1410	1409	IVR	M	UV	AR

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
PYRIDOXINE, continued from previous page							
pdx-1	39706(p)		1415	IVR	M	UV	AR
pdx-1	44204(p)	1413	1414	IVR	M	UV	AR
pdx-1	44602(p)	1412	1411	IVR	M	UV	AR
pdx-1	46904(p)	1417	1416	IVR	M	UV	AR
pdx-1	Y2329	1419	1418	IVR	M	UV	AR
pdx-1	Y30978	1313	3261	IVR	M	M	AR/ELT
pdx-1	Y31393	1314	1420	IVR	M	M	AR
pdx(Y12274)	Y12274	1312	1421	IVR	M	UV	AR
PEACH							
pe	L		567	IIR	L	S	ELT
pe	Y8743m	4036	4037	IIR	SL6	S?	EK
pe	no# (Sansome)		645	IIR	M		MJM
pe arg-12	Y874m, UM107	7656	7657	IIR,R			DDP
PERITHECIAL NECK							
pen-1	DL413	5830	5831	VII	SL	NG	DDP
PERITHECIAL COLOR							
Type I:							
per-1;ad-2	ABI1;STL2	2547		VR;IIIR	M	UV	TEJ
per-1;ad-2	ABT8;STL2	2551		VR;IIIR	M	UV	TEJ
per-1	AR174	7035	4318	VR	SL	UV	HBH/DDP
per-1	P760*	6708	6709	VR	SL6	S	DDP
per-1;pyr-3	PBE1;KS43	2546		VR;IVR	M	UV	TEJ
per-1	PBJ1	3309	3310	VR	SL	UV	DDP
per-1;csp-2	PBJ1;UCLA101	6662	6663	VR;VIIL	SL		DDP
per-1;pyr-3	PBP1;KS43	2550		VR;IVR	M	UV	TEJ
per-1;pyr-3	PBT4;KS43	2552		VR;IVR	M	UV	TEJ
per-1;pyr-3	PBT5;KS43	2553		VR;IVR	M	UV	TEJ
per-1 al-3; csp-2	AR174, RP100; UCLA 101	8412	8413	VR VR;VIIL			DDP
* originated in *N. intermedia*							
Type II:							
per-1	29-278	2954		VR	SL	NG	HBH
per-1	29-281	2955		VR	SL	S	HBH
per-1	DL126	5787	5788	VR	SL	NG	DDP
per-1	UG1837	4558	4559	VR	SL2	S	DDP
PERMEASE GENERAL AMINO ACID see *pmg*							
PUFF							
pf	B141	419	420	IVR	SL2	UV	DDP
POLYUNSATURATED FATTY ACIDS							
(*pfa-1* + a^{ml} ad-3B cyh-1)		7942		VII	SL		MT
(*pfa-2* +a^{ml} ad-3B cyh-1)			7943	-	SL		MT
(*pfa-3* + a^{ml} ad-3B cyh-1)		7944		-	SL		MT
(*pfa-4* + a^{ml} ad-3B cyh-1)		7945		VII	SL		MT
(*pfa-5* +a^{ml} ad-3B cyh-1)			7946	-	SL		MT
PHOSPHORUS GOVERNANCE							
$pgov^{C}$	5		3479	IIIR	SL	UV	RLM
$pgov^{C}$	12		3478	IIIR	SL	UV	RLM
$pgov^{C}$;*nuc-1*	R42;T28-M1	3480		IIIR;IR	M	UV	RLM

Locus	Allele	FGSC number mating type		Linkage group	Genetic background	Mutagen	Obtained from
		A	a				
PHENYLALANINE							
phe-1	H3791		504	IL	M	S35	RWB
phe-1	H6196	1096	492	IL	M	S35	DNP/RWB
phe-1	NM160	1294	1295	IL	SL2	UV	DDP
phe-1	UA119;89601	1167		IL;VR	M	NA	KKJ
phe-2	E5212	873		IIIR			AGD
phe-2 tyr-1;trp-2	E5212 C167;75001		3255	IIIR R;VIR			RLM
phe-2(phe-3)	Y16329	1332	1333	IIIR	SL3	X	DDP
PHENYLALANINE + TYROSINE see *pt*							
PHOSPHATASE-ACID							
pho-3;al-2	221(t);15300	3051	3052	IVR;IR	SL	UV	REN
PHOSPHATASE-ALKALINE							
pho-2	JFL134	3061	3062	VR	SL	UV	RLM
pho-2	JFL317		3063	VR	SL	UV	RLM
pho-2	JFL327	3064	3065	VR	SL	UV	RLM
pho-2	JFL341	3066	3067	VR	SL	UV	RLM
pho-2	JFL606	3068	3069	VR	SL	UV	RLM
pho-2	MKG-1	2535		VR	M	UV	RLM
pho-2	MKG-2	2536		VR	SL	UV	RLM
pho-2	RLM20	3057	3058	VR	SL	UV	RLM
pho-2	RLM72	3059	3060	VR	SL	UV	RLM
pho-2	KO	11192	11193	V	SL	KO	GP
PHOSPHORUS CONTROL see *pcon*^{C}							
PHOSPHORUS REGULATION see *preg*^{C}							
PHOSPHATE PERMEASE							
pho-4 (van)	BRY1	4636	4637	VIIL	L	UV	KEA
pho-4 (van)	BRY8		4638	VIIL	L	UV	KEA
pho-4 ; pyr-1	RIP; tt263	8344		VII; IV		RIP	RLM
pho–4; pho-5	RIP; RIP	8347	8348	VII; IV		RIP	RLM
pho-5	RIP	8346		IV		RIP	RLM
hkpp^{su}*; pho-4; pho-5*	su; RIP; RIP	8349	8350	?; VII; IV			HI
PHOTOREACTIVATION DEFICIENT							
phr	CR5-5-9		8929	IR			HI
PILE							
pi	B101	4026	4027	IIL	SL9	UV	EK
pi	R2438	6845	6868	IIL	SL3	UV	FGSC
PEAK (=*bis*)							
pk	B6	277	278	VR	SL	UV	DDP
pk	B12	805		VR	SL	UV	DDP
pk	B30	811		VR	SL	UV	DDP
pk	B230r	1250		VR	SL4	X	DDP
pk	C-1810-1	1074		VR	SL	S	DDP
pk	C-1810-1		1075	VR	SL	S	DDP
pk	D12		822	VR	M	UV	DDP
pk	D312	923	924	VR	M	UV	DDP
pk^{t1} *pab-l*	17-575 1633?	3420	3421	VR R	SL	UV	AMS
pk^{t2} *pab-1*	19-773(peak) 1633?	3422	3423	VR R	SL	DS	AMS
T(V;VII)17-088 pk^{D}	17-088(dominant peak)	3672	3418	V;VII			DDP/AMS
T(I;V)C-1670 pk	C-1670	483	2761	IR;VR			DDP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
PLUG							
pl	B118	96	97	VR	SL3	UV	DDP
PHOSPHOLIPASE C							
plc-1	plc1		9919	IIIR			OG
plc-1	KO		11411				GP
PLUMOSE *plm* - see *T(VI;VII)NCRL91 plm*, Part VI							
PERMEASE BASIC AMINO ACID							
pmb	UM535 (57A)	1683		IVR	M	UV	WMT
pmb	can-37(r)	4814	4815	IVR	SL		RMD
pmb	cnr-37(r)	2275		IVR	M	UV	LW
pmb;pmg	can-37(r);no#	4810	4811	IVR;IIL	SL		RMD
pmb;aga	DF101;UM906	7924	7925	IVR:VIIR		UV	RHD
PERMEASE GENERAL AMINO ACID							
pmg	FS667	4613	4614	IIL	M	UV	RMD
P-TYPE ATPase							
pmr, al-2	pmr 6-3	9356					BB
PERMEASE NEUTRAL AMINO ACID - see *mtr*							
POKY [*mi-1*] see Part IV							
PROTOPERITHECIA							
pp-1	Δpp-1::hph	9352				KO	DJE
pp-2	Δpp-2::RIP	9351		IIR		RIP	DJE
see *also gpi; pp*							
PLENTY OF IT							
poi-2		8939		VIIR			MAN
inl; poi-2		8936		VR; VIIR			MAN
al-2; poi-2		8938		IR; VIIR			MAN
al-2; inl; poi-2 arg-10 nt			8935	IR; VR; VII VIIR VIIR			MAN
poi-2 arg-10 nt			8937	VII VIIR VIIR			MAN
PARTIAL RESISTANCE TO SK-2 KILLING							
pr(Sk-2) mod(pr)	P2604		7398	IIIR			BCT
PERIOD							
prd-1;bd	no#;no#		4902	III;IVR	SL	NG	JFF
prd-2;bd	UVIV-2;no#	4903	4904	V;IVR	SL	UV	JFF
prd-3;bd	UVIV-4;no#	4905	4906	I;IVR	SL	UV	JFF
prd-4;bd	UVV-7;no#		4907	IR;IVR	SL	UV	JFF
PHOSPHORUS REGULATION							
$preg^{C}$	preg^{C2}	2532		IIR	M	UV	RLM
PERFORATED							
$(PrfA + Prf^{+}a^{m33})$	DL1227	6190		VR	SL	NG	NBR
$(Prfa^{m33} + Prf^{+}A)$	DL1227		6191	VR	SL	NG	NBR
PROLINE							
pro-1	21863	4516	4515	IIIR	SL	X	DDP
pro-3	44207	1310	1311	VR	SL2	UV	EGB

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
PROLINE, continued from previous page							
pro-3	51506	1308	1309	VR	SL2	UV	BVS
pro-4	35401	6	163	IIIR	SL3	UV	DDP
pro(51505)	51505	928	625 --	M	UV	MBM	
pro(K388)	K388		1159	--	E	UV	DGC
PROTEIN SYNTHESIS INITIATION							
psi-1	34C(t)	3044	3289	IVR	M	UV	DDP
PHOSPHORYLATION OF SMALL PROTEIN							
psp	KO1	8307	8308	VR	M		KH
PHENYLALANINE + TYROSINE							
pt	NS1	4695	4696	IVR	M		DDP
pt	P4418	8265		IVR	M		DDP
T(IV→III)S4342 pt	S4342	109	92	IVR;IIIR;IVR			DDP
PROTEASE							
pts-1 (Groveland-1c)	no#		1945	--			DDP
PUTRESCINE see SPERMIDINE							
PUTRESCINE UPTAKE							
puu-1	GB1	7044	7045	IVR	SL2	S	RHD
PYRIMIDINE							
pyr-1	H263	72	85	IVR	M	X	DDP
pyr-1	KS12p1	1301	8250	IVR	M		RHD
pyr-1	DFC33	8399		IVR	SL		RHD
pyr-2	37709		365	IVR	M	UV	MBM
pyr-2	38502	3465	3466	IVR	M	UV	DDP
pyr-2	DFC9	8398	8397	IVR	SL		RHD
pyr-3	1298(pyr-3e)		490	IVR	M	X	RWB
pyr-3	37301p	87	4356	IVR	M	UV	DDP/ELT
pyr-3;arg-12	37301p;37301s		894	IVR;IIR			RHD
pyr-3 col-4	37815(t) 70007c	392		IVR R	M	UV	MBM
pyr-3	37815(t)		366	IVR	M	UV	MBM
pyr-3	45502*	1900	937	IVR	M	UV	AR
pyr-3	49001	374		IVR	M	UV	MBM
pyr-3	67602	378		IVR	M	UV	MBM
pyr-3;arg-3?	43-101*;30300?	1890		IVR;IL	M	UV	AR
pyr-3;arg-3?	43-174*;30300?	1891		IVR;IL	M	UV	AR
pyr-3;arg-3?	43-180*;30300?	1892		IVR;IL	M	UV	AR
pyr-3;arg-3?	AR576*;30300?	1893		IVR;IL	M	A	AR
pyr-3 arg-2?	AR618* 33442?	1894		IVR R	M	A	AR
pyr-3 arg-2?	K0493-14* 33442?	1895		IVR R	M	NA	AR
pyr-3 arg-2?	K0493-54* 33442?	1896		IVR R	M	NA	AR
pyr-3 arg-2?	K0545-31* 33442?	1899		IVR R	M	NA	AR
pyr-3 arg-2?	K0545-122* 33442	1898		IVR R	M	NA	AR
pyr-3 arg-2?	K0556-185* 33442	1897		IVR R	M	NA	AR
pyr-3	KS1[†]		839	IVR	SL	UV	VWW
pyr-3	KS1[‡]	1964		IVR	M	UV	AR
pyr-3	KS3[†]	835	838	IVR	M	UV	VWW
pyr-3	KS3[‡]	1965		IVR	M	UV	AR
pyr-3	KS4[†]	843	828	IVR	M	UV	VWW
pyr-3	KS6[‡]	1980		IVR	M	UV	AR
pyr-3	KS7[‡]	1966		IVR	M	UV	AR
pyr-3	KS8[‡]	1967		IVR	M	UV	AR

PYRIMIDINE, continued from previous page

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
pyr-3	KS11[‡]	1968		IVR	M	UV	AR
pyr-3	KS12[†]	832	836	IVR	M	UV	VWW
pyr-3	KS12p[†]	1298	1299	IVR			RHD
pyr-3	KS13[†]	833	834	IVR	M	UV	VWW
pyr-3	KS15[‡]	1969		IVR	M	UV	AR
pyr-3	KS16[†]	829	831	IVR	M	UV	VWW
pyr-3	KS17[‡]	1970		IVR	M	UV	AR
pyr-3	KS20[†]	845	841	IVR	M	UV	VWW
pyr-3	KS23[‡]	846	842	IVR	M	UV	VWW
pyr-3	KS23p[†]	840		IVR	M	UV/KS23	VWW
pyr-3	KS24[‡]	1971		IVR	M	UV	AR
pyr-3	KS26[‡]	1972		IVR	M	UV	AR
pyr-3	KS40[‡]	1973		IVR	M	UV	AR
pyr-3	KS43*	844	837	IVR	M	UV	VWW
pyr-3	KS44[‡]	1974		IVR	M	UV	AR
pyr-3	KS45[‡]	1975		IVR	M	UV	AR
pyr-3	KS46[‡]	1976		IVR	M	UV	AR
pyr-3	KS47[‡]	1977		IVR	M	UV	AR
pyr-3	KS126[‡]	1978		IVR	M	UV	AR
pyr-3	KS139[‡]	1979		IVR	M	UV	AR
pyr-3	DFC3	8394	8396	IVR	SL		RHD
pyr-4	36601	4030	4031	IIL	SL6	UV	EK
pyr-4	DFC90	8395(nt)		IIL	SL		RHD
pyr-6	DFC37	2141	2111	VR	SL	NG	DDP

* Pyrimidine-specific CPS positive; ATCase negative

[†] Pyrimidine-specific CPS negative; ATCase positive

[‡] Pyrimidine-specific CPS negative; ATCase negative

PYRIMIDINE TRANSPORT see *uc-5*

PYRIMIDINE NUCLEOSIDE TRANSPORT see *ud-1*

QUINATE CATABOLISM

Locus	Allele	FGSC number mating type A	a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
qa-1F;aro-9	A4-18A;Y325M6	1747		VIIR;IIR	SL	UV	MEC
qa-1S qa-1F^{+}*;aro-9*	326-140;M6-11	5942		VIIR;IIR	SL	UV	MEC
qa-1S qa-1F^{+}*;aro-9*	326-105(t);M6-11	5943		VIIR;IIR	SL	UV	MEC
qa-1S qa-1F^{+}*;aro-9*	326-141;M6-11	6899		VIIR;IIR	SL	UV	MEC
qa-1S qa-1F^{+}*;aro-9*	326-105(t);M6-11	6900		VIIR;IIR	SL	UV	MEC
qa-1S qa-1F^{+}*;aro-9*	326-124;M6-11	6901		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-158;M6-11	5944		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-129;M6-11	6902		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-191(t);M6-11	6903		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-128;M6-11	6904		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-137;M6-11	6905		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-120;M6-11		6906	VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-181;M6-11	6907		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-189(t);M6-11	6908		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-108;M6-11	6909		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-177;M6-11	6910		VIIR;IIR	SL	UV	MEC
qa-1S^{+} *qa-1F;aro-9*	326-188(t);M6-11	6911		VIIR;IIR	SL	UV	MEC
qa-1S^{C} *qa-1F*$^{+}$*;aro-9*	105R12-1.5	5945		VIIR;IIR	SL	UV	MEC
qa-1S^{C} *qa-1F*$^{+}$	A1-1.4	5946		VIIR	SL	UV	MEC
qa-1S^{C} *qa-1F*$^{+}$	E2-3	6896		VIIR	SL	UV	MEC
qa-1S^{C} *qa-1F*$^{+}$	E1.1		6897	VIIR	SL	UV	MEC
qa-1S^{C} *qa-1F*$^{+}$	E4-3	6898		VIIR	SL	UV	MEC
qa-1F	KO	11035	11034	VII	SL	KO	GP
qa-2;pan-2	204;B23	3230		VIIR;VIR	SL		MEC

QUINATE CATABOLISM, continued from previous page

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
qa-2;pan-2	239;B36		3231	VIIR;VIR	SL		MEC
qa-2;aro-9	326M237;Y325M6	2718		VIIR;IIR	SL		MEC
qa-2;aro-9	M246;Y325M6	3957	3958	VIIR;IIR	SL		DDP
qa-3	Y330M16	2719		VIIR	M	UV	MEC
qa-4	Y330M18	2720		VIIR	M	UV	MEC

QUELLING DEFECTIVE

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
qde-1	qde-1^{UV}	9526	9527	VII		UC	RLM
qde-1::Bml^{R}; Sad-1$^{\Delta\text{::hygR}}$; fl		9528		VII; IL			RLM
qde-2::Bml^{R}; Sad-1$^{\Delta\text{::hygR}}$		9530		VI;I			RLM
qde-3::Bml^{R}, Sad-1$^{\Delta\text{::hygR}}$; fl			9535	IE, IL; IIR			RLM
qde-3::Bml^{R}, Sad-1$^{\Delta\text{::hygR}}$; fl		9534		IR, IL; IIR			RLM
qde-3::Bml^{R}, Sad-1$^{\Delta\text{::hygR}}$			9533	IR, IL			RLM
qde-3::Bml^{R}, Sad-1$^{\Delta\text{::hygR}}$		9532		IR, IL			RLM
qde-2::Bml^{R}; Sad-1$^{\Delta\text{::hygR}}$			9531	VII;I			RLM
qde-1::Bml^{R}; Sad-1$^{\Delta\text{::hygR}}$; fl			9529	VII;IL			RLM
qde-1++			9521				JAK
qde-1	KO	11157	11156	VII	SL	KO	GP

ROUND SPORE

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
R	35408	4022	4023	IR	SL7	UV	EK

RESPIRATORY DEFECTIVE [*rsp*] see Part III.

REGULATOR OF CONIDIATION

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
rco-1	CH119		9511				DJE
rco-1 con-10::lacZ::his-3 CH119			9510				DJE
rco-1	KO	11371	11372		SL	KO	GP
rco-3; fl	CH119		9509	I; II			DJE

RECOMBINATION AFFECTORS

rec-1 Dominant allele (*rec-1*$^{+}$) reduces allelic recombination at *his-1* and *nit-2*.Also called *rec-z.*

rec-2 Dominant allele (*rec-2*$^{+}$) reduces crossover between *pyr-3 his-5;h-3* and *ad-3;arg-3* and *sn*; also allelic recombination at *his-3*. Also called *rec-w,rec-4,rec-5*.

rec-3 Dominant allele (*rec-3*$^{+}$) reduces crossover between *sn* and *his-2* and allelic recombination at *am* and *his-2*. Allele *rec-3*^{L} differs from *rec-3*$^{+}$ by a reduced effect on allelic recobination at *am*. Also called *rec-x*

cog (recognition) allele *cog*$^{+}$ is a dominant promoter of recombination in the *his-3* - *ad-3* region, with predominant conversion in the *cog*$^{+}$ strand.

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
rec-1;rec-3; *cot-1;am his-1*	no#;no# C102(t);K314 K83		1567	VR;IL; IVR;VR R			DGC
rec-1;rec-3^{+}*;* *cot-1;his-1 inl*	no#;no# C102(t);K651 37401	1568		VR;IL; IVR;VR R			DGC
rec-1^{+}*;rec-3;cot-1;am*	no#;no#;C102(t);47305	1571		VR;IL;IVR;VR			DGC
rec-1^{+}*;rec-3*$^{+}$*;cot-1;am*	no#;no#;C102(t);47305	1570		VR;IL;IVR;VR			DGC
rec-1^{+}*;rec-3*$^{+}$*;* *cot-1;his-1 inl*	no#;no# C102(t);K651 37401	1569		VR;IL; IVR;VR R			DGC
rec-2;cog; *cot-1;arg-1 his-3*	no#;no#; C102(t);K166 K504	2570	2571	VR;IR; IVR;IR R			DGC
rec-2;cog; *cot-1;his-3 ad-3*	no#;no#; C102(t);K504 K118	2569	2566	VR;IR; IVR;IR R			DGC
rec-2;cog; *cot-1;his-3 ad-3*	no#;no#; C102(t);K874 K118	2565		VR;IR; IVR;IR R			DGC
rec-2;cog^{+} *cot-1;arg-1 his-3*	no#;Y8743cg; C102(t);K166 K26	2568		VR;IR IVR;IL R			DGC
rec-2;cog^{+} *cot-1;arg-1 his-3*	no#;Y8743cg; C102(t);K166 K874	2573	2574	VR;IR IVR;IL R			DGC

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
RECOMBINATION AFFECTORS , continued from previous page							
rec-2;cog^{+}*;cot-1;arg-1 T(I;VII)TM429 his-3*	no#;Y8743cg;C102(t);K166; TM429		2563	VR;IR;IVR;IL			DGC
rec-2;cog^{+} *cot-1;his-3 ad-3*	no#;Y8743cg; C102(t);K26 K118		2567	VR;IR IVR;IR R			DGC
rec-2;cog^{+}*;cot-1;his-3*	no#;Y8743cg;C102(t);K874		2564	VR;IR;IVR;IR R			DGC
rec-2;cog^{+}*;cot-1; his-3;am*	no#;Y8743cg;C102(t); K874;K314		2572	VR;IR;IVR; IR;VR			DGC
RAGGED							
rg-1	B187		287	IR	SL3	UV	DDP
rg-1	B53	296	4517	IR	SL/SL6	UV	DDP
rg-1	R2357	101	1219	IR	M/SL2	S	DDP
rg-2	no# (from *N. sitophila*)	4238	4239	IR	SL3		DDP
RIBOFLAVIN							
rib-1	51602(t)	4101	4102	VIR	SL7	UV	EK
rib-1;al	C107;--		1225	VIR;IR			WSM
rib-1	K28(t)	659	4350	VIR	M	S	MJM/ELT
rib-2	Y30539r	1873	83	IVR	M	M	DDP
rib(76R5)	76R5		1226	VI	M	UV	WSM
RIP DEFECTIVE							
rid-1 his-3	RIP1	9014		I IR			EUS
rid-1 his-3	RIP4		9015	I IR			EUS
rid-1 his-3^{+}*::Pccg-1-Bml*$^{+}$*-sgfp*$^{+}$	RIP1	9520					MHF
rid-1 his-3^{+}*::Pccg-1-hH1*$^{+}$*-sgfp*$^{+}$	RIP4		9517				MHF
rid-1 his-3^{+}*::Pccg-1-Bml*$^{+}$*-sgfp*$^{+}$	RIP4		9519				MHF
rid-1		9994	9995				DDP
rid-1; *In(IIR)UCLA191 eas*		9996	9997				DDP
RIBOSOME PRODUCTION DEFECTIVE							
rip-1	4M(t)	4041	4042	IIR	SL5		EK
ROPY							
ro-1	B15	4352	146	IVR			ELT/DDP
ro-1	B4	110	4351	IVR	SL3	UV	DDP/ELT
ro-2	B20	52	44	IIIR	SL3	UV	DDP
ro-3	R2354	3	43	IIL	L	UV	DDP
ro-3	R2354	2372		IIL	M	UV	ELT
ro-4	B38	2980	2981	VR	SL	UV	DDP
ro-4 (=ro-5)	R2428		1529	VR	M	UV	DDP
ro-4 inl	R2428 89601	1356		VR VR	M	UV	ELT
ro-4 (=ro-8)	R2520	1511	1379	VR	M	UV	DDP
ro-6	R2431	3626	3627	IR	SL3	UV	DDP
ro-7	P997	3321	3322	IIL	SL	S	DDP
ro-7	R2470	4024	4025	IIL	SL5	UV	EK
ro-9 see *da*							
ro-10	AR7	3618	3619	IL	M	UV	DDP
ro-11	P3053	7127	7128	IIIR	SL	RIP	DDP
ro-11	KO	11947	11946	III	SL	KO	GP
ro(P904)	P904	4355	1669	V			ELT/DDP
ro(P1798)	P1798	3910	3911	IR	M	S	DDP
ROPY-LIKE							
rol-1	B31	4353	1360	IVR	SL	UV	ELT
rol-2	R2459	3715	3716	VII	SL2	UV	DDP
rol-3 inl	R2498 89601	1354		VR R	M	UV	ELT

Locus	Allele	FGSC number mating type A	 a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
RUG							
rug (was *mat*)	B57	294	293	IVR	SL	UV	DDP
RESISTANT TO SPORE-KILLER							
r(Sk-2)-1	P527	7153		IIIL	M	S	DDP
r(Sk-2)	P112 (*N. intermedia*)	1832	1833		M	S	DDP
r(Sk-3)	P		7395	III			DDP
r(Sk-3)	P64 (*N. intermedia*)	1786			M	S	DDP
ROSY see *al-3*^{ros}							
SUPPRESSOR OF ASCUS-DOMINANT MUTANTS							
sad-1^{uv}			8737	I	OR	UV	RLM
sad-1$^{\Delta}$::hyg^{r}		8740	8741	I	OR		RLM
sad-1	KO	11152	11151	I	SL	KO	GP
SATELLITE-LESS							
sat	no#	944	945	VL			DDP
SCUMBO							
sc	5801	49	115	IIIR	M	X	DDP
sc	R2386	1377		IIIR	M	UV	ELT
sc (=col-14)	R2503	5075	5076	IIIR	M	UV	ELT
SULFUR CONTROL							
scon-1	scon^{C}		2142	VR	SL	UV	RLM
scon-2	PSD272	7452	7451	IIIR	SL	UV	RLM
SPREADING COLONIAL-TEMPERATURE SENSITIVE							
scot	P7806(t)	3265	3266	VR	M	S	DDP
SCRUFFY							
scr	24-013(t)	2317	3864	IIR	M	DS	AMS/DDP
SERINE							
ser-1	C127	3305	3306	IIIR	M	UV	DDP
ser-1	H605	116	118	IIIR	M	X	DDP
ser-2	65004	2169	2170	VR	SL2	UV	DDP
ser-3	47903	1213	1221	IL	SL2	UV	DNP
ser-3	UK3-23	8106		IL	M		DDP
ser-4	DW110	1756		IVR	SL	UV	JBM
ser-5	JBM9		2686	IIIR	M	UV	JBM
ser-6	DK42	3821	3822	VIL	O		DDP
T(V;VI)OY325 ser-6	OY325	3737	3738	VL;VIL	SL	UV	DDP
SLOW-FINE HYPHAE							
sf	C170sf	3732	1432	IL	SL2/M	S	DDP/MBM
SULFONAMIDE DEPENDENT							
sfo	E15172(d)	651	652	VIIC	M		MJM
sfo nt	E18829(d) 65001	576		VIIC	M		MJM
sfo	E18829(d)		506	VIIC	M		RWB
SHALLOW							
sh	R2371	88	13	VC	M/O	UV	DDP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
SHAGGY							
shg	KH160	3923	3924	IIIR	SL2	S	DDP
SIDEROPHORE TRANSPORT							
sit-1	GN140	4211	4212	--	M	UV	GWC
sit-2	GN328	4213	4214	--	M	UV	GWC
sit-3	GN235	4215	4216	--	M	UV	GWC
sit-4	GN435	4217		--	M	UV	GWC
sit-5;ota	GN218;UM78		4218	--;IIIR	M	UV	GWC
SKIN							
sk	B106	6659	276	VIIR	SL3/SL	UV	DDP
sk	B234	7148	7149	VIIR	SL	X	DDP
(*nic-3 wc-1 sk a+ a^{m1} ad-3B cyh-1*)	Y31881 P829 B234 + m1 2-17-114 KH52		7220	VIIR			FGSC
sk (mo(P1718))	P1718		6679	VIIR	M	S?	DDP
sk (mo-3)	R2466	6703	3823	VIIR		UV?	DDP/ELT
sk (moe-1)	Y6821		1388	VIIR	M/L	MC	DDP/ELT
SLIME							
fz;sg;os-1	no#;no#;B135	1118		--;--;IR	M	UV	SE
fz;sg;os-1	no#;no#;B135	4761		--;--;IR	M	UV	GAS
*fz;sg;os-1**	no#;no#;B135 (A/A)		1119	--;--;IR	M	UV	SE
fz;sg;arg-1 cr-1 al-1 os-1[†]	no#;no#;B369 B123 34508 B135 (A/A)		327	--;--;IL R R R	M	UV	SE
fz;sg;arg-1 cr-1 al-1 os-1 [‡]	no#;no#;B369 B123 34508 B135 (A/a)	2713		--;--;IL R R R	M	UV	REN

* In the heterokaryon (*fz;sg;os-1 A + arg-1 cr-1 al-1 os-1 A*)

[†] In the heterokaryon (*fz;sg;arg-1 cr-1 al-1 os-1 A + al-2 nic-1 lys-3 o1*)

[‡] In the mixed mating type heterokaryon (*fz;sg;arg-1 cr-1 al-1 os-1 A + tol pan-1 a*)

SLOW GROWTH							
slo-1	B149	57	59	IR	SL2	UV	DDP
slo-2	P3007	3940	1533	VII	M	S	DDP
slo-2	no#	2312	1169	VIIC	M	S	ELT/LG
SEMICOLONIAL							
smco-1	Y2330	1363		I	L	M	ELT
smco-3;inl	R2423;89601		1710	I;VR	M	UV	ELT
smco-4	R2435	8245	1367	IVR	M	UV	ELT
smco-5	R2442	8246	1361	I	M	UV	ELT
smco-6	R2477	4530	4531	VR	SL4	UV	DDP
smco-7	R2497	4253	4254	VR	SL	UV	DDP
smco-7, qa-2, aro-9 inl		8340					TM
smco-7	KO		12467	V	SL	KO	GP
smco-8	R2505	8247	1404	IVR	M	UV	ELT
smco-9	R2508	7365	7366	IVR			FGSC
smco-9;inl	R2508;89601		1405	IVR;VR	M	UV	ELT
SNOWFLAKE							
sn	C136	507	947	IC	M	S	RWB
sn	JL301		4338	IC	SL	UV	DDP
sn al-1	JL301 34508	4337		IC IR	SL	UV	DDP
SOFT							
so	B230	508	542	IR	SL3	X	RWB
so	P1490	1507	1506	IR	M	S	DDP
so	KO	11293	11292	I	SL	KO	GP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
SUPEROXIDE DISMUTASE							
sod-1	3C	7437	7438	IL	SL	RIP	DON
sod-1	KO		11215	I	SL	KO	GP
SORBOSE RESISTANT							
sor-1 (sor-A)	1(r)	2374		VIL	M	NA	WK
sor-3 (sor-C)	17(r)	2575		IIIR	SL	NA	WK
sor-4 (dgr-3)	BEX6	4334	4333	IL	SL	UV	BME
sor-4 (sor-DS)	DS(r)	1741		IL	SL2		DNP
sor-4 (dgr-3)	L5	4329	4330	IL	SL	UV	BME
sor-4 (dgr-3)	KHY19		8286	IL			SF
sor-4 (sor(T9))	T9M150(r)	3428	3429	IL	SL		TI
sor-4	CH10-7	9506	9513	I			DJE
sor-5	14(r)	2376		V	SL	NA	WK
sor-6	6(r)	2380	3583	IIIR?	SL	NA	WK/DDP
sor(15)	15(r)	2378		I	SL	NA	WK
SPORE KILLER see Part VI							
SPRAY							
sp	1405		1175	VR	M	UV	RRB
sp	B132	68	70	VR	SL3	UV	DDP
SPREADING COLONIAL							
spco-2 (allelic with *wa*)							
spco-3 (allelic with *spco-7*)							
spco-4	R2367	2233	1372	VIIL	M	UV	DDP/ELT
spco-5;inl	R2450;89601		1374*	VII;VR	M	UV	ELT
spco-6	R2456	4381	4382	VIIL	SL2	UV	DDP
spco-6	R2456	7766	7767	VIIL	SL3	UV	FGSC
spco-7	R2365	3195	3196	VIC	L	UV	DDP
spco-7	R2457		1392*	VIC	M	UV	ELT
spco-8;inl	R2462;89601		1383	IV;VR	M	UV	ELT
spco-9	R2480		1382*	VR	M	UV	ELT
spco-9 inl	R2480 89601	4366		VR R	M	UV	ELT
spco-10	R2488		1384	VR	M	UV	ELT
spco-11	R2502s	4383	4384	IL	SL2		DDP
spco-12	R2510	6946	6947	IL	SL2	UV	FGSC
spco-13;inl	R2530s;89601		1351	VI;VR	M	UV	ELT
spco(R2537)	R2537	2389		--	M	S	DDP

* Heterokaryon compatibility type C D E

SPERMIDINE							
spe-1	462JM	3323	3324	VR	SL	UV	KJM
spe-1 inl	462JM 89601	4265	4266	VR R	M		RHD
spe-1	521KW	3325	3326	VR	M	UV	KJM
spe-1	TP-138	4268	4277	VR	SL	UV	RHD
spe-1; aga	LV10; UM906		8386	VR; VIIR	SL		RHD
his-3; aga; spe-1::hph	Y155M261; UM906; spe-1::hph		8388	I; VII; V	SL	D	RHD
spe-2;aga	JP100;UM906	7040	7041	VR;VIIR	M	UV	RHD
spe-3;aga	LV105;UM906	7042	7043	VR;VIIR	M	UV	RHD

A variety of strains carrying *spe-1* constructs described in Hoyt *et al.*, Mol Cell Biol. 20:2760-2773 are available from the FGSC, as are a selection of spe mutants.

SPONGE							
spg	no#	6016	6017	III	SL3	S	DDP

		FGSC number mating type			Genetic		
Locus	Allele	A	a	Linkage group	back- ground	Muta- gen	Obtained from
SUPERSUPPRESSOR							
ssu-1;am	WRN33;am$_1$7	1687	1688	VIIR;VR		NA	TWS
ssu-1;nit-2;inl	WRN33;KGP0220;37401	6029		VIIR;IL;VR		UV	GAM
ssu-1;nit-3;inl	WRN33;KGP1211;37401	6023		VIIR;IVR;VR		UV	GAM
ssu-1;nit-3;inl	WRN33;KGP1222;37401	6030		VIIR;IVR;VR		UV	GAM
ssu-1(?)	Y319-44		1750	VIIR	SL	UV	MEC
ssu-2;am;al	WRU35;am$_{17}$;no#	1689		IR;VR;--		UV	TWS
ssu-3 am	WRU118 am$_{17}$		1851	IL;VR	M	UV	TWS
ssu-4 am	WRU18 am$_{17}$	1852		VIIC;VR	M	UV	TWS
ssu-5	Y319-45		1751	(III or IV)	SL	UV	MEC
*ssu-5**	Y319-45		2481	--			AJG
*ad-3B**	2-17-34		2485	IR			AJG
+ (wild type)*		2479					AJG
*ssu-5;ad-3B**	Y319-45;2-17-34	2483		--;IR			AJG
* Related stocks from the same tetrad							
ssu-6	Y319-26	1748		VR	SL	UV	MEC
ssu-8	Y319-37		1749	IR	SL	UV	MEC
ssu-8;ad-3B al-2; pan-2	Y319-37;12-21-22 Y112M38; Y153M96		2487	IR;R R;VIR	M	HA	AJG
ssu-8;ad-3B al-2; pan-2	Y319-37;12-21-76 Y112M38; Y153M96		2488	IR;R R;VIR	M	HA	AJG
ssu-9;am	WRU98;am$_{17}$		7584	--;VR	M	UV	MEC
ssu-10;am	WRU121(?);am$_{17}$		7574	--:VR	M		MEC
STICKY							
st	B128	50	35	IR	M	UV	DDP
STOPPER [*stp*] see Part IV							
SUPPRESSOR OF arg-6							
arg-1, al-2, sup-6	CD145, 15300, CAL-8	8918	8917	IR,L,L			RHD
SUPPRESSOR OF *bal*							
su(bal)	B	3486		I	M	S	SB
SUPPRESSOR OF COLONIAL-2							
su(col-2)	C	3482		IL	M	S	SB
SUPPRESSOR OF ISOLEUCINE							
su(ile-1);ile-1	no#;UK71-26	5886		V;VII	M	UV	JAK
SUPPRESSOR OF METHIONINE							
su(met-2)	no#		690	--	M	S	BSS
su(met-2);met-2	no#;H98		689	--;IVR	M	S	BSS
su(met-7) al-2	S1 15300		39	IR R	M		DDP
SUPPRESSOR OF [*mi-1*]							
su([mi-1])-f;[poky]	no#	385	386	VR;--	M	S	MBM
SUPPRESSOR OF [*mi-3*]							
su([mi-3])-1;[mi-3]		2472		IR;--	M	S	HB
SUPPRESSOR OF *mtr*							
su(mtr);fpr-3	18;no#	2999		IC;IIIR			JAK
su(mtr);mtr	21-2;21(r)	1718		IR;IVR	M	UV	DRS
su(mtr);mtr col-4	21-2;10(r) 70007c	1719		IC;IVR R	M	UV	DRS
su(mtr$_{26}$);mtr; his-2;pdx-1	26-R5035;26(r); Y152M43;37803	2732		VI;IVR; IR;IVR	M	NA	NGB

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
SUPPRESSOR OF *mtr*, continued from previous page							
su(mtr$_{26}$);mtr; *his-2;pdx-1*	26-R5037;26(r); Y152M43;37803	2733		VI;IVR; IR;IVR	M	NA	NGB
SUPPRESSOR OF *suc*							
su(suc)-1, suc, inl	su(163R2),KG163,89601		7783	-,IL,VR		UV	HK
su(suc)(R1), suc, inl	su(163R1),KG163,89601		7782	-,IL,VR		UV	HK
su(suc)(R4), suc, inl	su(163R4),KG163,89601		7784	IL,IL,VR		UV	HK
su(suc)(R6), suc, inl	su(163R6),KG163,89601		7785	IL,IL,VR		UV	HK
su(suc)-1	su(163R2)	7786				UV	HK
SUPPRESSOR OF *trp-3*							
su(trp-3^{td1})-1;trp-3	su$_{1-1}$;td1	5444		--;IIR			FJD
su(trp-3^{td2})-2;trp-3	su$_{2}$;S1952(td2)	6136		III;IIR			ELT
su(trp-3^{td201})-1;trp-3	su$_{201-1}$;td201		1618	VIIR;IIR	M	UV	SRS
su(trp-3^{td201})-1;trp-3	su$_{201-4}$;td201	1619		VIIR;IIR	M	UV	SRS
su(trp-3^{td201})-1;trp-3	su$_{201-6}$;td201	1620		VIIR;IIR	M	UV	SRS
su(trp-3^{td201})-1;trp-3	su$_{201-7}$;td201	1621		VIIR;IIR	M	UV	SRS
SUPPRESSOR OF *trp-5*							
su(trp-5);trp-5	77;A420		7575	VIL;VR	M	UV	JAK
SUPPRESSOR OF *ure-1*							
su(ure-1);ure-1 his-1	no#9;9 C91	4300		--;VR R			HGK
su(ure-1);ure-2 am	no#9;47 32213(am1)	4301		--;VR R			HGK
SUCCINATE							
suc	35402		655	IL	M	UV	MJM
suc	37807		759	IL	M	UV	DGC
suc	39311	1248	1249	IL	SL5	UV	DDP
suc	46005	1110	1111	IL	SL2	UV	KDM
suc	47807		656	IL	M	UV	MJM
suc	55901		762	IL	M	UV	DGC
suc	66702	1214	377	IL	SL2/M	UV	DNP/MBM
suc	KG163	3004		IL	M	NG	HK
suc	NM121		2441	IL	M	UV	DDP
SULFUR METABOLISM CONTROL see *scon*							
SUPERSUPPRESSOR see *ssu*							
TYROSINASE STRUCTURAL GENE							
T^{L}	4-137		320	IR	M	S	NHH
T^{S}	4-121	321		IR	M	S	NHH
T^{S}	69-1113		2963	IR	M		JFF
T	T^{PR}	1326		IR	M	S	NHH
al-2; aro-9; inv; qa-2; ccg-1:T::hph	GTH16		10006	I; II; V; VII			SF
TUFTED AERIAL							
ta	D317	1524	1525	IL	SL3	UV	DDP
TAD							
Tad Hyg^{r}			8609				JAK
TRYPTOPHAN SYNTHASE DEFECTIVE *td* see *trp-3*							

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
THIAMINE							
thi-1	56501	4010	4011	IR	SL9	X	EK
T(I;VII)17084 thi-1	17084	216	215	IR;VIIL			DDP
thi-2	9185	5906	5907	IIIR	SL	X	DDP
thi-2	9185	1222	1223	IIIR	M	X	DGC
thi-3	18558	4083	4084	VIIC	SL7	X	EK
thi-3	UT305	3824	3825	VIIL	M	UV	DDP
thi-4	85902	55	3941	IIIC	M	M	DDP
thi-5	50005	2171	375	IVR	M	UV	DDP
thi-lo;thi-1	no#;56501	934		IIIC;IR	M	S	BME
THREONINE							
thr-2	35423	2	40	IIL	L/M	UV	DDP
thr-3	44104(t)	24	12	IIL	SL/M	UV	DDP
thr-3	T42M59(t)	2294	2291	IIL	M	UV	DDP
thr(4V);inl	4V(t);89601		3763	--;VR	M	UV	DRS
thr(38E);inl	38E(t);89601		3760	II;VR	M	UV	DRS
thr(72C);inl	72C(t);89601		3758	II;VR	M	UV	DRS
TINY							
ti	B233(t)	309	310	IC	SL3	X	DDP
TANGERINE							
tng	P4474	3921	3922	IIL	SL2	S	DDP
TENUOUS							
tns	P4394	8281	8282	VIIR	M		DDP
TOLERANT							
tol	CZ30.7	3453		IVR	M	S	DDP
tol	N43	3452		IVR	M	S	DDP
tol	N83	2338	1946	IVR	S		DDP/DNP
tol	KO	11891	11890	IV	SL	KO	GP
TRANSPORT SYSTEMS see *bas,can,car,fpr,hlp,hgu,mod-5,mtr,nap,pm,pmg,pmn,uc,ud,trk*							
TREHALASE							
tre^{int}*;inl*	19-31;89601	4507		--;VR	M	NG	MLS
tre^{int}*;inl*	31-601;89601	4508		--;VR	M	NG	MLS
tre;inl	39-10;89601	4510		IR;VR	M	NG	MLS
tre;inl	39-21;89601	4511		IR;VR	M	NG	MLS
tre;inl	39-25;89601	4512		IR;VR	M	NG	MLS
tre;inl	39-30;89601	4513		IR;VR	M	NG	MLS
tre;inl	39-3;89601	4509		IR;VR	M	NG	MLS
tre;inl (mig^{f}*)*	no#;89601	497	498	IR;VR	M	M	RWB
tre (mig^{s}*)*	--	4514		IR			MLS
TRANSPORT OF POTASSIUM							
trk	R2449	1953	1954	IIIR	M	UV	CWS
TRYPTOPHAN							
trp-1	8	2038	2039	IIIR	M		JAD
trp-1	15	1848		IIIR	SL	UV	JHC
trp-1;am	15;am$_{17}$		1847	IIIR;VR	SL	UV	JHC
trp-1	20	2040	2041	IIIR	M	UV	JAD
trp-1	25	2042	2043	IIIR	M	NA	JAD
trp-1	28	2044	2045	IIIR	M	NA	JAD
trp-1	30	2046	2047	IIIR	M	NA	JAD

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
TRYPTOPHAN, continued from previous page							
trp-1	10575	4049	4050	IIIR	SL6	X	EK
trp-1	A9		1146	IIIR	M	UV	DGC
trp-1	A10		694	IIIR	M	UV	DGC
trp-1	A28		695	IIIR	M	UV	DGC
trp-1	A38		1148	IIIR	M	UV	DGC
trp-1	A50		1149	IIIR	M	UV	DGC
trp-1	A62		1150	IIIR	M	UV	DGC
trp-1	A63		1457	IIIR	E	UV	DGC
trp-1	A94		696	IIIR	M	UV	DGC
trp-1	C1	2048	2049	IIIR	M	UV	JAD
trp-1	C2	2050	2051	IIIR	M	UV	JAD
trp-1	K1032		1456	IIIR	M	UV	DGC
trp-1	K1442		1152	IIIR	M	UV	DGC
trp-2	10	1850		VIR	SL	UV	JHC
trp-2	41	4109	4110	VIR	SL6	NA	EK
trp-2	40008	758		VIR	M	UV	DGC
trp-2	45302	135	134	VIR	M	UV	DDP
trp-2	66110		4362	VIR	O	UV	ELT
trp-2	75001	4107	4108	VIR	SL6	N	EK
trp-2	S4266	990	4364	VIR	M	UV	LG
trp-2	TB31	1846		VIR	M	UV	JHC
trp-3	A16		697	IIR	M	UV	DGC
trp-3	A18		698	IIR	M	UV	DGC
trp-3	A20		1147	IIR	E	UV	DGC
trp-3	A42		699	IIR	M	UV	DGC
trp-3	A72		700	IIR	M	UV	DGC
trp-3	A73		701	IIR	M	UV	DGC
trp-3	A78		702	IIR	M	UV	DGC
trp-3	A78(tdA78 or td201)	860		IIR	M	UV	AML
trp-3	A78-101*	1026	1027	IIR	SL	UV	DMB
trp-3	A78-109*	1028	1029	IIR	SL	UV	DMB
trp-3	A78-110*	1030	1031	IIR	SL	UV	DMB
trp-3	A78-137*	1033	1032	IIR	SL	UV	DMB
trp-3	A78-149*	1035	1034	IIR	SL	UV	DMB
trp-3	A78-174*		1036	IIR	SL	UV	DMB
trp-3	C83	73	862	IIR	M/SL2	UV	DDP/AML
trp-3	S1952(td2)	861		IIR	SL2	MDAB	AML
trp-3	td3	854		IIR	SL3	UV	AML
trp-3	td6	858		IIR	SL3	UV	AML
trp-3	td7	857		IIR	SL2	UV	AML
trp-3	td16	855		IIR	SL	UV	AML
trp-3	td24	856	2070	IIR	SL2	UV	AML/DDP
trp-3	td37	4038	4039	IIR	SL7	X	EK
trp-3	td38	3535		IIR	SL	X	DDP
trp-3	td48[†]	1002		IIR	SL	UV	DMB
trp-3	td7	859		IIR	SL	X	AML
trp-3	td96		1003	IIR	SL	UV	DMB
trp-3	td97	1005	1004	IIR	SL	UV	DMB
trp-3	td100	1009	1008	IIR	SL	UV	DMB
trp-3	td101	1010 [‡]	1011	IIR	SL	UV	DMB
trp-3	td102	1013	1012	IIR	SL	UV	DMB
trp-3	td104	1014		IIR	SL	UV	DMB
trp-3	td120	1015	1016	IIR	SL	UV	DMB
trp-3	td128		1017	IIR	SL	UV	DMB
trp-3	td131		3536	IIR	SL		DDP
trp-3	td132[†]	1020		IIR	SL	UV	DMB
trp-3	td133	3537		IIR	SL	UV	DDP

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
TRYPTOPHAN, continued from previous page							
trp-3	td133		1021	IIR	SL	UV	DMB
trp-3	td138		1022	IIR	SL	UV	DMB
trp-3	td139	1023		IIR	SL	UV	DMB
trp-3	td140	3538		IIR	SL	UV	DDP
trp-3	td141		1025	IIR	SL	UV	DMB
trp-4	Y2198	4059	4060	IVR	SL6	M	EK
trp-5	A420	2332	2333	VR	M	UV	DDP

* Intragenic double mutant responding to tryptophan

† Contains intragenic suppressor resulting in partial reversion (derived strains use indole)

‡ Contains separable aberration. The FGSC has received numerous *trp-3* isolates from AML. Please inquire if you are interested.

TAN SPORE							
ts	no#	821		VR	M	S	KN
ts	m122		9355	VR			DK
TYROSINASE REGULATORY GENE							
ty-1	913-83	322		IIIR	M	S	NHH
ty-2	913-17		1194	IR			NHH
ty-3	T22	4878		IIIR			HCC
ty-3;ty-4;ff-3	T22;no#;HC725	4877		IIIR;--;IR	M		HCC
TYROSINE							
tyr-1(?)	C167		3258	IIIR			RLM
tyr-1	T145	874		IIIR		UV	AGD
tyr-1	Y6994	2259	2260	IIIR	SL2	M	DDP
tyr-1	acc^{phe}		3045	IIIR	SL	UV	AGD
tyr-2	STL1	36	25	IR	M	S	DDP
TYROSINE SENSITIVE							
tys	LW101(s)	2735		IL	M	UV	GAM
TYROSINASE STRUCTURAL GENE see *T*							
URACIL SALVAGE							
uc-1 pyr-4;uc-2	RW57 36601;RW135	2203		II L;I	M	UV	LGW
uc-1 pyr-4;uc-3	RW57 36601;RW203		2204	II L;--	M	UV	LGW
uc-2	RW135		2197	I	M	UV	LGW
uc-3	RW203		2198	--	M	UV	LGW
uc-4	RW341	2200	2199	VR	M	UV	LGW
PYRIMIDINE TRANSPORT							
uc-5 pyr-1	RW399 H263		2201	IVR R	SL	UV	LGW
PYRIMIDINE NUCLEOSIDE TRANSPORT							
ud-1;pyr-1	RW433;H263		2202	VIIR;IVR	SL	UV	LGW
URIDINE KINASE							
udk uc-4	FB-D425 RW341	4284	4285	VR R	SL	UV	FPB
UNSATURATED FATTY ACIDS							
ufa(P73B118)	P73B118	4440	4441	IVR	M	EMS	DDP
(ufa(P73B118)A + *a^{m1} ad-3B cyh-1)*	P73B118 + 1 2-17-114 KH52	4442	4443	IVR+IL R R		DDP	
ufa-3		7621		-	SL	γ	MT
ufa-4		7622		-	SL	γ	MT
ULTRAVIOLET PHOTOREACTIVATION see *upr*							

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
ULTRAVIOLET SENSITIVE see *uvs*							
UNKNOWN FUNCTION (Temperature sensitive lethal)							
un-1	44409(t)	6883	3942	IR	SL4	UV	DDP
un-1	KO		11164	I	SL	KO	GP
un-2	46006(t)	1956	931	IC	SL3/M	UV	DDP/MBM
un-2	ALS9(t)	2129	2130	IC	M		DDP
un-3	55701(t)	636	4529	IL	SL3/SL4	X	DNP/DDP
un-4	66204(t)	131	2172	VIL	M	UV	DDP
un-5	b39(t)	4000	4001	IL	SL6	M	EK
un-6	83106(t)	1328	1329	IIIR	M	X	DDP
un-7	T53M50(t)	2175	2176	IR	SL	UV	DDP
un-8	T27M9(t)	2173	2174	IVR	SL	UV	DDP
un-9	T54M96(t)	2339	2340	VR	SL	UV	DDP
un-10	T42M45(t)	2341	2342	VIIR	SL	UV	DDP
un-11	T42M30(t)	2343	2344	VR	M	UV	DDP
un-12	T51M118(t)	2345	2921	IVR	M	X	DDP
un-13	T42M24(t)	2346	2347	VIL	M	UV	DDP
un-14	T54M55(t)	2348	2349	IIIR	SL	UV	DDP
un-15	T54M50(t)	4040	2391	IIR	SL5/M	UV	EK/DDP
un-16	T42M38(t)	4306		IL	SL	UV	DDP
un-16	T42M69(t)	2392		IL	M	UV	DDP
un-16 acr-3	T42M69(t) KH14(r)		4303	IL L	SL		DDP
un-17	T51M171(t)	2356	2357	IIIR	SL	X	DDP
un-18	T54M94(t)	4020	4021	IR	SL6	UV	EK
un-19	P73B138(t)	2586	2587	VR	M	EMS	DDP
un-20	P2402(t)	3006	3007	IIR	M	S	DDP
un-21	T53M26(t)	3307	3320	IIIR	SL2		DDP
un-22	61C(t)	4323	4324	VII	SL	UV	DDP
un-22;inl	62C(t);89601		3786	VIIR;VR	M	UV	DRS
un-23	64D(t)	3926	3927	VIR	M	UV	DDP
un-24 het-6OR	DJ517 OR	7354		IIL L	SL	RIP	DJJ
un(6B);inl	6B(t);89601		3766	I;VR	M	UV	DRS
un(6T);inl	6T(t);89601		3781	IR;VR	M	UV	DRS
un(16J) inl	16J(t) 89601		3777	VR R	M	UV	DRS
un(19D);inl	19D(t);89601		3784	I;VR	M	UV	DRS
un(20J) inl	20J(t) 89601		3778	V VR	M	UV	DRS
un(21T) inl	21T(t) 89601		3782	V VR	M	UV	DRS
un(23M);inl	23M(t);89601		3779	--;VR	M	UV	DRS
un(58E) inl	58E(t) 89601		3775	V(?) VR	M	UV	DRS
un(74E);inl	74E(t);89601		3776	IV(?);VR	M	UV	DRS
un(74M);inl	74M(t);89601		3780	--;VR	M	UV	DRS
un(120C);inl	120C(t);89601		3768	IR;VR	M	UV	DRS
un(121C) inl	121C(t) 89601		3769	VR R	M	UV	DRS
un(134C) inl	134C(t) 89601		3770	VR R	M	UV	DRS
un(145C);inl	145C(t);89601		3783	I;VR	M	UV	DRS
un(151C);inl	151C(t);89601		3771	IL;VR	M	UV	DRS
un(165C) inl	165C(t) 89601		3772	VR R	M	UV	DRS
un(181C) inl	181C(t) 89601		3787	VR R	M	UV	DRS
un(209C);inl	209C(t);89601		3773	IL;VR	M	UV	DRS
un(71103) see *ilv(71103)*							
un(OY351)	OY351(t)	4316					DDP
un(P73G14)	P73G14(t)	4310		IR	SL	EMS	DDP
un(P8319)	P8319(t)	3849		IVR	M		DDP
un(STL6) see *fls*							
un(T28M15)	T28M15(t)	4304		I	SL	UV	DDP
un(T33M8)	T33M8(t)	4311			SL		DDP
un(T42M34)	T42M34(t)	4305			SL	UV	DDP

		FGSC number mating type			Genetic back-ground		
Locus	Allele	A	a	Linkage group		Muta-gen	Obtained from
UNKNOWN, continued from previous page							
un(T42M36)	T42M36(t)	4312			SL		DDP
un(T42M39)	T42M39(t)		4307		SL	UV	DDP
un(T42M46)	T42M46(t)	4308			SL		DDP
un(T42M54)	T42M54(t)	4309			SL	UV	DDP
un(T42M56)	T42M56(t)	2352	2353	VI	M	UV	DDP
un(T42M62)	T42M62(t)		4293	--	M	UV	DDP
un(T42M68)	T42M68(t)		4294		M	UV	DDP
un(T42M70)	T42M70(t)	4295			M	UV	DDP
un(T51M154	T51M154(t)	2354	2355	VIL	SL	X	DDP
un(T51M166	T51M166(t)	4313		II	SL	X	DDP
un(T52M23)	T52M23(t)		4296		M	UV	DDP
un(T54M57)	T54M57(t)	4314			SL		DDP
un(T54M58)	T54M58(t)		4297		M	UV	DDP
un(T54M68)	T54M68(t)	4315			SL		DDP
UV PHOTOREACTIVATION							
upr-1;	no#	4171		IL	SL2	M	EK
upr-1; cr-1 rg-1; pe fl; met(331)	no#	1705			M		RWT
upr-1;uvs-1; cr-1 rg-1; *pe fl; met(331)*	no#;no#	1703					RWT
UREASE DEFICIENT							
ure-1	9	1229	1230	VR	M	UV	HGK
ure-1	D1	3805		VR	SL	UV	HBH
ure-1	D2	3806		VR	SL	UV	HBH
ure-1	D3		3807	VR	SL	UV	HBH
ure-1	D23		3808	VR	SL	UV	HBH
ure-2	47	2056	2057	VR	M	UV	HGK
ure-2 am	47 32213		4299	VR R			HGK
ure-2	D74		3809	VR	SL	UV	HBH
ure-2	W2	3816		VR	SL	UV	HBH
ure-3	F29	3733	3734	IIR		UV	HBH
ure-4	601		3801	IR	SL	UV	HBH
ure-4	C21		3803	IR	SL	UV	HBH
ure-4	E12	3812		IR	SL	UV	HBH
ure(A7)	A7	3802		V	SL	UV	HBH
ure(C5)	C5		3804	--	SL	UV	HBH
ure(E3)	E3		3810	--	SL	UV	HBH
ure(E7)	E7	3811		--	SL	UV	HBH
ure(K3)	K3	3813		--	SL	UV	HBH
ure(R2)	R2		3814	--	SL	UV	HBH
ure(S3)	S3		3815	V	SL	UV	HBH
UV SENSITIVE							
uvs-1;cr-1 rg-1; pe fl;met(331)	no#	1630		--		UV	LTC
uvs-2	no#	4172	4173	IVR	SL6	UV	EK
uvs-2	KO	11444	11445	IV	SL	KO	GP
uvs-3	ALS11	4174	4175	IVL	SL8	UV	EK
uvs-3	FK016	4589	4590	IVL	SL8	UV	EK
uvs-3	KO	11167	11668	IV	SL	KO	GP
uvs-4	ALS12	4176	4177	IIIC	SL6	UV	EK
uvs-5	ALS13	2970	2971	IIIR	M	UV	DDP
uvs-6	ALS35	4178	4179	IR	SL6	UV	EK

Locus	Allele	FGSC number mating type A	FGSC number mating type a	Linkage group	Genetic back-ground	Muta-gen	Obtained from
VACUOLAR MEMBRANE ATPase							
(vma-1-RIP am^{132} +pvn-1-121 mat a^{ml} ad-3B cyh-1)		8628	8627	IR		RIP	BB
vma-3	brf-21-E-1	8613		V			BB
vma-3	brf-21-E-2		8614	V			BB
vma-3	brf-33-A-1	8615		V			BB
vma-3	brf-33-A-9		8616	V			BB
vma-3	brf-65-A-7	8617		V			BB
vma-3	brf-65-A-10		8618	V			BB
vma-3	brf-89-A-2		8619	V			BB
vma-3	brf-89-A-3	8620		V			BB
(*vma-13-RIP, his-3 +mat* a^{m1} *ad-3B cyh-1*)	10-5	8621		IR		RIP	BB
(*vma-5-RIP, +mat* a^{m1} *ad-3B cyh-1*)	2	8622				RIP	BB
(*vma-5-RIP, +mat* a^{m1} *ad-3B cyh-1*)	1	8623				RIP	BB
vma-3	bfr-314	8947	8948	V			BB
vma-3	bcr-31	8949	8950	V			BB
vma-3	bcr-69	8951	8952	V			BB
vma-3	bcr-118	8953	8954	V			BB
vma-3	bcr-149		8955	V			BB
vma-3 al-3	bfr-21		8956	V			BB
VACUOLAR PH-SENSITIVE ATPase							
(*vph-1-RIP, +mat* a^{m1} *ad-3B cyh-1*)	rk-1-3		8624			RIP	BB
(*vph-1-RIP, +mat* a^{m1} *ad-3B cyh-1*)	rk-1-1	8625				RIP	BB
VALINE							
val	33026	359	566	V	M	UV	MBM
val	33050	3614	3615	VR	M	UV	DDP
VANADATE RESISTANT see *pho-4*							
VARIANT							
var-1	X10a		2474	--	M	S	HB
VELVET							
vel	B18	2267	2268	IIIR	M	UV	DDP
vel	P1710		1655	IIIR	M	S	DDP
vel;inl	R2471;89601		1389	IIIR;VR	M	UV	ELT
VEGETATIVE INCOMPATIBILITY BLOCKED							
hetC^{OR} *pyr-4; vib-1*		9064					NLG
hetC^{OR} *; vib-1*		9065					NLG
het-c^{PA} *thr-2; vib-1*		9066					NLG
vib-1	KO	11309	11308		SL	KO	GP
VISIBLE							
T(I;III)3317 vis	3717	2682	2683	IR			DDP
VIVID							
vvd	SS-692	7852	7853	VIL	SL	UV	SNB
vvd	P4246	7854	7855	VIL	M		DDP
vvd	KO	11556	11555	VI	SL	KO	GP

Locus	Allele	FGSC number mating type		Linkage group	Genetic background	Mutagen	Obtained from
		A	a				
WASHED							
wa	R2359	6779	6780	VR	SL2	UV	DDP
WHITE COLLAR							
wc-1	ER45	4395	4396	VIIR	SL	UV	VEAR
wc-1	ER53	4397	4398	VIIR	SL	UV	VEAR
wc-1	ER57	4399	4400	VIIR	SL	UV	VEAR
wc-1	MK1	4401	4402	VIIR	SL	UV	VEAR
wc-1	MK2	4403	4404	VIIR	SL	UV	VEAR
wc-1	P4723	4444	4445	VIIR	SL3	S	DDP
wc-1	P829	128	143	VIIR	M	S	DDP
his-3; bd; $wc\text{-}1^{ko}$			9001	IR;IVR; VIIR			KL
wc-1	KO	11712	11711	VII	SL	KO	GP
wc-2	234w	3817	3818	IR	M	O	DDP
wc-2	ER24(t)	4405	4406	IR	SL	UV	VEAR
wc-2	ER33	4407	4408	IR	SL	UV	VEAR
wc-2	ER44(t)	4409	4410	IR	SL	UV	VEAR
wc-2	KO		11124	I	SL	KO	GP
WHITE SPORE							
ws-1	RP99	1434	1435	VIR	SL	DS	RLP
ws-2	NM122		1617	VI	M	UV	DDP
XANTHINE DEHYDROGENASE							
xdh-1	NMR11	2702		II	SL	UV	GAM
xdh-1	NMR27	2703		II	SL	UV	GAM
YELLOW							
ylo-1	P1193	1514		VIL	SL2	S	DDP
ylo-1	Y30539y	4099	4100	VIL	SL7	M	EK
ylo-2	Y256M230	1515		IL	SL	UV	DDP

PART II. Multiple Mutant Stocks

Markers within a linkage group are listed in order:left to right arm, insofar as order is known, and are listed according to map position of the left-most marker.Linkage groups are separated with a semicolon, C = vicinity of centromere; L,R = left and right arms respectively.Stocks having two or more linkage groups marked are presented according to the number of groups that contain markers other than mating type, and are listed in order of linkage group numbers (I;II.I;III.I;IV. etc.)

A. One Linkage Group Marked

Loci	Alleles	FGSC # mating type		Linkage group	Obtained from
		A	a		
Linkage Group I					
ro-10 un-5	AR7 b39(t)	7222	7223	L L	DDP
ro-10 nit-2 leu-3	AR7 nr37 R156	7224	7225	L L L	DDP
ro-10 In(IR;IL)OY323 al-2 arg-13		7481	7482	L R R	DDP
ro-10 al-2 un-18	AR7 15300 T54M94(t)	3789	3790	L R R	DDP
ro-10 un-18	AR7 T54M94(t)	3754	3755	L R	DDP
fr his-2 nic-2 al-2	B110 C94 43002 1-112-38		5302	L R R R	FJD
fr nic-2 al-2	B110 43002 1-112-38		5303	L R R	FJD
fr cr-1 al-1	B110 L 34508	237		L R R	DDP
fr al-1	B110 34508	314	238	LR	DDP
fr al-1 R	B110 ALS4 35408R	2087	2088	L R R	DDP
fr al-1 un-18	B110 ALS4 T54M94	2617	2618	L R R	DDP
un-5 nit-2	b39(t) nr37	7240		L L	DDP
un-5 leu-3 sn cr-1 cyh-1 al-2 nic-1	b39(t) R156 C136 B123 KH52(r) 15300 S1413	5160		L L C R R R R	EK
un-5 leu-3 nic-2 cyh-1	39(t) R156 43002 KH52(r)	4111		L L R R	EK
un-5 leu-3 cr-1 cyh-1 al-2 nic-1	b39(t) R156 B123 KH52(r) 15300 S1413	5219		L L R R R R	EK
un-5 leu-3 cyh-1 al-2 nic-1	b39(t) R156 KH52(r) 15300 S1413	5162	5163	L L R R R	EK
un-5 cyh-1 al-2 nic-1	b39(t) KH52(r) 15300 S1413	5164	5165	L R R R	EK
un-5 al-2 arg-13	b39(t) 15300 RU3	2282	2283	L R R	DDP
un-5 al-1 R	b39(t) ALS4 35408R	2177	2178	L R R	DDP
nit-2 leu-3	KGP0220 R156	6024		L L	GAM
nit-2 leu-3	nr37 R156		7226	L L	DDP
leu-3 arg-1	R156 B369	1210	1216	L L	DNP
leu-3 sn cr-1 cyh-1 al-2 nic-1	R156 C136 B123 KH52(r) 15300 S1413	5161		L C R R R R	EK
leu-3 ad-3B cyh-1	R156 2-17-34 KH52(r)	4147		L R R	EK
leu-3 ad-3B thi-1 cyh-1	R156 2-17-34 56501 KH52(r)	4146		L R R R	EK
leu-3 cr-1	47313 B122	257	247	L R	DDP
leu-3 cyh-1 un-18	R156 KH52(r) T54M49(t)	5159		L R R	EK
leu-3 mus-9	R156 FK129	6405		L R	EK
leu-3 al-2 nic-1 un-18	R156 15300 S1413 T54M49(t)		5158	L R R R	EK
cyt-1 leu-4	C115 R359		7227	L L	DDP
cyt-1 al-2 nic-1	C115 15300 3416		2473	L R R	HB
en(pdx-1) al(G2)	K30 G2		649	L R	MJM
ser-3 un-16 acr-3	47903 T42M69 KH14(r)		5079	L L L	DDP
mat a^{m1} *ad-3B cyh-1*	1 2-17-114 KH52(r)		4564	L R R	AJG
mat a^{m2} *ad-3B cyh-1*	2 2-17-114 KH52(r)		4565	L R R	AJG
mat a^{m5} *ad-3B cyh-1*	5 2-17-114 KH52(r)		4566	L R R	AJG
mat a^{m7} *ad-3B cyh-1*	7 2-17-114 KH52(r)		6840	L R R	DDP
mat a^{m10} *ad-3B cyh-1*	10 2-17-114 KH52(r)		6841	L R R	DDP
mat a^{m12} *ad-3B cyh-1*	12 2-17-114 KH52(r)		6842	L R R	DDP
mat a^{m24} *ad-3B cyh-1*	24 2-17-114 KH52(r)		6843	L R R	DDP

Linkage Group I, continued

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
mat a^{m26} *ad-3B cyh-1*	26 2-17-114 KH52(r)		4567	L R R	AJG
mat a^{m30} *ad-3B*	30 2-17-114		6844	L R R	DDP
mat a^{m33} *arg-3*	m33 30300		5383	L L	DDP
mat a^{m33} *ad-3B*	m33 2-17-128		4568	L R	AJG
mat a^{m1} *cyh-1*	1 KH52(r)		7448	IL R	RLM
mat A^{m42} *un-3 ad-3A nic-2 cyh-1*	42 55701(t) 2-17-814 43002 KH52(r)	4569		L L R R R	AJG
mat A^{m44} *un-3 ad-3A nic-2 cyh-1*	44 55701(t) 2-17-814 43002 KH52(r)	4570		L L R R R	AJG
mat A^{m54} *un-3 ad-3A nic-2 cyh-1*	54 55701(t) 2-17-814 43002 KH52(r)	4571		L L R R R	AJG
mat A^{m56} *un-3 ad-3A nic-2 cyh-1*	56 55701(t) 2-17-814 43002 KH52(r)	4572		L L R R R	AJG
mat A^{m64} *un-3 ad-3A nic-2 cyh-1*	64 55701(t) 2-17-814 43002 KH52(r)	4573		L L R R R	AJG
mat A^{m64} *nic-2 cyh-1*	64 43002 KH52(r)		7449	IL R R	
ta acr-3	D317 KH14(r)	7228		L L	DDP
un-16 acr-3	T42M69(t) KH14(r)		7558	L L	DDP
un-16 acr-3	T42M69(t) KH14(r)		4303	L L	DDP
cy sf	C170c C170sf	1433		L L	MBM
ad-5 his-2 cr-1	Y152M40 Y152M14 B123		246	L R R	DDP
ad-5 rg-1 cr-1	71104 B53 B123	5435		L R R	FJD
arg-1 mei-3	B369 N289		7229	L L	DDP
arg-1 arg-3	UM-245, 30300	8400		L L	RHD
arg-1 rg-1 cr-1 thi-1 al-2	46004 B53 B123 56501 15300	4964		L R R R R	ELT
arg-1 cr-1 al-1 os-1	B369 B123 34508 B135	329		L R R R	DDP
arg-1, arg-6	CD-145, CD-29		8401	L R	RHD
arg-1 al-1	29997 34508	5091		L R	DDP
arg-3 un-2	30300 46006(t)	2704		L R	DDP
arg-3 un-2 his-2	30300 46006(t) Y152M14	2750		L R R	DDP
arg-3 his-3 nic-2(?)	30300 1-226-566 43002(?)	5526		L R	FJD
arg-3 his-3 nic-2 al-1	30300 1710 43002 1-234-471	5544		L R R R	FJD
arg-3 nic-2 cr-1	30300 43002 B123	211		L R R	DDP
arg-3 ad-3B	30300 2-17-158		5529	L R	FJD
csp-1 nic-2	UCLA37 43002	2513		L R	CPS
sn his-2	C136 C94	399		C R	MBM
sn his-3	C136 C140	387		C R	MBM
sn cr-1	C136 B123	4158	4159	C R	EK
sn al-1	JL301 34508	4337		C C	DDP
un-2 his-2	46006(t) Y152M14	2748	2749	R R	DDP
his-2 ad-3A	C94 1-112-13		5527	R R	FJD
his-2 ad-3A nic-2	C94 1-112-13 43002		5528	R R R	FJD
his-2 his-3 nic-2 al-1	C94 1710 43002 1-234-471	5550		R R R	FJD
his-2 nic-2	C94 43002	5058	5059	R R	FJD
his-2 nic-2	Y152M14 43002	3219		R R	DDP
his-2 nic-2 al-2	C94 43002 Y112M38	5509	4933	R R R	FJD
his-2 al-2	C94 1-112-38		5057	R R	FJD
nuc-1 ad-3A	T28-M1 no#	1999		R R	TI
rg-1 his-3 nic-2	B53 Y152M9 43002		4770	R R R	FJD
rg-1 cr-1	B53 B123	624	418	R R	DDP
his-3 nic-2	Y269M5 43002	1855		R R	MEC
his-3 nic-2 al-1	1710 43002 1-234-471		5545	R R R	FJD
ad-3A nic-2	Y112M13 43002	4769		R R	FJD
ad-3A nic-2	38701 43002	142		R R	DDP
ad-3A al-2	1-112-15 1-112-38		5850	R R	FJD
ad-3B nic-2 al-2	3-10-446 43002 1-112-38	5325		R R R	FJD

Loci	Alleles	FGSC # mating type		Linkage group	Obtained from
		A	a		

Linkage Group I, continued

Loci	Alleles	A	a	Linkage group	Obtained from
ad-3B nic-2	2-17-37 43002	5286		R R	FJD
ad-3B al-2	1-112-4 15300		5263	R R	FJD
ad-3B thi-1 al-2	35203 56501 15300		259	R R R	DDP
cr-1 thi-1 nit-1 al-1 nic-1 os-1	L 56501 34547 34508 3416 B135		245	R R R R R R	DDP
cr-1 thi-1 al-2	B123 56501 15300	6658		R R R	DDP
cr-1 nit-1 al-1 os-1	B122 34547 34508 B135	258	288	R R R R	DDP
cr-1 al-1 os-1	B123 34508 B135	250		R R R	DDP
cr-1 os-1	B122 B135	289	280	R R	DDP
cys-9 un-1	T156 44409		7241	R R	DDP
thi-1 met-6	56501 35809	7856	7857	R R	DDP
thi-1 ad-9 nit-1 het-5^{PA}	56501 Y154M37 34547 PA	7348	7349	R R R R	DDP
cr-2 al-2	R2445 15300		2209	R R	ELT
fls al-1	STL6 34508		60	R R	DDP
wc-2 glp-1	234(w) 234	2742	2743	R R	HGK
nit-1 al-1 nic-1 os-1	34547 34508 3416 B135	228		R R R R	DDP
cyh-1 al-2 arg-6	KH52(r) 15300 29997	3450	3451	R R R	DDP
cyh-1 al-2 al-1	KH52(r) 15300 34508	4550	4551	R R R	DDP
cyh-1 al-2 nic-1	KH52(r) 15300 S1413		4148	R	EK
cyh-1 al-2 nic-1 arg-13	KH52(r) 15300 S1413 RU12		4112	R R R R	EK
cyh-1 al-1	KH52(r) 34508		4242	R R	DDP
cyh-1 al-1	KH52(r) JH216	6657		R R	DDP
mus-9 nic-2	FK129 43002	6407	6408	R R	EK
al-2 arg-6	15300 29997	313	272	R R	DDP
al-2 nic-1 het-I	15300 3416 no#	7343	7344	R R I or II	DDP
het-5^{PA} *arg-13*	PA RU3	7345		R R	DDP
al-2 nic-1 arg-13 un-18	15300 S1413 RU12 T54M94(t)	4113	4114	R R R R	EK
al-2 arg-13	15300 RU3	1728		R R	KJM
al-2 arg-13	15300 RU12	1723		R R	KJM
al-2 arg-13	15300 RU20	1722		R R	KJM
al-2 cnr^{S}	15300 no#(s)	99	263	R R	DDP
al-2 hom	15300 51504	5093	5094	R R	DDP
al-2 os-1	15300 P641	866		R R	DDP
al-2 su(met-7)	15300 S1		39	R R	DDP
al-2 cfs(OY306)	15300 OY306(s)		3529	R R	OCY
al-2 R un-18	15300 35408 T54M94(t)	7242		R R R	DDP
hom al-1	51504 34508		5092	R R	DDP
al-1 lys-3	JH612 4545	7231		R R	DDP
al-1 nic-1 os-1	34508 3416 B135	3603		R R R	DDP
al-1 nic-1 arg-13	34508 3416 RU3	3655	3656	R R R	DDP
al-1 aro-8	34508 DH8	1814	1815	R R	BCT
R un-18	35408 T54M94(t)	7232		R R	DDP

Linkage Group II

Loci	Alleles	A	a	Linkage group	Obtained from
pi trp-3	B101 td24	2071	2072	L R	DDP
pi un-15	B101 T54M50(t)	2435	2436	L R	DDP
ro-7 arg-5 rip-1	R2470 27947 4M(t)	6563	6564	L R R	DDP
ro-7 rip-1	R2470 4M(t)	3467	3468	L R	DDP
cys-3 arg-5	P22 27947	1290	4149	L R	DDP
cys-3 eas	NM27(t) UCLA191	4689	4690	L R	MLS
cys-3 fl	P22 P		1289	L R	DDP
un-24 het-6^{OR}	DJ517 OR	7354		L L	DDP
het-6^{PA} *arg-12*	PA UM107	7350	7351	L R	DDP
cot-5 het-C pyr-4 thr-2	R2479 C 36601 35423	7147		L L L L	DDP
cot-5 het-C^{OR} *pyr-4 thr-2*	R2479 C^{OR} 36601 35423	7355	7356	L L L L	DDP
cot-5 het-c	R2479	7447		L L	DDP
het-c pyr-4	c^{OR} 36601	7306	7307	L L	DDP

Linkage Group II, continued

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
het-c^{AD} *pyr-4 thr-2*	c^{AD} 36601 35423	7313		L L L	DDP
pyr-4 arg-12	36601 UM107	2997	2998	L R	DDP
ro-3 arg-5 pe	R2354 27947 Y8743m	2705	2705	L R R	DDP
ro-3 pe	R2354 Y8743m	3008	159	L R	DDP
thr-2 arg-5	35423 27947	7192	7193	L R	DDP
bal arg-5	B56 27447		2751	L R	DDP
arg-5 aro-3	27947 C167	7194		R R	DDP
arg-5 pe fl	27947 Y8743m L	4150	2706	R R R	EK
arg-5 fl	27947 L	312	155	R R	DDP
arg-5 pe fl trp-3	27947 Y8743m L td37	4115	4116	R R R R	EK
arg-5 arg-12^{S}	27947 37301s		895	R R	RHD
arg-5 mus-27	27947 FK124	6430	6431	R R	EK
arg-5 eas	CD6 UCLA191	4681	4682	R R	MLS
nuc-2 aro-1	T28-M2 Y7655	2000		R R	TI
pe aro-1 fl	Y8743m Y7655 L	1681		R R R	RWB
pe fl	Y8743m L	3072	3073	R R	KDM
pe fl	Y8743m L	4169	4170	R R	EK
pe fl	L L	5512	5511	R R	FJD
arg-12 ure-3	UM107 F29		7195	R R	DDP
arg-12 ure-3 un-20	UM107 F29 P2402		7196	R R	DDP
arg-12 ure-3 un-20	UM107 F29 P2402t		7308	R R R	DDP
arg-12 un-20	UM107 P2402	7197		R R	DDP
arg-12 fl rip-1	UM107 P 4M	7198	7207	R R R	DDP
mus-27 nuc-2	FK124 T28-M2	6432	6433	R R	EK
un-20 ace-1	P2402 Y2492	7199		R R	DDP
ace-1 eas	Y2492, JD105	8111		R R	DDP
fl trp-3	P605 td24		7200	R R	DDP
eas trp-3	td24, JD105	8596		RR	DDP
trp-3 un-15	td24 T54M50	7201	7202	R R	DDP

Linkage Group III

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
cum cyt-22 r(Sk-2)-1	P5241 289-4 P527	7154		L L L	DDP
cum r(Sk-2)-1	P5241 P527	7379	7380	L L	BCT
cum r(Sk-2)-1 acr-7	P5241 P527 P1676		7155	L L L	DDP
cum r(Sk-2)-1 acr-7	P5241 P527 P1676		7389	L L L	BCT
cum Sk-2^{K} *acr-7*	P5241 B P1676		7432	L L L	DDP
cum Sk-2^{K} *acr-2*	P5241 J KH5	7383	7384	L III C	BCT
cum Sk-3	P5241 P	7382	7381	L III	BCT
cum Sk-3 his-7	P5241 P Y152M31	7390	7391	L III R	BCT
cum r(Sk-3)	P5241 P		7396	L L	BCT
cum r(Sk-3) leu-1	P5241 P 33757		7394	L L R	BCT
cum acr-7	P5241 P1676	7156	7157	L L	DDP
cum acr-7 dow	P5241 P1676 P616	4540	4541	L L R	DDP
cum acr-2 his-7	P5241, KH5, Y152M31	8599	8600	L C R	DDP
cum dow	P5241 P616	4542	4543	L R	DDP
acr-7 dow	P1676 P616	7078	7079	L R	DDP
Sk-2^{K} *acr-7*	Borneo P1676	6930		L L	DDP
Sk-2^{K} *acr-7 leu-1 his-7*	Borneo P1676 33757 Y152M31		7373	III L R R	BCT
Sk-2 acr-2	P KH5	7385	7386	III III	BCT
Sk-2^{K} *acr-2*	Borneo KH5	6928	6929	L L	DDP
Sk-2^{K} *acr-2 leu-1*	Borneo KH5 33757	7375	7374	III C R	BCT
Sk-2^{K} *acr-2 his-7*	Borneo KH5 Y152M31	7376		III C R	BCT
Sk-2^{K} *acr-2 leu-1 his-7*	Borneo KH5 33757 Y152M31	7387	7388	III C R R	BCT
Sk-2^{K} *leu-1*	Borneo 33757	7371		III R	BCT
Sk-2^{K} *his-7*	Borneo Y152M31	7378		III R	BCT
Sk-2^{K} *phe-2 dow*	Borneo Y16329 P616	4538	4539	L R R	DDP

Linkage Group III, continued

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
Sk-2^{K} *dow*	Borneo P616	4260	4261	L R	DDP
Sk-3^{K} *acr-7*	-- P1676	6931	6932	L L	DDP
r(Sk-3) acr-7 ser-1	P P1676 C127	7397		L L R	BCT
acr-2 spg	KH5(r) no#	7158	7159	C C	DDP
acr-2 uvs-4 leu-1	KH5(r) ALS12 33757	4196		C R R	EK
acr-2 met-8 leu-1	KH5(r) P53 33757	7177		C R R	DDP
acr-2 leu-1 his-7	KH5(r) leu-1 his-7	7160	7178	C R R	DDP
acr-2 leu-1 trp-1 dow	KH5(r) 33757 10575 P616	4117	4118	C R R R	EK
acr-2 trp-1 mus-21	KH5(r) 10575 FK120	6420	6421	C R R	EK
acr-2 trp-1 nit-7 dow	KH5(r) 10575 V1M59 P616	6018		C R R R	DDP
acr-2 trp-1 dow	KH5(r) 10575 P616	4119	4120	C R R	EK
acr-2 dow	KH5(r) P616	2036	2037	C R	DDP
sc trp-1	5801 10575	190	239	C R	DDP
ad-4 pro-1	Y155M13(F10) 21863		468	R R	MEC
ad-4 leu-1	44206t 33757	7161		R R	DDP
ad-4 leu-1	Y112M160(F4) 33757		463	R R	MEC
uvs-4 leu-1	ALS12 33757		4197	R R	EK
leu-1 thi-2	33757 9185		7162	R R	DDP
acr-6 shg	KH19 KH160	2325	2326	R R	KSH
trp-1 mus-21	10575 FK121	6416	6417	R R	EK
trp-1 vel	10575 B18	173	298	R R	DDP
nit-7 dow	V1M59 P616	7163		R R	DDP
nit-7 erg-3	V1M59 UV41	7247	7248	R R	DDP
vel tyr-1	B18 Y6994	7179	7180	R R	DDP
dow erg-3	P616 UV41	7243	7244	R R	DDP

Linkage Group IV

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
uvs-3 trp-4 pan-1	ALS11 Y2198 5531	4194	4195	L R R	EK
cys-10 cut pyr-1	39816 LLM1 H263	2707		L R R	DDP
cys-10 pdx-1 pan-1	39816 37803 5531	4121	4122	L R R	EK
cys-10 pdx-1 pan-1 uvs-2	39816 37803 5531 no#	4123	4124	L R R R	EK
cys-10 col-4	39816 70007c	1534		L C	DDP
cys-10 col-4 cot-1	39816 70007c C102(t)	2752	2753	L R R	DDP
cys-10 cot-1 uvs-2	39816 C102(t) no#	2017	2018	L R R	DDP
cys-10rug	39816 B57	2615	2616	L R	DDP
cys-10 uvs-2	39816 no#	1989	2266	L R	DDP
cys-10 pmb	39816 cnr-37(r)	6884	6885	L R	DDP
cut psi-1	LLM1 34C	8253	8254	L R	DDP
psi-1 pdx-1	34C, 37803	8255	8256	R R	DDP
pyr-1 col-4 pyr-3	H263 70007c 37815(t)	390		R R R	MBM
pyr-1 arg-2	H263 33442	394		R R	MBM
pyr-1 rug	H263 B57	186	187	R R	DDP
pyr-1, pyr-3	DFC33, DFC3		8392	R R	RHD
pdx-1 col-4	35405 70007c		388	R R	MBM
pdx-1 col-4	37803 70007c	404		R R	MBM
pdx-1 col-4	39106p 70007c		345	R R	MBM
pdx-1 col-4 ad-6 pan-1 rug	37803 B148 28610 5531 B57	4962		R R R R R	BDM
pdx-1 tol	37803 N83	1948		R R	DNP
pdx-1 pan-1 pyr-2	37803 5531 38502	161	170	R R R	DDP
pdx-1 pan-1 cys-4	37803 5531 K7	4125	4126	R R R	EK
pdx-1 pan-1 cys-4 uvs-2	37803 5531 K7 no#	4127	4128	R R R R	EK
pdx-1 cot-1 cys-4	37803 C102(t) K7	4151	4152	R R R	EK
pdx-1 cys-4	37803 K7	1291		R R	DDP
mtr pmb	Pm-22(r) cnr-37(r)		2276	R R	LW
col-4 arg-2	70007c 33442		389	R R	MBM
col-4 pyr-3	70007c 37815(t)	392		R R	MBM

Linkage Group IV, continued

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
col-4 pyr-3	70007c 45502		344	R R	MBM
col-4 pan-1	B148 5531		188	R R	DDP
col-4 cot-1	NM164 C102(t)	7181		R R	DDP
col-4 pyr-2	70007c 38502	391		R R	MBM
pyr-3 arg-2?	K0493-14 33442?	1895		R R	AR
pyr-3 arg-2?	K0493-54 33442?	1896		R R	AR
pyr-3 arg-2?	K0545-122 33442	1898		R R	AR
pyr-3 arg-2?	K0556-185 33442?	1897		R R	AR
mus-30 met-2	FK115 K43	6448	6449	R R	EK
mus-30 pan-1	FK115 5531	6446	6447	R R	EK
tol trp-4	N83 Y2198	2336	2337	R R	DDP
tol pan-1	N83 5531		1949	R R	DNP
trp-4 pan-1	Y2198 5531		113	R R	DDP
leu-2 pan-1 rug	37501 5531 B57		335	R R R	DDP
ad-6 cot-1	28610 C102(t)	7208		R R	DDP
mod-(sc) pan-1	KH251 5531	1162	1163	R R	KSH
pan-1 uvs-2	5531 no#		4191	R R	EK
bd cel	no# R2366o		2947	R R	SB
cot-1 his-4	C102(t) C141	398		R R	MBM
cot-1 nit-3	C102(t) 14789	7209		R R	DDP
cot-1 cys-4	C102(t) K7	1201	1202	R R	DDP
cot-1 uvs-2	C102(t) no#	1709		R R	DRS
nit-3 pyr-2	14789 38502	7210		R R	DDP
pyr-2 cys-4	38502 K7		7211	R R	DDP

Linkage Group V

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
dgr-1 lys-1	KHY15 33933	7238	7239	L L	CTY
dgr-1 at al-3 his-6	KHY15 M111 RP100 Y152M105	7587	7560	L C R R	DDP
dgr-1 al-3 his-6	KHY15 RP100 Y152M105	7150	7151	L C R	DDP
caf-1 lys-1	KH101 33933	7164		L L	DDP
caf-1 lys-1 cyt-9 at cyh-2 al-3	KH101 33933 17 NM221 KH53 RP100	7182		L L L C R R	DDP
caf-1 at	KH101(r) M111	3657	3658	L C	DDP
caf-1 at al-3	KH101 M111 RP100		7165	L C R	DDP
caf-1 al-3 his-6	KH101(r)(t) RP100 Y152M105	3752	3753	L R R	DDP
lys-1 cyt-9	33933 17		7183	L L	DDP
lys-1 at	33933 M111	7166	7184	L C	DDP
lys-1 cyh-2 al-3 his-6	33933 KH53 RP100 Y152M105	4130		C R R R	EK
lys-1 cyh-2 al-3 inl his-6	33933 KH53(r) RP100 83201(t) Y152M105	4135		C R R R R	EK
lys-1 cyh-2 al-3 inl pab-2	33933 KH53(r) RP100 83201(t) H193		4132	C R R R R	EK
lys-1 cyh-2 al-3 inl pab-2 his-6	33933 KH53(r) RP100 83201(t) H193 Y152M105		4129	C R R R R R	EK
lys-1 al-3 inl pab-2	33933 RP100 83201(t) H193	4131		C R R R	EK
lys-1 inl	33933 37401	209	1097	C R	DDP
lys-1 inl his-6	33933 37401 Y152M105	1535	4136	C R R	DDP
lys-1 pk	33933 B6	192		C R	DDP
lys-1 asn	33933 S1007	1181	1182	C R	DDP
lys-1 mus-11	33933 FK117	6413		L R	EK
cyt-9 at	17 M111	7185		L C	DDP
at cyh-2 al-3	M111 KH53 RP100	7186	7167	C R R	DDP
at al-3 his-6	M111 RP100 Y152M105	2089	2090	C R R	DDP
at his-6	M111 Y152M105	1991	1992	C R	DDP
ilv(?6201) inl	?6201 37401	204	311	R R	DDP
ilv-1 inl	16117 64001	676		R R	MEC
rol-3 inl	R2498 89601	1354		R R	ELT

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
	Linkage Group V, continued				
cyh-2 leu-5	KH53(r) 45208		7168	R R	DDP
cyh-2 sp al-3	KH53(r) B132 RP100	7187	7188	R R R	DDP
cyh-2 al-3	KH53(r) RP100	7169		R R	DDP
cyh-2 al-3 inl pab-2	KH53(r) RP100 83201(t) H193	4133	4134	R R R R	EK
md cl	MW84 CL11		1297	R R	AS
ndc-1 inl	1(t) 89601		3441	R R	DRS
cot-4 inl	R2101(t) 89601	1357		R R	ELT
ure-2 am	47 32213		4299	R R	HGK
am inl	am132 37401	6649		R R	JAK
ure-1 his-1	9 C91		4298	R R	HGK
spe-1 inl	462JM 89601	4265	4266	R R	RHD
spe-1 inl	TP-138 89601	4267		R R	RHD
his-1 al-3	C84 Y234M470		7170	R R	DDP
his-1 al-3 inl	C84 RP100 89601	8257		R R R	DDP
his-1 met-3	K744 36104		780	R R	DGC
erg(RES208) al-3	RES208(r) al-3		3155	R R	RES
al-3 inl	RP100 83201(t)	2309	2300	R R	DDP
al-3 inl	RP100 89601	2308	2301	R R	DDP
al-3 pab-1	RP100 1633	7171	7172	R R	DDP
al-3 ad-7	RP100 P73B171	7173	7174	R R	DDP
al-3 pyr-6 oak	RP100 DFC37 R2358	7175		R R R	DDP
udk uc-4	FB-D425 RW341	4284	4285	R R	FPB
inl gln-l	89601 R1015	1450		R R	ER
inl met-3	37401 92935	2159		R R	GAM
inl pk pab-2	37401 B6 H193	242		R R R	WNS
inl col-9	89601 R2417		1385	R R	ELT
inl ro-4	89601 R2428	1356		R R	ELT
inl asn	37401 C123	284		R R	WNS
inl acu-1	R233 JI48	1731		R R	RBF
inl his-6	37401 Y152M105	1285	1286	R R	DDP
pk asp	B6 S1007		243	R R	DDP
pk^{t1} *pab-l*	17-575 1633?	3420	3421	R R	AMS
pk^{t2} *pab-1*	19-773(peak) 1633?	3422	3423	R R	AMS
ro-4 inv	B38 no#		7176	R R	DDP
un-9 his-6	T54M96 Y152M105		7189	R R	DDP
met(152C) inl	152C(t) 89601		3759	(?) R	DRS
un(20J) inl	20J(t) 89601		3778	R R	DRS
un(21T) inl	21T(t) 89601		3782	R R	DRS
un(121C) inl	121C(t) 89601		3769	R R	DRS
un(134C) inl	134C(t) 89601		3770	R R	DRS
un(165C) inl	165C(t) 89601		3772	R R	DRS
un(16J) inl	16J(t) 89601		3777	R R	DRS
un(181C) inl	181C(t) 89601		3787	R R	DRS
un(58E) inl	58E(t) 89601		3775	(?) VR	DRS
	Linkage Group VI				
chol-2 nit-6	47904(t) OP4	7212		L L	DDP
chol-2 nit-6 ser-6 het-8^{PA}	47904 OP4 DK42 het-8^{PA}	7470	7471	L L L L	JFL
chol-2 nit-6 ser-6 het-8^{HO}	47904 OP4 DK42 het-8^{P516}	7485	7486	L L L L	JFL
chol-2 nit-6 het-8^{OR} *ser-6 ad-8*	47904 OP4 no# DK42 Y112M343	7404	7405	L L L L L	JFL
chol-2 ad-8 lys-5 un-4 pan-2	47904(t) Y226M58 DS6-85 66204(t) Y153M96	3251	3252	L L L L R	OMM
chol-2 trp-2	47904(t) 75001	1087	1088	L R	DDP
chol-2 ylo-1 rib-1 pan-2 trp-2	47904(t) Y30539y 51602(t) Y153M96 41		5179	L L R R R	EK
chol-2 ylo-1 trp-2	47904(t) Y30539y 41	5180	5181	L L R	EK
chol-2 ylo-1 ws-1	47904(t) Y30539y RP99	3519	3520	L L R	DDP

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from

Linkage Group VI, continued

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
nit-6 pan-2	OP4 B36	2977		L R	GJS
nit-6 ylo-1 un-23	OP4 Y30539y 64D	7563	7564	L L R	DDP
mus-29 ylo-1 pan-2	FK119 Y30539y Y153M96	6442	6443	L L R	EK
mus-29 trp-2	FK119 41	6440	6441	L R	EK
ser-6 ad-8	DK42 Y226M58		7213	L L	DDP
het-8^{PA} *ad-8*	het-8^{PA} Y112M343	7469		L L	JFL
ad-8 lys-5	Y226M58 DS6-85	7214		L L	DDP
ad-8 ylo-1	Y152M7(E6) Y30539y	448	449	L L	TI
lys-5 ylo-1	DS6-85 Y30539y		4	L L	DDP
lys-5 ylo-1 pan-2 cho-2	DS6-85 Y30539y Y153M96 47904(t)		5185	L L R R	EK
asco (lys-5) trp-2	37402 75001	210		L R	DDP
un-4 trp-2	66204(t) 75001	393		L R	MBM
cys-2 ylo-1	80702 Y30539y	125	489	L L	BDM
cys-1 ylo-1	84605 Y30539y	1092	2086	L L	NEM
sor-1 ylo-1	10(r) Y30539y	2375		L L	WK
ylo-1 pan-2 trp-2	Y30539y B3(Y153M96) 75001	469		L R R	MEC
ylo-1 del trp-2	Y30539y B137 45302		7215	L R R	DDP
ylo-1 trp-2	Y30539y S4266	953		L R	DDP
ad-1 pan-2	3254 B5(Y154M64)	3121	3122	L R	DDP
ad-1 glp-4	3254 G660		7216	L C	DDP
rib-1 pan-2 trp-2	51602(t) B2(Y153M66) 41	4139	4140	C R	EK

Linkage Group VII

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
spco-4 wc-1 nt	R2367 P829 65001	2284	2285	L R R	DDP
nic-3 met-7	Y31881 4894	152	153	L R	DDP
nic-3 met-7 arg-10	Y31881 4894 B317	4141	4142	L R	EK
nic-3 mus-25	Y31881 FK123	6426	6427	L R	EK
nic-3 wc-1	Y31881 P829	154	156	L R	DDP
nic-3 wc-1 arg-10	Y31881 P829 B317	157		L R R	DDP
nic-3 wc-1 sk	Y31881 P829 B234	2073	2074	L R R	DDP
thi-3 met-7	18558 NM251		3915	R R	DDP
thi-3 met-7 nt	18558 4894 65001	4143	4144	L R R	EK
csp-2 nic-3	FS590 Y31881	2516		L L	CPS
csp-2 nic-3	FS591 Y31881	2517		L L	CPS
csp-2 nic-3	UCLA101 Y31881	2520		L L	CPS
csp-2 nic-3	UCLA102 Y31881	3872		L L	CPS
ace-8 met7	KG570 4894		7781	L R	HK
sfo nt	E18829(d) 65001	576	506	C R	ELT
met-7 met-9 wc-1	NM331 NM43(t) P829	3607		R R R	AR
met-7 wc-1	NM56 P829		3928	R R	DDP
met-7 wc-1	NM251 P829	3914		R R	DDP
met-7 wc-1 nt	4894 P829 C86		158	R R R	DDP
wc-1 nt sk	P829 65001 P1718	6660	6661	R R R	DDP
arg-*10 nt*	B317 65001	7217		R R	DDP

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
B. Two Linkage Groups Marked					
I;II					
fr;arg-5	B110;27947	328	279	IL;IIC	DDP
sod-1;fl	3C;P	7439	7440	IL;IIL	DON
ylo-2;eas	Y256M230;UCLA191	4671	4672	IL;IIR	MLS
rg-1 cr-1;pe fl	B53 B123;Y8743m L	331		IC R;IIR R	DDP
sn cr-1;pe fl	C136 B123;Y8743m L	4162	4163	IC R;IIR R	EK
ad-3B;pe fl	2-17-51;Y8743m L	5537	5536	IR;IIR R	FJD
ad-3B;pe fl	2-17-74;Y8743m L	5535		IR;IIR R	FJD
ad-3B;pe fl	2-17-75;Y8743m L	5534		IR;IIR R	FJD
al-1;arg-5	34508;27947	1205	1206	IR;IIC	DDP
al-1;pe	34508;Y8743m	1203	1204	IR;IIR	DDP
cr-1;pe fl	B123;Y8743m L	4167	4168	IR;IIC R	EK
Fsp-2;Fsp-1	DL709;ALS141	5069	5070	IR;IIR	NBR
nuc-1;nuc-2	T28-M1;T28-M2	1998		IR;IIR	TI
uc-2;pyr-4 uc-1	RW135;36601 RW57	2203		I;IIL II	LGW
wc-2;fl	ER33 P	7203	7204	IR;IIR	FRL
I;III					
acr-4;shg	KH16(r);KH160	2322		IL;IIIR	KSH
leu-4;leu-1	FLR92;D221	1501		IL;IIIR	SRG
sn cr-1;acr-2 leu-1 dow	C136 B123;KH5(r) 33757 P616	5177	5178	IC R;IIIC R R	EK
sn cr-1;acr-2 leu-1 trp-1 dow	C136 B123;KH5(r) 33757 10575 P616	5174	5175	IC R;IIIC R R R	EK
sn cr-1;acr-2 trp-1 dow	C136 B123;KH5(r) 10575 P616		5176	IC R;IIIC R R	EK
su(mtr);fpr-3	18;no#	2999		IC;IIIR	JAK
al(Y234M468);ad-2	Y234M468al;Y175M256	956		IR;IIIR	AMK
arg-3 ad-3A nic-2;ad-2	30300 1-112-13 43002;1-175-256	5553		IL R R;IIIR	FJD
arg-3 ad-3A ad-3B nic-2 al-1;ad-2	30300 1-112-13 35203 43002; 1-234-471;1-175-256	5555		IL R R R R; IIIR	FJD
ff-3;ty-3(T22)	no#;135-333(T22)	2962		IR;IIIR	JFF
his-2 ad-3A ad-3B nic-2;ad-2	C94 1-112-13 35203 43002; 1-175-256	5307		IR R R R;IIIR	FJD
his-2 ad-3A ad-3B nic-2 al-1;ad-2	C94 1-112-13 35203 43002 1-234-471;1-175-256	5539	5540	IR R R R R; IIIR	FJD
his-2 ad-3A ad-3B nic-2 al-2;ad-2	C94 1-112-13 35203 43002 1-112-38;1-175-256	5532		IR R R R R; IIIR	FJD
nuc-1;pgov[c]	T28-M1;R42	3480		IR;IIIR	RLM
I;IV					
acr-3 nic-1 pdx-1	KH14(r) S1413;37803		4630	IL R;IVR	JL
ad-5 nic-2 thi-1;cot-1	Y152M40 43002;56501;C102(t)	256		IL R R;IVR	DDP
arg-3; arg-2, pyr-3	CD186; CD80, DFC3	8393		IL; IVR, IVR	RHD
csp-1;bd	UCLA37;no#	2948	4547	IL;IVR	SB
csp-1;cel bd	UCLA37;R2366o no#	3484		IL;IVR R	SB
En(pdx-1);pdx-1	K30;44602p	422		IL;IVR	DDP
fmf-1;pyr-3	PB-J6;KS43	3108		IL;IVR	TEJ
fmf-1;tol pan-1	PB-J6;N83 5531	3109	3110	IL;IVR R	TEJ
leu-3 arg-1 ad-3B al-1 tol C D	R156 36703 2-17-114 car-10 N83		3819	IL L R R;IVR	AJG
leu-3;cot-1	R156;C102(t)	2253		IL;IVR	RKL
leu-3 cyt-1 arg-3;tol	R156 C115 30300;N83	7337		IL L L;IVR	DDP
leu-3 suc;tol pan-1	R156 66702;N83 5531		7322	IL L;IVR R	DDP
leu-3 his-2 cr-1 al-1 cot-1	R156 Y152M14 B123 34508;C102(t)		249	IL C I I;IVR	DDP

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
	I;IV, continued				
mei-3;tol	N289;N83		2765	IL;IVR	DNP
mei-3;uvs-2	N289;no#	4616	4617	IL;IVR	ALS*un-3 ad-3A*
nic-2 al-2 tol c D	E55701(t) 2-17-814 43002 Y112M38 N83	3820		IL R R R;IVR	AJG
upr-1;uvs-3	no#;ALS11	2288	2289	IL;IVL	RWT
sn cr-1;cys-10 pdx-1 pan-1 uvs-2	C136 B123;39816 37803 5531 no#	5186	5187	IC R;IVL R R R	EK
su(mtr);mtr col-4	21-2;10(r) 70007c	1719		IC;IVR R	DRS
ad-3A ad-3B nic-2;cot-1	B110 C94 43002 1-112-38		5301	IR R R;IVR	FJD
ad-3B;cot-1	1-263-111 C102(t)		5277	IR;IVR	FJD
ad-3B;cot-1	C-18-972;C102(t)	2250		IR;IVR	RKL
al-2;cot-1	15300;C102(t)	2251	4701	IR;IVR	RKL
al-2;cot-1	1-112-38;C102(t)	5270	5269	IR;IVR	FJD
his-3;ad-6	Y306M176;Y175M30		6125	IR;IVR	MEC
his-3;cot-1	1-152-9 C102(t)		5274	IR;IVR	FJD
nic-2 al-2;cot-1	43002 1-112-38 C102(t)	5273		IR R;IVR	FJD
al-2;pan-2 cot-1 uvs-2	Y112M38;Y153M96 C102(t) no#	4583	4584	IR;IVR R R	FJD
al-2 pan-1;fpr-5	15300;5531;no#(r)	3001	3002	IR R;IVR	JAK
al-2;pho-3	15300;221(t)	3051	3052	IR;IVR	REN
al-1 col-4	34508 70007c		286	IR;IVR	DDP
cr-1 al-2;cot-1	B123 1-112-38;C102(t)	5619		IR R;IVR	FJD
cr-1;cot-1 grey	L;C102(t) KH165	2327		IR;IVR R	KSH
cr-1 thi-1 nit-1 al-1 nic-1 os-1;cot-1	L 56501 34547 34508 3416 B135;C102(t)	236		IR R R R R R;IVR	DDP
his-2 cr-1 thi-1 nit-1 al-1 nic-1 os-1;cot-1	Y152M14 L 56501 34547 34508 3416 B135;C102(t)		248	IR R R R R R R;IVR	DDP
his-2 ad-3A ad-3B nic-2 al-2;cot-1	C94 1-112-13 35203 43002 1-112-38;C102(t)		5454	IR R R R R; IVR	FJD
his-2;mtr col-4	Y152M43;10(r) 70007c	1720		IR;IVR R	DRS
his-2;mtr col-4	Y152M43;14(r) 70007c		3016	IR;IVR R	DRS
his-2;mtr col-4	Y152M43;30(r) 70007c		3017	IR;IVR R	DRS
his-3 al-1;mtr col-4	1-152-111 1-234-471;17-1-64	5604		IR R;IVR R R	FJD
his-3 al-1;mtr col-4 cot-1	1-152-111 1-234-471;17-2-14 70007 C102(t)	5506		IR R;IVR R R	FJD
his-3;pt	C1710;S4342		206	IR;IVR	DDP
su(mtr);mtr	21-2;21(r)	1718		IR;IVR	DRS
uc-2;pyr-1	RW135;H263		2206	I;IVR	LGW
uvs-6;mtr met-2 pan-1	ALS35;15(r) P159 5531	4198		IR;IVR	EK
	I;V				
arg-3 his-3 nic-2 al-1;inl	30300 1710 43002 1-234-471;JH319		5546	IL R R R;VR	FJD
Ban mei-3;inl	N452P63 N289;89601		2990	IL L;VR	DNP
leu-3;inl	R117;89601		1320	IL;VR	SRG
sor(T9);ad-7	T9M150;Y186M423	3430		IL;VR	TI
ssu-3;am	WRU118;am_{17}		1851	IL;VR	TWS
un(151C);inl	151C(t);89601		3771	IL;VR	DRS
un(209C);inl	209C(t);89601		3773	IL;VR	DRS
fpr-4;su(mtr)	no#;17-2	3000		IC;VR	JAK
rg-1 cr-1;Mei-2	B53 B123;ALS181		2622	IC R;VR	DAS
sn cr-1;al-3 inl	C136 B123;RP100 83201(t)	4160	4161	IC R;VR R	EK
sn cr-1;al-3 inl	C136 B123;RP100 89601	2303	2306	IC R;VR R	DDP
sn cr-1;cyh-2 al-3 inl his-6	C136 B123;KH53(r) RP100 83201(t) Y152M105		5191	IC R;VR R R R	EK
sn cr-1;lys-1 cyh-2 al-3 inl pab-2	C136 B123;33933 KH53(r) RP100 83201(t) H193	5192	5193	IC R;VC R R R R	EK
sn cr-1;lys-1 cyh-2 al-3 inl pab-2 his-6	C136 B123;33933 KH53(r) RP100 83201(t) H193 Y152M105	5189	5190	IC R;VC R R R R R	EK

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
	I;V continued				
ad-3A;inl	1-155-314;JH319	5611		IR;VR	FJD
ad-3A;inl	38701;JH319	5448		IR;VR	FJD
ad-3A;inl	38709;JH319	5451		IR;VR	FJD
ad-3A;inl	68306;JH319	5453		IR;VR	FJD
al-2;am	15300;am$_{17}$	1685	1686	IR;VR	TWS
al-2;am	15300;RU1(am$_{21}$)	1737	1738	IR;VR	KJM
al-2;am	15300;am$_{10}$		1679	IR;VR	JRS
al-2 al-1;al-3	15300 34508;RP100	4552		IR R;VR	DDP
al^S*;am*	al^S;47305(pr)(am$_{2a}$)		782	IR;VR	RWB
al^S*;am*	al^S;S2929(pr)(am$_{3b}$)	784		IR;VR	RWB
al^S*;am*	al^S;K314(am$_6$)		786	IR;VR	RWB
al^S*;am*	al^S;am$_9$		789	IR;VR	RWB
cr-1 al-2;inl	B123 1-112-38;JH319	5618		IR R;IVR;VR	FJD
cr-3;inl	R2509;89601	2210	2211	IR;VR	ELT
cyh-1 al-2 al-1;al-3	KH52(r) 15300 34508;RP100	4553		IR R R;VR	DDP
his-3;inl	1-224-26;JH319	5531		IR;VR	FJD
rg-1;inl	B53;37401	1375		IR;VR	ELT
tre;inl	39-3;89601	4509		IR;VR	MLS
tre;inl	39-10;89601	4510		IR;VR	MLS
tre;inl	39-21;89601	4511		IR;VR	MLS
tre;inl	39-25;89601	4512		IR;VR	MLS
tre;inl	39-30;89601	4513		IR;VR	MLS
un(120C);inl	120C(t);89601		3768	IR;VR	DRS
un(6T);inl	6T(t);89601		3781	IR;VR	DRS
lys(60C);inl	60C(t);89601		3757	I;VR	DRS
smco-3;inl	R2423;89601		1710	I;VR	ELT
un(145C);inl	145C(t);89601		3783	I;VR	DRS
un(19D);inl	19D(t);89601		3784	I;VR	DRS
un(47D);inl	47D(t);89601		3785	I;VR	DRS
un(6B);inl	6B(t);89601		3766	I;VR	DRS
	I;VI				
fs-3;pan-2	52-2;Y1531796	3240		IL;VIR	OMM
arg-3 al-2;pan-2	30300 1-112-38;1-153-96	5854		IL R;IVR;VIR	FJD
aro-7 ad-3 aro-8;aro-6	DH7 K118 DH8;DH1		4491	IR R;VIL	DDP
aro-7 aro-8 nic-1;aro-6	DH7 DH8 3416;DH1	4489	4490	IR R;VIL	DDP
aro-7 aro-8;ad-8 aro-6	DH7 DH8;Y193M22 DH1	4492		IR;VIL L	DDP
sn cr-1;chol-2 lys-5 ylo-1 pan-2 trp-2	C136 B123;47904(t) DS6-85 Y30539y B2(Y153M66) 41	5182		IC R;VIL L L R R	EK
sn cr-1;chol-2 ylo-1 pan-2 trp-2	C136 B123;47904(t) Y30539y B2(Y153M66) 41	5183		IC R;VIL L R R	EK
ad-3A;pan-2	1-112-9;1-153-96	5612		IR;VIR	FJD
ad-3A;pan-2	1-152-36;1-153-96	5607		IR;VIR	FJD
ad-3A;pan-2	1-153-6;1-153-96	5608		IR;VIR	FJD
ad-3A;pan-2	1-154-28;1-153-96	5609		IR;VIR	FJD
ad-3A;pan-2	1-155-64;1-153-96	5610		IR;VIR	FJD
ad-3A;pan-2	38701;1-153-96	5449		IR;VIR	FJD
ad-3A;pan-2	38709;1-153-96	5450		IR;VIR	FJD
ad-3B al-2;pan-2	3-10-384 1-112-38;1-153-96	5052		IR R;VIR	FJD
al;rib-1	no#;C107		1225	IR;VIR	WSM
al-1;ylo-1	34508;Y30539y	3116	3117	IR;VIL	DDP
cr-1 al-2;pan-2	B123 1-112-38;1-153-96	5617	5616	IR R;IVR;VIR	FJD
erg-4;pan-2	UVC53;Y153M66	3606		IR;VIR	MG
his-3 nic-2 al-2;pan-2	Y152M9 43002 Y112M38;Y387-15.7		2457	IR R R;VIR	FJD
his-3 nic-2 al-2;pan-2	1-152-9 43002 1-112-38 1-153-96	5265	5264	IR R R;VIR	FJD

I;VI, continued

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
ssu-8 ad-3B al-2;pan-2	Y319-37;12-21-22 Y112M38; Y153M96	2487		IR R R;VIR	AJG
ssu-8 ad-3B al-2;pan-2	Y319-37;12-21-76 Y112M38; Y153M96	2488		IR R R;VIR	AJG

I;VII

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
csp-1;nic-3	UCLA37;Y31881	2514		IL;VIIL	CPS
fr;nic-3	B110;Y31881		254	IL;VIIL	DDP
fs-3;nic-3	52-2;Y31881		3239	IL;VIIL	OMM
sn cr-1;csp-2	C136 B123;UCLA101	2697	2002	IC R;VII	REN
sn cr-1;csp-2	C136 B123;UCLA101	4157		IC;VII	EK
sn cr-1;nic-3 met-7 arg-10	C136 B123;Y31881 4894 B317	5219		IC R;VIIl R R	EK
is-3;hlp-2	K458;HC114		2319	IR;VIIR	HCC
his-3 aga	Y155M261; UM906		8387	IR; VIIR	RHD
nic-2;csp-2	43002;FS590	2515		IR;VII	CPS
nic-2;csp-2	43002;UCLA102	3871		IR;VII	CPS
uvs-6;nic-3	ALS35;Y31881	4199		IR;VIIL	EK

I;--

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
arg-3;mei-4	30300;N395	2763		IL;--	DNP
tyr(LW101);glt	LW101(s);D240(r)	2736		IL;--	GAM
ad-3B;ssu-5	2-17-34;Y319-45	2483		IR;--	AJG
ad-3B;ssu-5	2-17-34;Y319-45	2484		IR;--	AJG
suc;ma-1	46005;M20	1112		IR;--	KDM
suc;ma-2	46005;M24	1113		IR;--	KDM

II;III

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
arg-5 pe fl;acr-2	27947 Y8743m L;KH53(r)	5169	5170	IIR R R;IIIC	EK
aro-1;trp-1	Y7655;10575a	1145		IIR;IIIR	RBC
fl;Sk-2	P;no#	3297	3298	IIR;III	DDP
fl;Sk-3	P;no#	3579	3580	IIR;IIIC	DDP
trp-3;su(trp-3^{td2}*)-2*	S1952;su2		6136	IIR;III	ELT

II;IV

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
pmg;pmb	no#;can-37(r)	4810	4811	IIL;IVR	RMD
pmg;pmn	no#;Pm-22(r)	4808	4809	IIL;IVR	RMD
arg-12^{S}*;pyr-3*	37301s;37301p		894	IIR;IVR	RHD
col-1;pe	Y8743c;Y8743m		535	IIR;IVR	ELT
fl;dn	P;38502d	3517	3518	IIR;IVR	DDP
pe fl cot-1	Y8743m L;C102(t)		639	IIR R;IVR	RWB
pe fl;le-1	Y8743m L;S4355		1402	IIR R;IVR	ELT
pe fl;gul-3 pt cot-1	Y8743m L;845 NS1(t) C102(t)		1174	IIR R;IVR R R	HFT
pe fl;pan-1	Y8743m L;5531		3532	IIR R;IVR	ELT

II;V

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
cyb-3;his-6	A10;Y175M16		3427	IIL;VR	DVW
ro-3;inl	R2354;89601	2311		IIL;VR	ELT
aro-3;inl	R2202;89601	1098		IIR;VR	MEC
aro-4;inl	R2219;89601	1105		IIR;VR	MEC
en(am)-2;am	C24;32213	1624		IIR;VR	MS
fl;his-6	P605;Y152M105	1537	1538	IIR;VR	DDP

		FGSC # mating type		Linkage	Obtained
Loci	Alleles	A	a	group	from
II;V, continued					
fl;inl	P;37401	3631	3632	IIR;VR	DDP
fl;per-1	P;PB-J1	3311	3312	IIR;VR	DDP
fl;per-1 al-3	P;AR174 RP100	3960	3120	IIR;VR R	DDP
glp-2;inl	JC1444;83201(t)	2969		IIR;VR	JBC
nuc-5;inl	276;83201(t)		4912	IIR;VR	NCM
nuc-6;inl	936;83201(t)		4914	IIR;VR	NCM
pe en(am)-2;am	Y8743m C24;32213		1625	IIR R;VR;	MS
spco-14;inl	R2536;89601	1397		II;VR	ELT
thr(38E);inl	38E(t);89601		3760	II;VR	DRS
thr(72C);inl	72C(t);89601		3758	II;VR	DRS
II;VI					
arg-12^S;cpc-1	37301s;CD-15	4262	4263	IIR;VIL	RHD
glp-2;ylo-1	JC17;Y30539y	2968		IIR;VIL	JBC
nuc-3;pan-2	701;1-153-96		4910	IIR;VIR	NCM
nuc-7;pan-2	24;1-153-96		4916	IIR;VIR	NCM
II;VII					
aro-1;met-7	Y7655;4894	4555	4556	IIR;VIIR	DDP
aro-9;qa-1	Y325M6;A4-18A	1747		IIR;VIIR	MEC
aro-9;qa-2	Y325M6;326M237	2718		IIR;VIIR	MEC
fl;wc-1	P;P829	7052	7053	IIR;VIIR	DDP
ro-3;nic-3	R2354;Y31881	260	261	IIL;VIIL	DDP
trp-3 aro-9;qa-2	td24 Y325M6;M246		4546	IIR R;VII	DDP
trp-3;su(trp-3^{td201})	td201;su201-4	1619		IIR;VIIR	SRS
trp-3;su(trp-3^{td201})	td201;su201-6	1620		IIR;VIIR	SRS
trp-3;su(trp-3^{td201})	td201;su210-7	1621		IIR;VIIR	SRS
trp-3;su(trp-3^{td201})	td201;su201-1		1618	IIR;VIIR	SRS
fl;wc-1	ER45;P	7205	7206	IIR;VIIR	FRL
II;--					
uc-1 pyr-4;uc-3	RW57 33601;RW203		2204	II IIL;--	LGW
III;IV					
acr-2;cys-10 pdx-1 pan-1	KH53(r);39816 37803 5531	5195		IIIC;IVL R R	EK
acr-2;cys-10 pdx-1 pan-1 uvs-2	KH53(r);39816 37803 5531 no#	5194		IIIC;IVL R R R	EK
sc;pdx-1	5801;37803	336		IIIR;IVR	DDP
III;V					
ad-2;inl	1-175-256;JH319	5042	5046	IIIR;VR	FJD
ad-2;per-1	STL2;ABT8	2551		IIIR;VR	TEJ
leu-1;mus-28	33757;FK118	6436	6437	IIIR;VL	EK
sc;inl	R2503;89601		1398	IIIR;VR	ELT
trp-1;am	15;am$_{17}$	1848	1847	IIIR;VR	JHC
trp-1;inl	25;37401		4544	IIIR;VR	DDP
III;VI					
acr-2 dow;chol-2 trp-2	KH5(r) P616;47904(t) 75001		4154	IIIL R;VILR	EK
acr-2 dow;chol-2 ylo-1 trp-2	KH5(r) P616;47904(t) Y30539y 75001	4153		IIIL R;VILR	EK
phe-2 tyr-1;trp-2	E5212 C167;75001		3255	IIIR R;VIR	RLM
sor-3 ad-4;sor-1 ylo-1	17(r) K5-M27;10(r);Y30539y	2377		IIIR R;VIL L	WK
trp-1;ylo-1	10575;Y30539y	1207	1208	IIIR;VIL	DDP

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
		III;--			
ota;sit-5	UM728;GN218		4218	IIIR;--	GWC
		IV;V			
cot-1;lys-1	C102(t);33933		2254	IVR;VC	RKL
ilv-3;lys-1	T344;33933	1053		IVR;VC	RPW
bd;inv	no#;no#	1860	1861	IVR;VR	MLS
chol-1;inl	34486;89601		2950	IVR;VR	SB
cot-1;al-3	C102(t);RP100	4155	4156	IVR;VR	EK
cot-1;gul-1	C102(t);CA1	1962	1963	IVR;VR	DS
cot-1;inl	C102(t);37401	1243	1244	IVR;VR	DDP
met(26U);inl	26U(t);89601		3762	IVR;VR	DRS
oxD met-1;inl	8 38706;89601	1325	889	IVR R;VR	NHH
pan-1;mus-11	5531;FK117	6411	6412	IVR;VR	EK
pan-1;mus-12 inl	5531;SC15 83201(t)		3906	IVR;V VR	NCM
pdx-1;scon cyh-2	37803;$scon^C$;KH53(r)		2143	IVR;VR R	RLM
psi-1;inl	1;89601		2651	IVR;VR	ML
pyr-3;per-1	KS43;PBE1	2546		IVR;VR	TEJ
pyr-3;per-1	KS43;PBJ1	2548		IVR;VR	TEJ
spco-8;inl	R2462;89601		1383	IV;VR	ELT
un(74E);inl	74E(t);89601		3776	IV(?);VR	DRS
uvs-2;mei-2	no#;ALS181		4618	IVR;VR	ALS
		IV;VI			
uvs-3;ylo-1 pan-2	ALS11;Y30539y B5(Y154M64)	4192	4193	IVL;VIL R	EK
chol-1;chol-2	34486;47904(t)	2949		IVR;VIL	SB
cot-1;gul-5	C102(t);BAT26-2		2956	IVR;VI	JLR
cot-1;ylo-1	C102(t);Y30539y	4621	212	IVR;VIL	DDP
cot-1;pan-2	C102(t);1-153-96	5271	5272	IVR;VIR	FJD
mtr;ylo-1	6(r);ylo-1		1117	IVR;VIL	DRS
ad-6;ws-1	RP102;RP99	2078		IVR;VIR	RLP
		IV;VII			
cys-10;nic-3	39816;Y31881	1541	1542	IVL;VIIL	DDP
bd;csp-2	no#;UCLA101	4548	4549	IVR;VIIL	DDP
pt;ylo-1	NS1(t);Y30539y	137	10	IVR;VIIL	DDP
pyr-1;ud-1	H263;RW433		2202	IVR;VIIR	LGW
arg-14, pyr-3; aga	CD21, DFC3; UM906	8391	8390	IVR, IVR, VIIR	RHD
		IV;--			
cot-1;gluc-1	C102(t);CM26(3-8)		1224	IVR;--	BME
gpi;pp	T66M37g;T66M37p	3432		IV;--	TI
leu-2;glt	37501;D240(R)		2737	IVR;--	GAM
pan-1;mus(SC1)	5531;SC1(s)	3902		IVR;--	NCM
pyr-1;uc-3	H263;RW203		2205	IVR;--	LGW
		V;VI			
lys-1 cyh-2;chol-2 ylo-1 trp-2	33933 KH53(r);47904(t) Y30539y 41	5207	5208	VC R;VIL L R	EK
ad-7;ylo-1	44411;Y30539y	89		VR;VIL	DDP
al-3;ws-1	RP100;RP99	2084		VR;VIR	RLP
am;trp-2	am_{17};10	1849		VR;VIR	JHC
cyh-2 al-3 inl;nic-3 met-7 arg-10	KH53(r) RP100 83201(t);Y31881 4894 B317	5197	5198	VR R R;VIIL R R	EK

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
	V;VI, continued				
erg-1;pan-2	uv1;Y153M66	2722		VR;VIR	MG
erg-2;pan-2	NAN25;Y153M66	2724		VR;VIR	MG
his-1 pk;ylo-1	C84 B6;Y30539y		233	VR R;VIL	WNS
inl;chol-2	89601;47904(t)	2951		VR;VIL	SB
inl;ylo-1	83201(t);Y30539y		285	VR;VIL	WNS
inl;spco-13	89601;R2530s		1351	VR;VI	ELT
inl;moe-2	89601;R2532	1386		VR;VIC	ELT
lys-2 pk ad-7;ylo-1	37101 C-1810-1 44411;Y30539y	241		VR R R;VIL	WNS
met-3;ylo-1	36104;Y30539y		251	VR;VIL	DDP
pab-2;ylo-1	H193;Y30539y	225		VR;VIL	DDP
	V;VII				
am;ssu-4	am_{17};WRU18	1852		VR;VIIC	TWS
am;ssu-1	am_{17};WRN33	1687	1688	VR;VIIR	TWS
inl;le-2	89601;R2411	1395		VR;VIIR	ELT
inl pab-2;slo-2	37401 H193;no#	202		VR R;VIIC	WNS
inl;un-22	89601;61C(t)		3767	VR;VIIR	DRS
per-1;csp-2	PBJ1;UCLA101	6662	6663	VR;VIIL	DDP
	V;--				
inl;cni-1	89601;1;	3232		VR;--	DLE
inl;met(105W)	89601;105W(t)		3764	VR;--	DRS
inl;met(119W)	89601;119W(t)		3765	VR;--	DRS
inl;met(29T)	89601;29T(t)		3761	VR;--	DRS
inl;thr(4V)	89601;4V(t)		3763	VR;--	DRS
inl;tre^{in}*t*	89601;19-31		4507	VR;--	MLS
inl;tre^{int}	89601;31-601		4508	VR;--	MLS
inl;un(23M)	89601;23M(t)		3779	VR;--	DRS
inl;un(74M)	89601;74M(t)		3780	VR;--	DRS
ure-1 his-1;su[ure-1(9)]	9 C91;no#	4300		VR R;--	GK
ure-2 am;su[ure-1(9)]	47 32213;no#	4301		VR R;--	GK
	VI;VII				
chol-2;spco-4 wc-1 nt	47904;R2367 P829 65001	2924	2925	VIL;VIIL R R	DDP
pan-2;qa-2	B23;204	3230		VIR;VIIR	MEC
pan-2;qa-2	B36;239		3231	VIR;VIIR	MEC
	VI;--				
cpc-1;slo	j-5;17	4433	4434	VIL;--	IB
pan-2;fs-2	Y153M96;10-4(t)		3237	VIR;--	MM
pan-2;fs-4	Y153M96;2326	3242		VIR;--	MM
pan-2;fs-6	2351;Y153M96	3244		VIR;--	OMM
	VII;--				
kyn-1;leu	RC71-3;no#		2512	VII;--	PJR
nic-3;fs-1	Y31881;19-2	3235	3236	VIIL;--	OMM
nic-3;fs-4	Y31881;2326		3241	VIIL;--	OMM
nic-3;fs-5	Y31881;5-5		3243	VIIL;--	OMM

		FGSC # mating type		Linkage	Obtained
Loci	Alleles	A	a	group	from
--;--					
sit-1;sit-2	GN328;GN140	4226	4227	--;--	GWC
sit-2;sit-3	GN328;GN235	4221	4222	--;--	GWC
sit-3;sit-5	GN235;GN218		4230	--;--	GWC

C. Three Linkage Groups Marked

Loci	Alleles	A	a	Linkage group	Obtained from
I;II;III					
sn cr-1;arg-5 pe fl;acr-2	C136 B123;27947 Y8743m L;KH5(r)		5168	IC R;IIR R R;IIIC	EK
I;II;IV					
al-1;arg-5;cot-1	15300;27947;C102(t)	2252		IR;IIR;IVR	RKL
al-2;pe;col-1	15300;Y8743m;Y8743c	536		IR;IIR;IVR	ELT
cyh-1 al-2;ro-7;pan-1 cys-4	KH52(r) 15300;R2470;5531 K7		5201	IR R;IIL;IVR R	EK
nic-2 cyh-1 al-2;arg-5;cys-4	S1413 KH52(r) 15300;27947;K7		5157	IR R R;IIR;IVR	EK
un-5 al-2;pi;cys-10	b39(t) 15300;B101;39816	2922	2923	IL R;IIL;IVL	DDP
I;II;V					
al-2;rip-1;inl	15300;4M(t);89601	2650		IR;IIR;VR	ML
cr-1;pe fl;al-3 inl	B123;Y8743m L;RP100 83201(t)	4166		IC;IIR R;VR R	EK
sn cr-1;pe fl;al-3 inl	C136 B123;Y8743m L;RP100 83201(t)	4164	4165	IC;IIR;VR	EK
I;II;VII					
his-3;ff-1;hlp-1	K458;T30;B538	2320		IR;IIR;VIIR	HCC
nic-2 cyh-1 al-2;arg-5;met-7	S1413 KH52(r) 15300;27947 4894	5153		IR R R;IIR;VIIR	EK
al-1;arg-5;csp-2	34508;27947;UCLA101	6942	6943	IR;IIR;VIIL	DDP
I;III;IV					
al-1;ad-2;col-4 cot-1	1-234-471;1-175-256;70007c C102(t)	5594	5593	IR;IIIR;IVR R	FJD
al-1;ad-2;cot-1	1-234-471;1-175-256;C102(t)	5588	5589	IR;IIIR;IVR	FJD
al-1;ad-2;mtr col-4 cot-1	1-234-471;1-175-256;17-1-64 70007c C102(t)	5605		IR;IIIR;IVR R R	FJD
al-2;ser-5;cot-1	15300;JBM9;C102(t)	2612		IR;IIIR;IVR	JBM
his-3 al-1;ad-2;col-4 cot-1	1-152-111 1-234-471;1-175-256; 70007c C102(t)	5595	5596	IR R;IIIR; IVR R	FJD
his-3 al-1;ad-2;cot-1	1-152-111 1-234-471;1-175-256; C102(t)	5590		IR R;IIIR;IVR	FJD
his-3 al-1;ad-2;mtr col-4	1-152-111 1-234-471;1-175-256; 17-1-64 70007c	5601	5602	IR R;IIIR;IVR R	FJD
sn cr-1;acr-2;cys-10 pdx-1 pan-1 uvs-2	C136 B123;KH5(r);39816 37803 5531 no#		5188	IC R;IIIC;IVL R R R	EK
I;III;V					
al-2;sc;lys-1	15300;5801;33933	230	231	IR;IIIR;VC	DDP
arg-3 ad-3A ad-3B nic-2; ad-2;inl	30300 1-112-13 35203 43002; 1-175-256;JH319	5556		IL R R R;IIIR VR	FJD
arg-3 ad-3A ad-3B nic-2 al-1;ad-2;inl	30300 1-112-13 35203 43002; 1-234-471 1-175-256;JH319	5554	5552	IL R R R R IIIR;VR	FJD

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
I;III;V, continued					
his-2 ad-3A ad-3B nic-2 al-2;ad-2;inl	C94 1-112-13 35203 43002 1-112-38;1-175-256;JH319	5533		IR R R R R; IIIR;VR	FJD
his-2 ad-3A ad-3B nic-2 al-1;ad-2;inl	C94 1-112-13 35203 43002 1-234-471;1-175-256;JH319		5538	IR R R R R; IIIR;VR	FJD
his-2 ad-3A ad-3B nic-2;ad-2;inl	C94 Y112M13 35203 43002;Y175M256;JH319	2582		IR R R R; IIIR;VR	FJD
I;III;VI					
sn cr-1;acr-2;chol-2 ylo-1 trp-2	C136 B123;KH5(r);47904(t) Y30539y 41	5172	5173	IC R;IIIC;VIL L R	EK
sn cr-1;mtr uvs-2;lys-5 trp-2		7882		IC R;IVR R;VIL R	DRS
sn cr-1 cyh-1;ad-2;trp-2		7883		IC R R;IIIR;VIR	
I;III;--					
ff-3;ty-3;ty-4	HC725;T22;no#	4877		IR;IIIR;--	HCC
I;IV;V					
un-5;cys-10 uvs-2;al-3 inl his-6	b39(t);39816 no#;15300 83201(t) Y152M105	5202	5203	IL;IVL R;VR R R	EK
mus(SC25) sn cr-1 al-2;pan-1;inl	SC25;C136 B123 15300; 5531;83201(t)	3908		I C R R; IVR;VR	NCM
sn cr-1;mtr met-2 pan-1; al-2 inl	C136 B123;15 P159 5531; 15300 83201(t)	5217		IC R;IVR R R; VR R	EK
his-3 cyh-1 al-1;mtr;inl	1-234-723 KH52(r) 34508;SR62;89601	7507	7508		
al-2;pan-1;inl;mus(SC17)	15300;5531;83201(t);SC17		3907	IR;IVR;VR;V	NCM
cr-1 al-2;cot-1;inl	B123 1-112-38;C102(t);JH319		5618	IR R;IVR	FJD
his-2;mtr;pdx-1	Y152M43;120(r);37803	3021		IR;IVR;VR	DRS
nic-1;cot-1;inl	39113;C102(t);JH319		5530	IR;IVR;VR	FJD
un-18;rug;his-6	T54M94(t);B57;Y152M105	2944	2945	IR;IVR;VR	DDP
I;IV;VI					
al-2;cot-1;pan-2	Y112M38;C102(t);Y387-15.7	2583	4934	IR;IVR;VIR	FJD
al-2;pan-1;mus(SC13)	15300;5531;SC13		3905	IR;IVR;VI	NCM
al-2;pan-1;mus-14	15300;5531;SC3		3903	IR;IVR;VI	NCM
al-2;cot-1;pan-2 ad-8	Y112M38;Y387-15.7;C102(t) E146		5071	IR;IVR;VIR L	HI
al-2;cot-1;pan-2 ad-8	Y112M38;Y387-15.7;C102(t) E193		5072	IR;IVR;VIR L	HI
al-2 nic-1;cot-1;pan-2	1-112-38 39113;C102(t);1-153-96		5543	IR R;IVR;VIR	FJD
cr-1 al-2;cot-1;pan-2	B123 1-112-38;C102(t);1-153-96	5617	5616	IR R;IVR	FJD
cr-1;cot-1 grey;ylo-1	L;C102(t) KH165 Y30539y		2328	IR;IVR R;VI	KSH
cr-1;cot-1;ylo-1	L;C102(t);Y30539y	191		IR;IVR;VIR	DDP
al-2;uvs-3 cot-1;pan-2	Y112M38;ALS11 C102(t);Y387-15.7	2714	2715	IR;IVL IVR;VIR	FJD
ad-3A al-2;cot-1;pan-2	N23 Y112M38;C102(t);Y387-15.7	3331		IR R;IVR;VIR	TMO
ad-3A al-2;cot-1;pan-2	N24 Y112M38;C102(t);Y387-15.7	3332		IR R;IVR;VIR	TMO
ad-5 his-2 al-1;pt;ylo-1	Y152M40 Y152M14 34508; NS/t;Y30539y		235	IL R R;IVR;VIL	DDP
arg-3 nic-2 al-1;pt;ylo-1	30300 43002 34508;NS1(t);Y30539y	240		IL R R;IVR;VIR	DDP
his-2 ad-3A ad-3B nic-2 al-2;cot-1;pan-2	C94 1-112-13 35203 43002 1-112-38;C102(t);1-153-96		5454	IR R R R R; IVR;VIR	FJD
his-2;mtr;pdx-1;su(mtr26)	Y152M43;26(r);37803;26-R5035		2732	IR;IVR;R;VI	NGB

Loci	Alleles	FGSC # mating type A	a	Linkage group	Obtained from
	I;IV;VI, continued				
his-2;mtr;pdx-1;su(mtr26)	Y152M43;26(r);37803;26-R5037		2733	IR;IVR;R;VI	NGB
his-3 al-2;cot-1;pan-2	1-152-111 1-112-38;C102(t); 1-153-96	5603		IR R;IVR;VIR	FJD
ro al-2;cot-1;pan-2	P1798 1-112-38;C102(t);1-153-96	5597	5598	IR R;IVR;VIR	FJD
sn cr-1;mtr;lys-5 trp-2		7881		IC R;IVR;VIL R	
	I;IV;VII				
csp-1;bd;oli	UCLA37;no#;no#(r)	3483		IL;IVR;VIIR	SB
arg-1, arg-6; pyr-3, pyr-1; aga	CD145, CD29; DFC8, DFC33; UM906		8389	IL, IR; IVR, IVR; VIIR	RHD
	I;IV;--				
pmg;pmn pmb;lox	no#;no# no#;rd9	4246	4247	IL;IVR R;--	RMD
al-2;pan-2 cot-1 uvs-1	Y112M38;Y153M96 C102(t) no#		4581	IR;IVR R;--	FJD
	I;V;VI				
al-1 al-2;al-3;wc-1	34508 15300;RP100;ER45	5140	5141	IR R;VR;VIIR	MGS
al-1;his-1;pk;ylo-1	34508;C84;B6;Y30539y		234	IR;VR R;VIL	WNS
al-1;inl pab-2;ylo-1	34508;37401 H193;Y30539y	150		IR;VR R;VIL	DDP
al-2;inl;mus(SC10)	15300;83201(t);SC10		3904	IR;VR;VI(?)	NCM
al-2;inl;pan-2	1-112-38;JH319;1-153-96	5515	5514	IR;VR;VIR	FJD
nic-1 al-2;inl;pan-2	39113 1-112-38;JH319;1-153-96		5624	IR R;IVR	FJD
sn cr-1;lys-1 cyh-2; chol-2 ylo-1 trp-2	C136 B123;33933 KH53(r) 47904(t) Y30539y 41		5213	IC R;VC R;VIL L R	EK
sn cr-1;lys-1 cyh-2; ylo-1 pan-2	C136 B123;33933 KH53(r) Y30539y B2(Y153M66)	5216		IC R;VC R;VIL R	EK
un-18;cyh-2;chol-2 ylo-1 trp-2	T54M94;KH53(r);47904(t) Y30539y 41		5204	IR;VR;VIL L R	EK
	I;V;VII				
al-1;inl pab-2;slo-2	34508;37401 H193;no#	203		IR;VR R;VIIC	WNS
sn cr-1;cyh-2 al-3 inl; nic-3 met-7 arg-10	C136 B123;KH53(r) 15300 83201; Y31881 4894 B317		5196	IC R;VR R R; VIIL R R	EK
	I;V;--				
ssu-2;am;al	WRU35;am$_{17}$;no#	1689		IR;VR;--	TWS
	I;--;--				
suc;ma-1;ma-2	46005;M20;M24		1114	IR;--;--	KDM
	II;III;VI				
rip;dow;trp-2	4M(t);P616;45302	3313	3314	IIR;IIIR;VIR	DDP
un-15;dow;trp-2	T54M50(t);P616;45302	2926	2927	IIR;IIIR;VIR	DDP
	II;III;VII				
bal;acr-2;wc-1	B56;KH5(r);P829	1539	1540	IIL;IIIC;VIIC	DDP
arg-5;ota;aga	27947;UM728;UM906	2744		IIR;IIIR;VIIR	RHD

Loci	Alleles	FGSC # mating type		Linkage group	Obtained from
		A	a		
II;IV;V					
acr-2;uvs-2;his-6	KH5(r);no#;Y152M105	4190		IIC;IVR;VR	EK
ff-1;ylo-1;inl	744;Y30539y;83201(t)	2967		IIR;IVL;VR	JBC
fl;dn;inl	P;38502d;37401	3633	3634	IIR;IVR;VR	DDP
II;V;VII					
aro-9;qa-2;inl	M6-11;89601;M246	3952		IIR;VR;VIIR	MEC
II;VI;VII					
bal;ylo-1;met-7	B56;4894;Y30539y		330	IIL;VIL;VIIR	DDP
arg-5;sit-2;sit-5	no#;GN328;GN218		4223	IIR;--;--	GWC
III;IV;V					
acr-2;uvs-2;his-6	KH5(r);no#;Y152M105		4190	IIIC;IVR;VR	EK
III;IV;VI					
trp-1;cot-1;ylo-1	10575;C102(t);Y30539y	1095		IIIR;IVR;VIL	DDP
III;--;--					
ota;sit-2;sit-3	UM728;GN328;GN235		4219	IIIR;--;--	GWC
ota;sit-2;sit-5	UM728;GN328;GN218		4224	IIIR;--;--	GWC
VI;VII;--					
pan-2;nic-3;fs-2	Y153M96;Y31881;10-4(t)	3238		VIR;VIIL;--	OMM
D. Four Linkage Groups Marked					
sn cr-1 cyh-1;ad-2;uvs-2;trp-2		7880		IC R R;IIIR;IVR;VIR	DRS
al-1;arg-5;trp-1;ylo-1	34508;27947;10575;Y30539y	2124	1888	IR;IIC;IIIR;VIL	DDP
al-1;arg-5;cot-1;inl	34508;27947;C102(t);37401	1885	1886	IR;IIC;IVR;VR	DDP
al-2;fl;cot-1;inl	1-112-38;L;C102(t);JH319	5621		IR;IIR;IVR;VR	FJD
al-2;pe fl;cot-1;pan-2	1-112-38;L L;C102(t);1-153-96	5516		IR;IIR R;IVR;VIR	FJD
cr-1 al-2;fl;cot-1;inl	B123 1-112-38;L;C102(t);JH319	5622		IR;IIR;IVR;VR	FJD
nic-2 cyh-1 al-2;arg-5; pan-1;met-7	43002 KH53(r) 15300;27947; 5521;4894	5152		IR R R;IIIR;IVR VIIR	
al-2;uvs-4;cot-1;pan-2	Y112M38;ALS12;C102(t);Y153M96	4585	4586	IR;IIIR;IVR;VIR	FJD
al-2;uvs-5;cot-1;pan-2	Y112M38;ALS13;C102(t);Y153M96	4587	4588	IR;IIIR;IVR;VIR	FJD
al-2;uvs-5;cot-1;pan-2	Y112M38;ALS13;C102(t); Y387-15.7	2716	2717	IR;IIIR;IVR;VIR	FJD
al-2;cot-1;inl;pan-2	1-112-38;C102(t);JH319;1-153-96	5542		IR;IVR;VR;VIR	FJD
arg-3 al-2;cot-1;inl;pan-2	30300 1-112-38;C102(t);JH319; 1-153-96	5614		IL R;IVR;VR;VIR	FJD
cr-1 al-2;cot-1;inl; pan-2	B123 1-112-38;C102(t);JH319; 1-153-96	5615		IR R;IVR;VR;VIR	FJD
his-3 al-2 cot-1 inl pan-2	1-152-111 1-112-38;C102(t); JH319;1-153-96	5040		IR R;IVR;VR;VIR	FJD
lys-4 al-2 cot-1 inl pan-2	ST3954 1-112-38;C102(t); JH319;1-153-96	5039	5048	IR R;IVR;VR;VIR	FJD
nic-1 al-2;cot-1;inl;pan-2	39113 1-112-38;C102(t);JH319; *1-153-96*	5623	5625	IR R;IVR;VR;VIR	FJD
cyh-1 al-2 al-1;bd;inl al-3;csp-2	KH52(r) 15300 34508;no# 83201(t);RP100(t);UCLA101		4554	IR R R;IVR VR R;VIIL	DDP

Four Linkage Groups Marked, continued

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
al-2;pan-1;inl;mus(SC29)	15300;5531;83201(t);SC29	3909		IR;IVR;VR;--	NCM
al-2;cot-1;pan-2;arg-10	1-112-38;C102(t);1-153-96;B317	5510		IR;IVR;VIR;VIIR	FJD
sn cr-1;lys-1 cyh-2;ylo-1 pan-2;nic-3	C136 B123;33933 KH53(r); Y30539y Y153M96;Y31881	5211		IC R;VC R;VIL VIR;VIIL	EK
sn cr-1;lys-1;ylo-1 pan-2;nic-3 met-7	C136 B123;33933;Y30539y Y153M96;Y31881 4894	5215		IC R;VC;VIL R; VIIL R	EK
pe fl;cot-1;inl;gul-2	Y8743m L;C102(t);37401;264	1173		IIR R;IVR;VR;--	HFT
arg-5;acr-2;pdx-1 mtr pan-1;al-3 inl	27947;KH53(r);37803 5531;15300 83201(t)	5209		IIR;IIIC;IVR R R;VR R	EK
aro-9;trp-1;inl;qa-2	Y325M6;20;89601;M246	4545		IIR;IIIR;VR;VII	DDP
arg-5 acr-2 ylo-1 wc-1	27947 KH5(r) Y30539y P829	3118		IIC;IIIL;VIL;VIIC	DDP
rip-1;acr-2 dow;ylo-1 nic-3 arg-10	4M(t);KH53(r) P616;Y30539y Y31881 B317	5199	5200	IIL;IIIC R;VIL; VIIL R	EK
arg-5;ota;sit-2;sit-3	no#;UM728;GN328;GN235	4220		IIR;IIIR;--;--	GWC
arg-5;ota;sit-2;sit-5	no#;UM728;GN328;GN218	4225		IIR;IIIR;--;--	GWC
arg-5;ota;sit-4;sit-5	no#;UM728;GN435;GN218	4228	4229	IIR;IIIR;--;--	GWC
pe col-1;su(pe);acon	Y8743m;Y8743c;no#;no#(t)	781		IIR;IVR;--;--	GWG
trp-1;cot-1;al-3;ylo-1	10575;C102(t);RP100;Y30539y	4321	4322	IIIR;IVR;VR;VIL	DDP
trp-1;cot-1;inl;ylo-1	10575;C102(t);37401;Y30539y	1987	1988	IIIR;IVR;VR;VIL	DDP
cot-1;inl;ylo-1;nt	C102(t);37401;Y30539y;C86	333		IVR;VR;VIL;VIIR	DDP
gul-4;pe fl;cot-1;inl	42;Y8743m L;C102(t);37401	1605		VII;IIR R;IVR;VR	JLR

E. Five Linkage Groups Marked

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
al-2;fl;cot-1;inl;pan-2	1-112-38;L;C102(t);JH319;1-153-96		5620	IR;IIR;IVR;VR;VIR	FJD
al-2;cot-1;inl;pan-2; arg-10	1-112-38;C102(t);JH319; 1-153-96;B317	5627	5626	IR;IVR;VR;VIR; VIIR	FJD
acr-2;pdx-1;at;ylo-1;wc-1	KH5(r) 37803 M111 Y30539y P829	1985	1986	IIIC;IVC;VC;VIL;VIIR	DDP
sn cr-1;arg-5;acr-2;pdx-1 mtr pan-1;al-3 inl	C136 B123;27947;KH53(r); 37803 5531;15300 83201(t)	5214		IC R;IIR;IIIC; IVR R R;VR R	EK

F. Six Linkage Groups Marked

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
arg-5;acr-2;mtr;al-3 inl; rib-1;met-7	27947;KH53(r);15;RP100 83201(t);51602(t);4894	5205	5206	IIR;IIIC;IVR; VR R;VIR;VIIR	EK
bal;acr-2;pdx-1;at; ylo-1;wc-1	B56;KH5(r);37803;M111; Y30539y;P829	2014	2015	IIR;IIIR;IVR; VC;VIR;VIIR	DDP
arg-5;acr-2;psi-1;at; ylo-1;wc-1	27947;KH5;34C(t);M111; Y30539y;P829	6828	6829	IIR;IIIL;IVR VC;VIL;VIIR	DDP

G. Seven Linkage Groups Marked

Loci	Alleles	FGSC # mating type A	FGSC # mating type a	Linkage group	Obtained from
al-2;fl;sc;pan-1;inl; ylo-1;nt	15300;L;5801;5531;37401; Y30539y;C86		281	IR;IIR;IIIR; IVR;VR;VIL;VIIR	DDP
al-2;trp-3;tyr-1;pdx-1 inl;chol-2;thi-3 ars(101)	15300;td37;Y6994;37803; no#;47904(t);18558 101	2053	2054	IR;IIR;IIIR; IVC;VR;VIL;VIIR	RLM
In(IL;IR)OY323;arg-5; acr-2;pdx-1;at;ylo-1;wc-1	OY323;27947;KH5;37803;M111 Y30539y;P829	6824	6825	I;IIR;IIIL;IVR VC;VIL;VIIR	DDP
In(IL;IR)OY323;arg-5; acr-2;psi-1;at;ylo-1;wc-1	OY323;27947;KH5;34C(t);M111 Y30539y;P829	6832	6833	I;IIR;IIIL;IVR VC;VIL;VIIR	DDP

PART III. Mitochondrial Mutant Stocks

When designating the genotype of extrachromosomal mutants, the symbol is enclosed in brackets (Barratt, R.W. 1967. Neurospora Newslett. 12:11).

Symbol	Isolation designation or stock #	MT	FGSC #	Nuclear gene markers present	Genetic back-ground	Obtained from
ABNORMAL						
[*abn-1*]	no#	*a*	1448	*inl*(37401)	M	DJL
[*abn-2*]	no#	*A*	1458		M	JFW
CYANIDE INSENSITIVE						
[*cni-3*]	1	*A*	3304	*inl*(89601)	M	DLE
EXTRANUCLEAR						
[*exn-1*]	N4-9-4	*a*	2475	*pan-2*(B3)		HB
[*exn-2*]	X-21	*a*	2476	*al-2*(15300),*nic-1*(3416)	M	HB
[*exn-4*]	P85	*a*	2477	*al-2*(15300);*pan-2*(B3)	M	HB
[*exn-5*]	exn-5-1	*a*	2478		M	HB
[*exn(C93)*]*	C93	*A*	3557		SL	THP
* Probably ATPase mutant; complements in heterokaryon with [*poky*].						
MATERNAL INHERITANCE						
[*mi-2*]	mi-2-3.3	*A*	1580		SL3	PSL
[*mi-2*]	mi-2-3.5	*a*	1581		SL3	PSL
[*mi-2*]	mi-2R1	*a*	1233		M	MBM
[*mi-2*]	mi-2-3.1	*A*	1579	*ad-4*(F4)	SL3	PSL
[*mi-2*]	mi-2-3.7	*a*	1582	*ad-4*(F4)	SL3	PSL
[*mi-3*]	no#	*A*	1729		SL	NJW
[*mi-3*]	2543	*A*	2472	*su-1([mi-3])*(CR-52A)	M	HB
[*mi-3*]	2543	*a*	7595	*su-1([mi-3])*(CR-52A)pan-2-B3	M	FEN
[*mi-3*]	3754	*a*	382		M	MBM
[*mi-3*]	3754	*A*	4691	*eas*(UCLA191)		MLS
[*mi-3*]	3754	*a*	4692	*eas*(UCLA191)		MLS
[*mi-4*]	mi-4	*A*	1234		M	MBM
[*mi-4*]	mi-4-3.1	*A*	1583		SL3	PSL
[*mi-4*]	mi-4-3.5	*a*	1585		SL3	PSL
[*mi-4*]	mi-4-3.3	*A*	1584	*pan-1*(5531)	SL3	PSL
[*mi-4*]	mi-4-3.7	*a*	1586	*pan-1*(5531)	SL3	PSL
[*mi-5*]	mi-5-1.2	*A*	1587		SL3	PSL
[*mi-5*]	mi-5-1.4	*a*	1588		SL3	PSL
[*mi-5*]	mi-5R1	*A*	1235		M	MBM
[*mi-5*]	mi-5-1.6	*a*	1589	(F4)	SL3	PSL
[*mi-5*]	mi-5-1.8	*A*	1590	(F4)	SL3	PSL
[*mi-6*]	mi-6-2.2	*a*	1591		SL3	PSL
[*mi-6*]	mi-6-2.8	*A*	1594		SL3	PSL
[*mi-6*]	mi-6R1	*A*	1236		M	MBM
[*mi-6*]	mi-6-2.2	*a*	1592	*ad-4*(F4)	SL3	PSL
[*mi-7*]	mi-7	*A*	1237		M	MBM
[*mi-7*]	mi-7-4.2	*a*	1595		SL4	PSL
[*mi-7*]	mi-7-4.6	*A*	1597		SL4	PSL
[*mi-7*]	mi-7-4.4	*a*	1596	*ad-4*(F4)	SL4	PSL
[*mi-7*]	mi-7-4.8	*A*	1598	*ad-4*(F4)	SL4	PSL
[*mi-8*]	mi-8-1.4	*a*	1600		SL3	PSL
[*mi-8*]	mi-8-1.6	*A*	1601		SL3	PSL
[*mi-8*]	mi-8R6*	*a*	1238		M	MBM
[*mi-8*]	mi-8-1.2	*a*	1599	*ad-4*(F4)	SL3	PSL
[*mi-8*]	mi-8-1.8	*A*	1602	*ad-4*(F4)	SL3	PSL

* [*mi-8*] was originally isolated from the cross of wild type 8a X C83(trp-3); in turn C83 was isolated from 8a X 7A by Mary B. Mitchell.

Symbol	Isolation designation or stock #	MT	FGSC #	Nuclear gene markers present	Genetic back-ground	Obtained from
POKY (also called [*mi-1*])						
[*poky*]	3627-2	*A*	384		M	MBM
[*poky*]	mi-1-1.4	*A*	1575		SL3	PSL
[*poky*]	mi-1-1.8	*a*	1578		SL	PSL
[*poky*]	[13-5]	*A*	3485	*bd*(no#);inl(89601?)		SB
[*poky*]	3627-4	*A*	4693	*eas*(UCLA191)		MLS
[*poky*]	3627-4	*a*	4694	*eas*(UCLA191)		MLS
[*poky*]	mi-1-1.6	*a*	1577	*nic-2*(?)	SL3	PSL
[*poky*]	mi-1-1.2	*A*	1576	*nic-2*(?)	SL3	PSL
[*poky*]	3627-3	*a*	386	*su([mi-1*])-f	M	MBM
[*poky*]	3627-4	*A*	385	*su([mi-1*])-f	M	MBM
RESPIRATORY DEFECTIVE						
[*rsp-1*]	1	*A*	3233		M	DLE
[*rsp-2*]	1	*A*	3301	*inl*(89601)	M	DLE
[*rsp-3*]	1	*A*	3303	*inl*(89601)	M	DLE
[*rsp-4*]	1	*A*	3302	*inl*(89601)	M	DLE
SLOW GROWTH						
[*SG-1*]	RL3202-23	*a*	1702		SL	AMS
[*SG-3*]	RL3120-10	*a*	1452		M	AMS
STOPPER						
[stp-B1]	30a-1	*A*	1574	*al-2*(15300);*ad-4*(F4)	M	HB
[*stp*]	17-2a-1	*A*	1573	*al-2*(15300);*ad-4*(F4)	M	HB
[*stp*]	E35	*A*	5061	*al-3*(RP100);*inl*(89601)		HDV
[*stp*]	Iar155	*A*	6654	*met-2*(no#);*inl*(89601	M	SRG
[*stp*]	ER-3	*A*	6716	*inl*(89601)	RL	AA
ULTRAVIOLET SENSITIVE (NON-NUCLEAR)						
[*uvs(cyt)*]	no#	*A*	1631	*cr-1*(B123),*rg-1*(B53); *pe*(Y8743m,*fl*(L)	M	RWT

Strains shown to contain Mitochondrial Plasmids

N. crassa	FGSC #	Reference
Mauriceville-1c	2225	1,6
Mauriceville M2-8	6008	6
Mauriceville M3-24	6009	6
Roanoke-1	2228	5

N. intermedia	FGSC #	Reference
Fiji N6-6	435	2
LaBelle-1b	1940	2
Varkud-1c	1823	3,6
Varkud 1-2	6006	6
Varkud V2-7	6037	6
Varkud V3-8	6007	6

N. tetrasperma	FGSC#	Reference
85A	1270	4
Hanalei-1bv1	2510	4
Lihue-1v2	2509	4
Waimea Falls-2	3296	4

Please note, this list is not exhaustive, but rather illustrative. For a more thorough description of strains carrying mitochondrial plasmids, please consult the following references.

1. Collins, R.A. et al. 1981. Cell 24:443
2. Stohl, L.L. et al. 1982. Nuc. Acid Res. 10:1439
3. Stohl, L.L. et al. 1983. Fed. Proc. 42:1972
4. Natvig, D.O. et al. 1984. J. Bact. 159:288
5. Taylor, J.W. et al. 1985. Mol. Gen. Genet. 201:161
6. Akins, R.A. et al. 1986. Cell 47:505
7. Yang, X., and AJF Griffiths 1993 Mol Gen Genet 237:177-186
8. Arganoza et al 1994 Curr Genet 26:62-73
9. Nargang, F.E. 1985 Exp Mycol 9:285-293
10. Court et al. 1991 Curr Genet 19:129-137
11. Bok and Griffiths 2001 Plasmid 43:176-80

kalilo strains of *N. intermedia* (Griffiths and Bertrand, 1984. Current Genetics 8:387-398)

Strain designation	FGSC #	Strain designation	FGSC #
Hanalei (P790)	3722	Koloa-1hv1 (P647)	2366
Hanalei-1g (P561)	5014	Lihue-3b (P627)	2365
Kekaha-1 (P589)	2363	Waimea (P612)	3718

maranhar strains of *N. crassa*: (Court et al. 1991. Curr. Genet. 19:129-137)

Strain designation	FGSC #	Strain designation	FGSC #
Aarey-1e	2499	Aarey-1	2500

PART IV. Wild Type Strains

Wild type and wild collected *N. crassa* strains; wild type, wild collected and mutant strains of other Neurospora species; stocks representing related genera. For a general review of wild-collected strains and their uses, see Turner, Perkins, and Fairfield. 2001. Fungal Genet. Biol. 32:67-92. or Exp. Mycol. 12:91-131. For derivation of certain *N. crassa* laboratory stocks see Newmeyer et al., 1987. Fungal Genetics Newsl. 34:46-51 and Perkins, D.D., B.C. Turner and E.G. Barry, 1976. Evolution 30:281-313.

For a conventional key to Neurospora species, see Frederick, L. et al., 1969. Mycologia 61:1077-1084. For a key based on crossing behavior and/or information on origins and characteristics of wild-collected strains, see Perkins et al., 1976, or Perkins, D.D. and N.B. Raju, 1986, Experimental Mycol. 10:323-338. Tester strains for determining species are listed in Part VI of this issue. Usually one A and a pair has been deposited from each locality.

Additional isolates from many localities that were in the Perkins collection are available from the FGSC. These are not listed in the catalog. They are stored according to their 'P' number. Some wild-collected strains from DDP may be mixtures.
FGSC 2489 and 4200 are the recommended wild-type strains. 2489 is the strain that was used for the genome project.
Please see Perkins, 2004. Fungal Genet.Newsl 51:7-8

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
			NEUROSPORA AFRICANA			
Africana N200	1740 (homothallic)		Nsukka, Eastern Nigeria	N200		DPM

NEUROSPORA CRASSA

Standard reference strains and derived wild types. For a detailed pedigree showing origins and relationships, see Newmeyer et al. 1987. FGN 34:46-51. The following stocks are indicated not to be authentic: 351,354,424,541, 687,739,1757 and 1758.

FGSC 2489 and 4200 are the recommended wild-type strains. 2489 is the strain that was used for the genome project. Please see Perkins, 2004. Fungal Genet.Newsl 51:7-8

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
ABBOTT						
Abbott 4 *mei-1*	1228			Abbott 4A		MBM
Abbott	757		(Possibly 4A)	832		DGC
Abb4	1757			10336		ATCC
Abbott 12		351*			12a	MBM
Abb12		1758	contains *un(P8319)* in LG IV		10337	ATCC
Abbott	687					MJM
Abbott	739			831		DGC
CHILTON						
Chilton a	683					MJM
Chilton a	740			837		DGC
Chilton a	1691		Ryan NC5 (R.Goos→FGSC) from Ryan collection via ATCC	42860		ATCC
EMERSON						
Em5256	424		progeny of Abbott X Lindegren			RF
Em5297		352				
Em5296;Em5297	626	627	progeny of Abbott X Lindegren	5256	10816	ATCC
1534.12;1535.11	691	692	from Em5256A X 5297a	1535.12	1535.11	DGC
Em(KJT1960)	2440		from Em5256A X 5297a	KJT1960A		RPW
Em(LSDT1969)	2460	2461	from KJT1960A X KJT1960a	LSDT1969A;a		RPW
LEIN						
Lein 7A	847		C.E. Harrold → NRRL	2332		NRRL
Lein 8a		1693	Ryan NC10 via ATCC		NC10	ATCC

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
LINDEGREN						
Lindegren 1A;25a	5222*	353*	Beadle and Tatum wild type (FGSC 5410 genuine 1A)			MBM
(+)	853		Presumably orig. Lindegren (+)	#239.37		CBS
ROCKEFELLER-LINDEGREN (*het C D E*)						
RL3-8;RL21	2218*	2219*	From 1A X 25a	RL3-8A	RL21a	ELT
* contain *scot* (VR)						
ST. LAWRENCE (het C d e)						
Sta(73a)		3834*	St. Lawrence Standard wild type		8015	DDP
STA4	262		Veg. reisolate of St. Lawrence 74A	8001		DNP
74-OR23-1A;OR8-1a	987	988	Derived Oak Ridge wild type			FJD
74-OR23-1VA	2489		Veg. reisolate of 74-OR23-1A via 8 serial single conidial isolations			OMM
ORSa		2490	Ascospore isolate from 7 generations of backcrosses to 74-OR23-1A			
74-ORS-6a		4200			M527	EK
5.5;3.1	936	935		5.5A	3.1a	MEC
* may differ at a 4th compatability locus. ST73a not compatible with other OR stocks						
YALE (TATUM)						
SY4f3a		621	contains *scot* (VR)		SY4f3a	RWB
SY7A	622		contains *scot* (VR)	SY7A		RWB
HC462		2556			H462	HCC

Other *N. crassa* wild types

1-2A;1-77a	5729	5730	Fast growing isolates.	See Mullaney E.J. and K.E. Papa J. Hered. 73:245-246. 1982		
2A;43a	5731	5732	Slow growing isolates			

Original *N. crassa* strains collected from nature

BANGLADESH						
Dacca	4704		1984	P2525		DDP
BRITISH WEST INDIES						
Old Man Bay-1		8175	Grand Cayman, J. Leslie		P4694	BCT
Old Man Bay-2	8182		Grand Cayman, J. Leslie	P4784		BCT
CONGO						
Bouanza		4819	1985		P3853	DDP
Loubomo		4820	1985		P3826	DDP
Madingo	4822		1985	P3838		DDP
Makaba-2		4821	1985		P3816	DDP
CONTINENTAL UNITED STATES						
Bayou Chicot-5	3227		Louisiana 1977	P873		DDP
Coon-4; -1	3199	3200	Louisiana 1977	P882	P879	DDP
Elizabeth-4; -8	3223	3224	Louisiana 1977	P864	P868	DDP
Everglades	3972		Florida 1980	P1441		DDP
Florida City	3973	3974	Florida 1980	P1453	P1448	DDP
Franklin, LA	7833	7834		P4448	P4449	BCT
Franklin, Louisiana	8870		Single conidium isolate from P4448	D110		DJJ
Franklin, Louisiana		8871	Single conidium isolate from P4449		D111	DJJ

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. crassa CONTINENTAL UNITED STATES, continued from previous page						
Franklin, Louisiana	8872		Single conidium isolate from P4453	D112		DJJ
Franklin, Louisiana		8873	Single conidium isolate from P4454		D113	DJJ
Franklin, Louisiana	8874		Single conidium isolate from P4464	D114		DJJ
Franklin, Louisiana	8875		Single conidium isolate from P4480	D115		DJJ
Franklin, Louisiana		8876	Single conidium isolate from P4481		D116	DJJ
Franklin, Louisiana	8877		Single conidium isolate from P4490	D117		DJJ
Franklin, Louisiana		8878	Single conidium isolate from P4491		D118	DJJ
Franklin, Louisiana		8879	Single conidium isolate from P4500		D119	DJJ
Fred-2		3225	Texas 1977		P828	DDP
Georgia Plantation		8104	Louisiana		P4506	BCT
Groveland-1c		1945	Florida 1970 (*pts-1*)	P438		DDP
Homestead-2	3970	3971	Florida 1980	P1409	P1405	DDP
Homestead, Florida		8879	Single conidium isolate from P4500		D19	DJJ
Homestead, Florida	8783		Single conidium isolate from P1409	D23		DJJ
Homestead, Florida	8784		Single conidium isolate from P1410	D24		DJJ
Homestead, Florida	8787		Single conidium isolate from P1417	D27		DJJ
Homestead, Florida		8788	Single conidium isolate from P1460		D28	DJJ
Homestead, Florida	8789		Single conidium isolate from P1465	D29		DJJ
Homestead, Florida		8790	Single conidium isolate from P1470		D30	DJJ
Houma-1l		3943	Louisiana 1972		P501	DDP
Houma-1n; -1	2220	2221	Louisiana 1972	P503	P491	DDP
Iowa-1; -1f	2222	2223	Louisiana 1972	P527	P532	DDP
Marrero-1d		2224	Louisiana 1972		P474	DDP
Marrero	8903		Single conidium from FGSC 987	D143		DJJ
Mauriceville-1c; -1d	2225	2226	Texas 1972	P538	P539	DDP
Northside Planting	7838	7839	Louisiana 1990	P4514	P4517	BCT
Northside Planting		8141	Louisiana 1990		P4519	BCT
Okeechobee	3968		Florida 1980	P1352		DDP
Perma #2		8571	MT		W619	DJJ
Ravenswood-1	3212		Louisiana 1977	P888		DDP
Roanoke-1m; -1	2227	2228	Louisiana 1972	P526	P516	DDP
Saratoga-11	3226		Texas 1972	P825		DDP
Scott A	3885		Mt. Wilson, CA 1965 (W.A. Scott)	Scott A		GWC
Spurger-3; -7	3201	3202	Texas 1977	P838	P842	DDP
Sugartown-1; -7	3210	3211	Louisiana 1977	P852	P858	DDP
Sweetwater-2		3975	Florida 1980		P1476	DDP
Welsh-1e; -1d	2229	2230	Louisiana 1972	P508	P507	DDP
Yeehaw Junction	3969		Florida 1980	P1365		DDP
COSTA RICA						
Agudas Rd-1	6203	6204	1986 (R. Metzenberg)	P3972	P3974	DDP
Agudas Rd-2		6205	1986 (R. Metzenberg)		P3982	DDP
Costa Rica	851		Coto, 1958 (R. Goos)	UFC #205a		RDG
Costa Rica	852		Coto, 1958 (R. Goos)	UFC #205b		RDG
Covolar	6212		1986 (R. Metzenberg)	P4021		DDP
Esterillo Este	6208	6209	1986 (R. Metzenberg)	P4002	P4003	DDP
Esterillo Este Rd-3	6206	6207	1986 (R. Metzenberg)	P3992	P3994	DDP
Jaco-1	6202	6201	1986 (R. Metzenberg)	P3963	P3962	DDP
Jaco-2	6211	6210	1986 (R. Metzenberg)	P4012	P4011	DDP
GABON						
Libreville	4823		1985	P3951		DDP

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. crassa wild type strains, continued						
HAITI						
Bas Quartier		4707	1984		P3471	DDP
Berard	4708	4709	1984	P3479	P3478	DDP
Carrefour Dufort	4710		1984	P3424		DDP
Carrefour Dufort	8816		Single conidium isolate from P3424	D56		DJJ
Carrefour Dufort		8819	Single conidium isolate from P3427		D59	DJJ
Carrefour Mme. Gras	4824		1984	P3491		DDP
Carrefour Mme. Gras	8822		Single conidium isolate from P3491	D62		DJJ
Haut Diquini	4711		1984	P3420		DDP
Leogane		4712	1984		P3433	DDP
Leogane		8820	Single conidium isolate from P3433		D60	DJJ
Merger	4713		1984	P3437		DDP
Merger	8821		Single conidium isolate from P3437	D61		DDP
Pescail	4714	4715	1984	P3454	P3453	DDP
Puilboreau Mt.	4716		1984	P3441		DDP
INDIA						
Aarey-1e; -1	2499*	2500*	Bombay, Maharashtra 1974	P680	P676	DDP
Aarey-1g		2712	Bombay, Maharashtra 1974		P682	DDP
Chennai	9055		KCP Pressmud Sugar Dump			PMM
Dagguluru-1	3360	3361	Andhra Pradesh 1978 (N.B. Raju)	P1120	P1121	NBR
Golur		8771	Karnataka		D11	DJJ
Golur		8772	Karnataka		D12	DJJ
Lankala Koderu-1; -2	3358†	3359	Andhra Pradesh 1978 (N.B. Raju)	P1105	P1117	NBR
Madurai	4717	4718	Tamil Nadu 1984	P2540	P2533	DDP
Madurai	8802		Tamil Nadu	D42		DJJ
Madurai	8864	8865	Tamil Nadu	D104	D105	DJJ
Mallilinatham		4719	Tamil Nadu 1984		P2565	DDP
Mallilinatham	8858		Tamil Nadu	D98		DJJ
Mallilinatham	8859		Tamil Nadu	D99		DJJ
Mallilinatham		8860	Tamil Nadu		D100	DJJ
Mallilinatham		8863	Tamil Nadu		D103	DJJ
Rameshwaram	8866	8867	Tamil Nadu	D106	D107	DJJ
Vallancheri	4720	4721	Tamil Nadu 1984	P2560	P2559	DDP
Vehar		8316	Vehar-1j		P675	
Venkatavarum		4722	Tamil Nadu 1984		P2576	DDP
Vickramam	6688		Tamil Nadu 1976 (R. Maheshwari)			DDP
ITALY						
Turchino Est.		10042	2003		W-1331	DJJ
Turchino Est		10036	2003		W-1318	DJJ
Turchino Est		10037	2003		W-1320	DJJ
Turchino Est		10038	2003		W-1324	DJJ
Turchino Est		10040	2003		W-1327	DJJ
Genoa		10054	2003		W-1400	DJJ
Genoa	10056			W-1436		DJJ
Genoa	10051			W-1393		DJJ

* Senescent, due to maranhar plasmid - see Court et al. 1991. Curr. Genet. 19:129-137.

† Requires thiamine

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. crassa wild type strains, continued						
IVORY COAST						
Adiopodoume	430*		D. Muller, 1955 (Called North Africa I)			NHH
Adiopodoume	8856		Single conidium isolate from P4305		D96	
Adiopodoume	8890		Single conidium isolate from M17		D140	DJJ
Asikro		4828	1985		P3753	DDP
Foro-Foro		4829	1985		P3720	DDP
Golikro	4830		1985		P3726	DDP
Golikro	8830		Single conidium isolate from P3726		D70	DJJ
Grabiokoko		4831	1985		P3591	DDP
Eremankono		4832	1985		P3707	DDP
Ibogue	4833		1985	P3607		DDP
Issia	4834		1985	P3617		DDP
N'Douci	4835	4836	1985	P3695	P3696	DDP
Sakota		4837	1985	P3557		DDP
Tiassale	4825	4826	1985	P3681	P3684	DDP
Tiassale	4827	1985			P3679	DDP
Tiassale	8828		Single conidium isolate from P3681		D68	DJJ
Tiassale	8829		Single conidium isolate from P3684	D69		DJJ
* Original source of transposon, Tad						
LIBERIA						
Liberia	961	967*	1957 (Harbel)	UA-1	UA-2	JW
* Requires threonine						
MALAYA						
Batu Ferringi-1		5359	Penang 1984		P2681	DDP
Georgetown-4	4723	4724	Penang 1984	P2605	P2606	DDP
Georgetown-5	4725		Penang 1984	P2614		DDP
Georgetown-6	4726	4727	Penang 1984	P2618	P2617	DDP
Georgetown-7		4728	Penang 1984		P2623	DDP
Tanjong Tokong		4729	Penang 1984		P2674	DDP
MEXICO						
Chemax	6634	6636	Yucatan 1988 (R. Metzenberg)	P4108	P4118	DDP
Chichen Itza		8854	Single conidium isolate from P4160		D 94	DJJ
Kabah	6638	6637	Yucatan 1988 (RLM)	P4127	P4125	DDP
Kabah		8845	Yucatan, Segregant from P4130		D85	DJJ
Sayil		8848	Yucatan, Segregant from P4150		D88	DJJ
Uxmal	8850		Yucatan, Segregant from P4154	D90		DJJ
Uxmal	8851		Yucatan, Segregant from P4155	D91		DJJ
PAKISTAN						
Lahore-1; -1b	1824	1825	1969	P349	P350	DDP
PANAMA						
Cristobal	8904		Single conidium from FGSC 1131 D144			DJJ
Panama	1165		1944 (Hutchinson)	QM#4834		EGS
Panama CZ30.6	1131		*het-5*, *-6*, *-8*, *-9*. Canal Zone 1944 (Hutchinson)	QM#4838		EGS
Panama CZ30.7	1132		Canal Zone 1944 (Hutchinson)	QM#4839		EGS
Panama CZ30.9	1133		Canal Zone 1944 (Hutchinson)	QM#4841		EGS
Panama CZ304	1130		Canal Zone 1944 (Hutchinson)	QM#8436		EGS

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. crassa wild type strains, continued						
PORTUGAL						
Penedo Furado	10018		2006	W-1244		DJJ
Tapada de Mafra	10020		2006	W-1246		DJJ
Tapada de Mafra		10021	2006		W-1247	DJJ
Tapada de Mafra	10024		2006	W-1252		DJJ
Troviscal Sertã	10017		2006	W-1243		DJJ
Monchique		10027	2006		W-1265	DJJ
Monchique		10028	2006		W-1268	DJJ
PUERTO RICO						
Colonia Paraiso	3693	3694	1979	P1295	P1291	DDP
Puerto Rico 18	429	(H. Teas)				NHH
SOUTH AMERICA						
Arena Reser	7547		Trinidad 1992 (N. Giles)	P4581		BCT
Digitima Creek-1		5910	Guyana 1984 (G. Samuels)		P4065	DDP
Ile St. Joseph		7553	French Guiana 1992 (N. Giles)		P4589	BCT
Maripasoula	6240	6241	French Guiana 1987 (G. Samuels)	P4087	P4088	DDP
Orinoco Delta-2	7552		Venezuela 1992 (N. Giles)	P4588		BCT
Puerto Ayachucho	4730	6233	Venezuela 1984 (G. Samuels)	P3410	P4035	DDP
Rondon	4705	4706	Brazil 1984 (G. Samuels)	P3393	P3396	DDP
Torani Canal	5914		Guyana 1984 (G. Samuels)	P4078		DDP
Tucamanduba	7556		Brazil 1992 (N. Giles)	P4592		BCT
Tucamanduba-2	7851		Brazil	P4607		BCT
SPAIN						
Platja d'Aro	10049		2006	W-1387		DJJ
Sevilla	10058		2006	W-1566		DJJ
Seros		10043	2006		W-1355	DJJ
Seros	10046		2006	W-1378		DJJ
Platja d"Aro	10050		2006	W-1390		DJJ
Platja d"Aro		10048	2006		W-1382	DJJ
Sevilla		10059	2006		W-1567	DJJ
Seros	10044		2006	W-1356		DJJ
Seros		10045	2006		W-1367	DJJ
Macanet de la Sevla		10033	2006		W-1296	DJJ
THAILAND						
Khao Eto	6490	6797	1984	P4085	P4248	DDP
Klong Rangsit-57	6488		1984	P2913		DDP
TRINIDAD						
Caroni Swamp	8147		(N. Giles)	P4585		BCT

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
			NEUROSPORA DISCRETA			
CENTRAL AMERICA, MEXICO AND SOUTH AMERICA						
Serra Araca	6793		Brazil 1984 (G. Samuels)	P3388		DDP
Serra Araca	9958		Single conidium isolate from P3388	D166		DJJ
Chichen Itza	9976		Single conidium isolate from P4159	D184		DJJ
Santa Maria		3319	Guatamala 1972 (N. Franklin)		P755	DDP
Santa Maria	5066	5067	5th backcross P755 to P851	8161	8162	DDP
Santa Maria		9943	Single conidium isolate from P0755		D151	DJJ
CONGO						
Port du Djoue-2	9970		P3796	D178		DJJ
Loudima	9971		P3836	D179		DJJ
CONTINTENTAL UNITED STATES						
Belen	8579	8578	New Mexico	W683	W682	DJJ
Belen		8906	Single conidium isolate from W766		D146	DJJ
Bernalillo	8980	8979	New Mexico	W782	W781	DJJ
Blodgett Trailhead	8558		Montana	W477		DJJ
Chelan Lake	8994	8995	Washington	W1070	W1071	DJJ
Chiquita Loma Rd.	9000		California	W1106		DJJ
Cobalt	8567	8568	Idaho	W593	W594	DJJ
Coleville	8583	8584	California	W09	W710	DJJ
Hayfork		8993	California		W1004	DJJ
Homestead-1k		3268	Florida 1970		P390	DDP
Homestead	5064	5065	7th backcross P390 to P851	8143	8144	DDP
Homestead-1	8780		Single conidium isolate from P1406	D120		DJJ
Homestead-1		9941	Single conidium isolate from P0389		D149	DJJ
Homestead-1		9942	Single conidium isolate from P0390		D150	DJJ
Iceland Rd.	8988	8989	California	W922	W923	DJJ
Kennedy Meadows	8561	8560	California	W514	W512	DJJ
Kirbyville-6, -1	3228	3229	Texas 1977	P851	P846	DDP
Kirbyville 8127		4378	4th backcross P846 to P851		P8127	DDP
Kirbyville-6	8777		Single conidium isolate from P851		D17	DJJ
Kirbyville-6		9944	Single conidium isolate from P0846		D152	DJJ
Laird Creek	8556	8555	Sula, Montana	W467	W466	DJJ
lwn (lawn)	5922	5923	Morph. variant in Homestead-1k	8240	8241	DDP
La Joya	8581	8582	New Mexico	W693	W694	DJJ
Los Alamos #1	8591		New Mexico	W776		DJJ
Los Alamos #2	8588	8589	New Mexico	W755	W756	DJJ
Los Alamos #1	8591		New Mexico	W776		DJJ
Los Alamos #2	8588	8589	New Mexico	W755	W756	DJJ
Los Alamos #2		9984	New Mexico W751		D203	DJJ
Los Alamos #2	9985		New Mexico W752	D204		DJJ
Los Lunas	8577	8576	New Mexico	W648	W645	DJJ
Los Lunas	9076		New Mexico	W763		DJJ
Manter Meadow	8562	8563	California	W531	W532	DJJ
Murphy Meadow	8986	8987	California	W885	W886	DJJ
Napais Creek	8554	8553	Idaho	W458	W457	DJJ
Northwest Peak	8548		Montana	W441		DJJ
Panther Creek Road	8550		Idaho	W443		DJJ
Pecos #1	8585		New Mexico	W736		DJJ
Pecos #2	8587	8586	New Mexico	W741	W740	DJJ
Pecos #2		9982	New Mexico W744		D201	DJJ
Pecos #2	9983		New Mexico W745	D202		DJJ
Perma #1	8569	8570	Montana	W606	W607	DJJ

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. discreta wild type strains, CONTINTENTAL UNITED STATES, continued						
Perma #2	8573	8572	Montana	W621	W620	DJJ
Perma #2		9977	W862		D196	DJJ
Plumas		8564	California		W538	DJJ
Ramey Creek		8551	Idaho		W449	DJJ
Skalaho		8978	Montana		W777	DJJ
Sula	8557		18 Mile post, Montana	W474		DJJ
Susanville	8985	8984	California	W869	W868	DJJ
Tok	8983	8982	Alaska	W808	W807	DJJ
Tok	9980		Alaska W855	D199		DJJ
Tok		9981	Alaska W814		D200	DJJ
Tok		9978	Alaska W853		D197	DJJ
Tok	9979		Alaska W854	D198		DJJ
Turner Creek Road	8549		Montana	W442		DJJ
Weaverville	8991	8992	California	W963	W964	DJJ
Wells	8565	8566	Nevada	W564	W565	DJJ
Yankee Fork	8552		Idaho	W452		DJJ
Yellowstone NP	8990		Wyoming	W938		DJJ
Laird Creek	8556	8555	Sula, Montana	W467	W466	DJJ
GABON						
Ekowong		9972	P3920		D180	DJJ
Ekowong	9973		P3927	D181		DJJ
Makokou-5	9974		P3928	D182		DJJ
Makokou-7		9975	P3931		D183	DJJ
INDIA						
Bandipur		6789	India 1974 (R. Maheshwari)		P2511	DDP
Bandipur		8797	Single conidium isolate from P2511		D37	DJJ
IVORY COAST						
Fougbesso		8827	Single conidium isolate from P3660		D67	DJJ
Golikro		8831	Single conidium isolate from P3728		D71	DJJ
Gahelile	9959		Single conidium isolate from P3602	D167		DJJ
Gahelile		9960	Single conidium isolate from P3603		D168	DJJ
Issia		9961	Single conidium isolate from P3619		D169	DJJ
Issia		9962	Single conidium isolate from P3621		D170	DJJ
Carrefour Couessesso	9963		Single conidium isolate from P3635	D171		DJJ
Carrefour Couessesso		9964	Single conidium isolate from P3639		D172	DJJ
Gouana	6794		Ivory Coast 1985	P3642		DDP
Gouana	9965		Single conidium isolate from P3642	D173		DJJ
Gouana		9966	Single conidium isolate from P3644		D174	DJJ
Fougbesso	9967		Single conidium isolate from P3650	D175		DJJ
Foro-Foro	9968		Single conidium isolate from P3722	D176		DJJ
Foro-Foro		9969	Single conidium isolate from P3723		D177	DJJ
MOOREA and TAHITI						
Moorea	8975		From N. Giles, 1997	W550		DJJ
NEW ZEALAND						
Brookby	9952		Single conidium isolate from P2315	D160		DJJ
Brookby		9953	Single conidium isolate from P2324		D161	DJJ
Waipu		9954	Single conidium isolate from P2349		D162	DJJ

Strain designation	FGSC # and mating type A	 a	Comments	Number in other culture collection A	 a	Obtained from
N. discreta wild type strains, continued						
PAPUA NEW GUINEA						
Hiri	6788		Papua New Guinea 1983	P1992		DDP
Hiri	9951		Single conidium isolate from P1992	D159		DJJ
Tiaba-1		8765	Single conidium isolate from P0047		D5	DJJ
Tiaba-1		9940	Single conidium isolate from P0048		D148	DJJ
Wau-6		6784	Papua New Guinea 1983		P1692	DDP
Wau-6		9945	Single conidium isolate from P1692		D153	DJJ
Marinville	6785		Papua New Guinea 1983	P1859		DDP
Marinville	9946		Single conidium isolate from P1859	D154		DJJ
Sogeri Road-1	6786		Papua New Guinea 1983	P1913		DDP
Sogeri Road-1		9947	Single conidium isolate from P1911		D155	DJJ
Sogeri Road-1	9948		Single conidium isolate from P1913	D156		DJJ
Rouna-8		6787	Papua New Guinea 1983		P1966	DDP
Rouna-8		9949	Single conidium isolate from P1964		D157	DJJ
Rouna-8	9950		Single conidium isolate from P1966	D158		DJJ
PORTUGAL						
Boticas		10011	2003		W-1231	DJJ
Boticas	10014		2003	W-1237		DJJ
Boticas		10025	2003		W-1260	DJJ
Boticas	10013		2003	W-1236		DJJ
Boticas		10010	2003		W-1230	DJJ
Boticas		10012	2003		W-1234	DJJ
Boticas		9986	2003 W-1232		D215	DJJ
Boticas	9987		2003 W-1233	D216		DJJ
Boticas		9988	2003 W-1235		D217	DJJ
Monchique	9989		2003 W-1254	D218		DJJ
Monchique	9990		2003 W-1269	D220		DJJ
Monchique		10025	2003 W-1260			DJJ
SPAIN						
Macanet de la Selva		10030	2003 W-1290			DJJ
Macanet de la Selva	9991		2003 W-1289	D221		DJJ
THAILAND						
Kang Koi		6792	1983		P3016	DDP
Kang Koi		8814	Single conidium isolate from P3016		D54	DJJ
Khao Yai-4		6790	1983		P3002	DDP
Khao Yai-4		9955	Single conidium isolate from P3002		D163	DJJ
Khao Yai-4		9956	Single conidium isolate from P3003		D164	DJJ
Pakchong-2		6791	Thailand 1983		P3004	DDP
Pakchong-2		9957	Single conidium isolate from P3004		D165	DJJ
SWITZERLAND						
Leuk	9992		2003 W-1303	D224		DJJ
Leuk	9993		2003 W-1304	D225		DJJ
***NEUROSPORA DISCRETA*-like**						
Brabadougou	8317		Ivory Coast	P4297		DDP

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
NEUROSPORA DODGEI						
PR300	1692 (homothallic)		Luquillo Mtns., Puerto Rico,	15509		ATCC
NEUROSPORA GALAPAGOSENSIS						
G349	1739 (homothallic)		Isla Santa Cruz, Galapagos Islands	18746		ATCC
var. *dominicana*						
D301	4628 (homothallic)		From soil, Dominica Island (L.H. Huang)	D301		DDP
NEUROSPORA INTERMEDIA						
Reference strains; derived wild types						
N. intermedia Tai		962	Dowding collection (presumed original from Nanking, China)			JW
NIT		1754	CBS→A.M. Srb, 1956.	CBS 268.36		AMS
268.36		2540	Nanking, China (corncob), 1927. Tai	CBS 268.36		CBS
Shp-1A; -1a	3416	3417	f_5 inbred progeny FGSC 1766x1767	WS912	WS911	HWS
P420;P405	2316	1940	Clewiston and LaBelle, Florida	P420	P405	DDP
			(recommended as species reference tester)			
fl^P	5798	5799	*fl*^{P} from *N. crassa* introgressed via 7 backcrosses to ShP	8238	8239	DDP
Original *N. intermedia* strains collected from nature						
AUSTRALIA						
8 Mile Plain		8778	Queensland, Australia		D18	DJJ
Bambaroo	3996	3997	Queensland 1981 (M. Bjorkman)	P1545	P1546	MB
Berry Springs	7845	7846	Northern Territory	P4568	P4569	BCT
Brisbane-1f; -1g	1882	1883	Queensland 1969	P82	P83	DDP
Cairns-1c; -1d	1830	1831	Queensland 1969	P91	P92	DDP
Daintree-1	5100	5101	Queensland 1983	P2060	P2063	DDP
Daintree-4	8089	8090	Queensland	P4183	P4192	BCT
Ku-Rin-Gai Nat'l Park	7849		New South Wales	P4605		BCT
8 Mile Plain		5647*	Queensland 1983		P898	DDP
Miallo	5114	5115	Queensland 1983	P2220	P2221	DDP
New Italy		6626*	N.So. Wales 1983 (E. Maynard)		P3379	DDP
Feluga	5108	5109	Queensland 1983	P2138	P2137	DDP
Harwood Island	6624	6625*	N.So. Wales 1984 (D. Strong)	P3383	P3384	DDP
Jacobs Well Bee Baskets		8095	Queensland		P4245	BCT
Japoonvale	5111	5110	Queensland 1983	P2163	P2160	DDP
Mareeba	5105	5104	Queensland 1983	P2102	P2101	DDP
Shaw's Corner	5112	5113	Queensland 1983	P2177	P2178	DDP
Townsville-1b; -1	1832	1833	Queensland 1969	P113	P112	DDP
Walkerston Bee Baskets	8087	8088	Queensland	P4032	P4179	BCT
Wangetti	5106	5107	Queensland 1983	P2121	P2122	DDP
Windaroo-2		6221*	Queensland 1984 (D. Shaw)		P3523	DDP
Wonderoo	6627*	6628*	New South Wales 1983	P2233	P2232	DDP
Wonga	5102	5103	Queensland 1983	P2087	P2090	DDP
* Yellow ecotype						
BORNEO						
Kota Kinabalu-2	5384	5385	Sabah 1984	P3142	P3147	DDP
Lokawi Camp	5375	5374	Sabah 1984	P3114	P3112	DDP
Menggajal	5376	5377	Sabah 1984	P3127	P3130	DDP
Mt. Kinabalu	5379	5378	Sabah 1984	P3136	P3132	DDP
Kuching-3	5373	5372	Sarawak 1984	P3107	P3105	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. intermedia, continued from previous page						
BRAZIL						
Campinas-1	3338	3339	Brazil 1978	P973	P972	DDP
Capivari-1	3346	3347	Brazil 1978	P1025	P1026	DDP
Dois Corregos-1	3342	3343	Brazil 1978	P1016	P1013	DDP
Itirapina-1	3351	3352	Brazil 1978	P1047	P1046	DDP
Jaboticabal-1	3353	3354	Brazil 1978	P1053	P1055	DDP
Mombuca-1	3340	3341	Brazil 1978	P1005	P1004	DDP
Monte Alegre-1	3336	3337	Brazil 1978	P940	P943	DDP
Piracicaba-1	3334	3335	Brazil 1978	P910	P912	DDP
Piracununga-1	3350		Brazil 1978	P1040		DDP
Porto Ferreira-1	3348	3349	Brazil 1978	P1032	P1033	DDP
Rio Das Pedras-1	3344	3345	Brazil 1978	P1018	P1021	DDP
CENTRAL AMERICA and MEXICO						
Coba-2		6645	Mexico 1988 (R. Metzenberg) >50% white spores x *N. intermedia* tester		P4171	DDP
Honduras		1300	From R.H. Stover, United Fruit Co. (via Srb)			CFC
Honduras-5; -7	1543	1544	Guaruma I, Cortes 1968 (K. Hsu)	P8045	P8046	DDP
CHINA						
(Collected with the help of the Genetics Society of the Peoples Republic of China and Dr. T.C. Sheng. Sent via N.Giles)						
Baoding		3991	Hebei 1980		P1530	DDP
Beijing	3976	3977	1979, yellow ecotype	P1510	P1512	DDP
Beijing	3982		1979, yellow ecotype	P1517		DDP
Changdu	3979		Xizang (Tibet) 1980, yellow ecotype	P1514		DDP
Chengdu	3992		Sichuan 1980, yellow ecotype	P1531		DDP
Gongzhuling	3990		Jilin 1980, yellow ecotype	P1529		DDP
Guiyang	3985		Guizhou 1980, yellow ecotype	P1522		DDP
Hangzhou	3978		Zhejiang, yellow ecotype	P1513		DDP
Harbin		3983	Heilongjiang 1980, yellow ecotype		P1518	DDP
Harbin		3988	Heilongjiang 1980, yellow ecotype		P1525	DDP
Taiyuan		3984	Shanxi 1980, yellow ecotype		P1520	DDP
Hefei	3989		Anhui 1980	P1526		DDP
Hefei	3980		Anhui 1980, yellow ecotype	P1515		DDP
Hefei	8791		Single conidium isolate from P1515	D31		DJJ
Hefei	8792		Single conidium isolate from P1526	D32		DJJ
Jinan	3981		Shandong 1980, yellow ecotype	P1516		DDP
Liaoning		3986	Shenyang 1980, yellow ecotype		P1524	DDP
Shanxi		3993	Shanxi, yellow ecotype		P1532	DDP
CONGO						
Brazzaville		6264	1985		P3780	DDP
Bouanza		6276	1985		P3852	DDP
Bouanza		8841	Single conidium isolate from P3852		D81	DJJ
Dimonika Village	6269	6270	1985, yellow ecotype	P3818	P3822	DDP
Djoue	6267		1985	P3786		DDP
Djoue		6268	1985, yellow ecotype		P3788	DDP
Jacob	6272	6273	1985	P3831	P3834	DDP
Kinkala-1		6278	1985		P3891	DDP
Loubomo		6271	1985		P3824	DDP
Loubomo		8836	Single conidium isolate from P3824		D76	DJJ
Madingo		6274	1985		P3839	DDP
Madingo Market	6275		1985, yellow ecotype	P3848		DDP
Madingo		8839	Single conidium isolate from P3839		D79	DJJ
Madingo	8840		Single conidium isolate from P3843	D80		DJJ

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. intermedia						
CONGO, continued from previous page						
Missafou-1		6277	1985		P3886	DDP
Missafou-2	6279	6280	1985	P3895	P3897	DDP
Port du Djoue-3	6265		1985	P3782		DDP
Port du Djoue-3		6266	1985, yellow ecotype		P3783	DDP
CONTINENTAL UNITED STATES						
Canal Point	6599	6600	Florida 1980	P1312	P1314	DDP
Clewiston-1h	2316	6598	Florida 1970	P420	P416	DDP
Dunedin	3994	3995	Florida 1981	P1536	P1539	FD
Fred-6		3213	Texas 1977		P831	DDP
Fred		8776	Single conidium isolate from P831		D16	DJJ
Groveland-1d; -1b	2236	2237	Florida 1970	P439	P437	DDP
Homestead	6596	6597	Florida 1970	P384	P385	DDP
Homestead-2	6603	6604	Florida 1980	P1407	P1411	DDP
Homestead	8781		Single conidium isolate from P1407	D21		DJJ
Homestead		8782	Single conidium isolate from 1408P		D22	DJJ
Homestead		8785	Single conidium isolate from P1413		D25	DJJ
Homestead	8786		Single conidium isolate from P1415	D26		DJJ
Jakes Branch	8996		New Jersey	W1006		DJJ
LaBelle-1d; -1b	1939	1940	Florida 1970	P407	P405	DDP
Saratoga		6605	Texas		P824	DDP
Yeehaw Junction	6601	6602	Florida 1980	P1358	P1359	DDP
DOMINICAN REPUBLIC						
Bani	7840	7841	Near San Cristobal, 1991	P4529	P4531	BCT
FIJI						
Levuka	8902		Single conidium isolate from FGSC435	D142		DJJ
FRENCH GUIANA and GUYANA						
Big Emma		5908	Guyana 1984 (G. Samuels)		P4055	DDP
Digitima Creek-2	5910	5911	Guyana 1984 (G. Samuels)	P4067	P4068	DDP
Ile St. Joseph	7555	7554	French Guiana 1992 (N. Giles)	P4591	P4590	BCT
Lookout Village	5915		Guyana, 1984 (G. Samuels)	P4082		DDP
GABON						
Ekowong		6281	1985, yellow ecotype		P3926	DDP
Libreville	6231		1985	P3950		DDP
Makokou-6		6226	1985, yellow ecotype		P3930	DDP
Makokou-7	6282		1985	P3932		DDP
Makokou-8	6229		1985, yellow ecotype	P3938		DDP
Makokou-9		6230	1985, yellow ecotype		P3944	DDP
GUAM						
Malojloj	6551	6550	1984	P3221	P3220	DDP
Merizo	6548	6547	1984	P3217	P3214	DDP
Taelayag	6544	6543	1984	P3200	P3199	DDP
Taleysay	6552		1984	P3226		DDP
Taleytac	6542	6541	1984	P3192	P3191	DDP
Umatac Bay	6545	6546	1984	P3206	P3211	DDP
HAITI						
Au Borgne-1	6249		1985	P3457		DDP
Carrefour Mme. Gras	6251		1985	P3495		DDP
Carrefour Mme. Gras	8824		Single conidium isolate from P3495	D64		DJJ

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. intermedia,						
HAITI, continued from previous page						
Gran Sous		6252	1985		P3509	DDP
Haut du Cap	6250		1985	P3487		DDP
Kenscoff	6242		1985	P3422		DDP
Leogane	6243		1985	P3430		DDP
Merger		6244	1985		P3439	DDP
Pescail	6248	6247	1985	P3455	P3450	DDP
Puilboreau Mt.	6245	6246	1985	P3442	P3443	DDP
HAWAII						
Hanalei	3722*	3723	Kauai 1976	P790	P789	DDP
Hanalei-1f; -1	2360	2361	Kauai 1972	P560	P555	DDP
Hanalei-1g		5014*	Kauai 1972		P561	DDP
Hanapepe	3720	3721	Kauai 1972	P605	P602	DDP
Kahalui-1	3292	3293	Maui 1976	P786	P782	DDP
Kekaha	6238	6239	Kauai 1988 (BCT)	P4104	P4105	DDP
Kekaha-1b; -1	2362	2363	Kauai 1972	P590	P589	DDP
Kekaha-3	7843	7842	Kauai 1991	P4557	P4554	BCT
Koloa-1hv1; -1hv4	2366*	2367	Kauai 1972	P647	P648	DDP
Laie	6236		Oahu 1988 (BCT), Yellow ecotype	P4093		DDP
Laie		6237	Oahu 1988 (BCT),		P4097	DDP
Laie,	8844		Single conidium isolate from P4095	D84		DJJ
Lihue-3d; -3b	2364	2365*	Kauai 1972	P629	P627	DDP
Wailua Falls-1	3294	3295	Kauai 1976	P807	P808	DDP
Waimea	3718*	3719	Kauai 1972,	P612	P613	DDP
Waimea Falls-2	3290	3291	Oahu 1976	P768	P769	DDP

* shows [*kal*] phenotype. See Griffiths and Bertrand. 1984. Current Genetics 8:387

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
HONDURAS						
Puerto Cortes	8882		Single conidium isolate from P8045	D122		DJJ
INDIA						
Channapatna-1	1803		Karnataka 1969	P348		DPP
Chickkadana-1; -1j	2495	2496	Karnataka 1974	P697	P706	DDP
Dagguluru-1	3362		Andhra Pradesh 1978 (N.B. Raju)	P1124		NBR
Goa 9-10A; 9-7a	2655	2654	from soil, Goa			RM
Golur-1b; -1c	1804	1805	Karnataka 1969	P330	P331	DDP
Kadakola-1; -1g	1806	1807	Karnataka 1969	P321	P327	DDP
Kalastwadi-1c; -1	1810	1811	Karnataka 1969	P291	P289	DDP
Konappatti	5344	5343	Tamil Nadu 1984	P2546	P2545	DDP
Konappatti		8803	Single conidium isolate from P2544		D43	DJJ
Konappatti	8804		Single conidium isolate from P2546	D44		DJJ
Konappatti		8805	Single conidium isolate from P2550		D45	DJJ
Konappatti	8806		Single conidium isolate from P2551	D46		DJJ
Konappatti		8857	Single conidium isolate from P4331		D97	DJJ
Kurubara Shettihally-1f; -1	1808	1809	Karnataka 1969	P301	P296	DDP
Lankala Koderu-2	3363	3364	Andhra Pradesh 1978 (N.B. Raju)	P1118	P1115	NBR
Madaurai		8798	Single conidium isolate from P2533		D38	DJJ
Madaurai		8799	Single conidium isolate from P2536		D39	DJJ
Madaurai	8800		Single conidium isolate from P2538	D40		DJJ
Madaurai	8801		Single conidium isolate from P2542	D41		DJJ
Madaurai	8868		Single conidium isolate from P4363	D108		DJJ
Madaurai		8869	Single conidium isolate from P4364		D109	DJJ
Maddur		8885	Maheshwari stock M10		D125	DJJ
Maddur	8886		Maheshwari stock M101	D126		DJJ
Maddur		8887	Maheshwari stock M105		D127	DJJ

	FGSC # and mating type			Number in other culture collection		Obtained
Strain designation	A	a	Comments	A	a	from
N. intermedia						
INDIA, continued from previous page						
Maddur	8888		Maheshwari stock M110	D128		DJJ
Maddur	8889		Maheshwari stock M14	D129		DJJ
Maddur		8890	Maheshwari stock M17		D130	DJJ
Maddur	8891		Maheshwari stock M19	D131		DJJ
Maddur	8892		Maheshwari stock M2	D132		DJJ
Maddur		8893	Maheshwari stock M64		D133	DJJ
Maddur	8894		Maheshwari stock M65	D134		DJJ
Maddur		8895	Maheshwari stock M71		D135	DJJ
Maddur		8896	Maheshwari stock M77		D136	DJJ
Maddur	8897		Maheshwari stock M86	D137		DJJ
Maddur	8898		Maheshwari stock M92	D138		DJJ
Maddur	8899		Maheshwari stock M95	D139		DJJ
Maddur	9599			60A		RM
Maddur	9600			107A		RM
Mallilinatham	8810		Single conidium isolate from P2567	D50		DJJ
Mallilinatham	8861		Single conidium isolate from P4336	D101		DJJ
Mysore-1; -1e	1820	1821	Karnataka 1969	P285	P287	DDP
Nandi Hill 1-1A; 1-4a	2652	2653	from soil, Karnataka			RM
Pulikeezhu-1b; -1	2497	2498	Kerala 1974	P688	P687	DDP
Rameshwaram	5346	5345	Tamil Nadu 1984	P2555	P2552	DDP
Rameshwaram		8807	Single conidium isolate from P2552		D47	DJJ
Rameshwaram	8808		Single conidium isolate P2554	D48		DJJ
Rameshwaram	8809		Single conidium isolate P2555	D49		DJJ
Varkud-1c; -1b	1823	1822	Karnataka 1969	P343	P342	DDP
INDONESIA						
Besakih-1; -1c	1826	1827	Bali 1969, yellow ecotype	P190	P192	DDP
Bodjongloa Djalan		2560	peanut ontjom, Bandung		H2137	HCC
Bogor-2c; -2g	1792	1793	Java 1969	P142	P146	DDP
Bogor-3		2215	Java 1969		P147	DDP
Bogor Java	5643		Java, 1969, yellow ecotype	P151		DDP
Bogor-4	5644		Java 1969, yellow ecotype	P153		DDP
Bogor Pasar	2558	2559	soybean ontjom, Bogor	H2121	H2125-1	HCC
Bogor-7	7835		Kampung Sempur	P4504		BCT
Gianjor-1c; -1d	1836	1837	Bali 1969	P204	P205	DDP
Jakarta-1	1881		Java 1969, yellow ecotype	P181		DDP
Jalan Kopo		5097	peanut ontjom, Jalan Kopo, Java		H2140	HCC
Java		431	from Ryan?			NHH
Kampong Babakan	2562		peanut ontjom, Bandung (C.C. Ho)	H2147		HCC
Kelungkung		5646	Bali, yellow ecotype		P201	DDP
Kopo Djalan		2561	peanut ontjom, Kopo Djalan (C.C. Ho)	H2139		HCC
Leuwi Malang-1c; -1e	1834	1835	Java 1969, 1835 contains *T(I;IV)P170*	P168	P170	DDP
Pasar Balubur		5099	peanut ontjom, Pasar Balubur, Java	H2158		HCC
Pasar Bandung	5098		peanut ontjom, Pasar Bandung, Java	H2156		HCC
Tampaksiring-1c; -1b	1796	1795	Bali 1969	P212	P211	DDP
Tjikini Pasar	2557		Standard ontjom strain (soybean), Jakarta (Ho Coy Choke)	H2065		HCC
Tjipanas-1		5645	Java, yellow ecotype		P176	DDP
BOR32	3257		from soil, Brunei, Borneo (Warcup) with *nit-4*, *Sk-2*^{K}	P8108		DDP
14151	2613		ontjom, Bandung, Java 1959	14151		ATCC
IVORY COAST						
Adiopodoume-1	6262		1985	P3758		DDP
Adiopodoume-4		6263	1985		P3770	DDP

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. intermedia						
IVORY COAST, continued from previous page						
Adiopodoume		8833	Single conidium isolate from P3770		D73	DJJ
Adiopodoume	8855		Single conidium isolate from P4277	D95		DJJ
Brobo		6260	1985		P3732	DDP
Hermankono	6259		1985	P3709		DDP
Kovasiblekro		6261	1985		P3741	DDP
Mt. Tonkgui		6258	1985		P3669	DDP
Ran Adjame	6253		1985	P3533		DDP
Tiassole	6257		1985, yellow ecotype	P3565		DDP
Universite d'Abidjan		6256	1985		P3549	DDP
Yopougon	6254	6255	1985	P3540	P3543	DDP
Yopougon	8825		Single conidium isolate from P3540	D65		DJJ
Yopougon		8826	Single conidium isolate from P3543		D66	DJJ
JAPAN						
Unzen	1768		Kyushu 1968	P3		DDP
JAVA						
Bogor	8767		Single conidium isolate from P142	D7		DJJ
Bogor		8768	Single conidium isolate from P147		D8	DJJ
Tjipanas	8769		Single conidium isolate from P176	D9		DJJ
LIBERIA						
Liberia 4	434		H. Teas			NHH
Monrovia	8901		Single conidium from FGSC 434	D141		DJJ
MALAYA						
Batu Ferringi-1	5358	6606	Penang 1984	P2680	P2679	DDP
Bayan Lepas		5355	Penang 1984		P2662	DDP
Bukit Penara	5230	5229	Penang 1984	P2720	P2719	DDP
Cheras	5247	5248	Penang 1984	P2821	P2822	DDP
Damansara Jaya	5235	5236	1984	P2737	P2740	DDP
Georgetown-1	5347	5348	Penang 1984	P2579	P2585	DDP
Georgetown-6	5349	5350	Penang 1984	P2620	P2621	DDP
Georgetown	8811		Single conidium isolate from P2632	D51		DJJ
Gertak Sangul	5353	5354	Penang 1984	P2655	P2656	DDP
Kajang	5249	5250	1984	P2825	P2829	DDP
Kampung Cempaka	5238	5237	1984	P2746	P2743	DDP
Kampang Pengakalan	8154	8166	J. Leslie	P4650	P4652	BCT
Karak Highway	5244	5243	1984	P2795	P2792	DDP
Klang-6d; -6b	1799	1800	1969	P266	P264	DDP
Kuala Lumpur-1b; -1e	1801	1802	1969	P271	P274	DDP
Kuala-Selengor-4; -4b	1797	1798	1969	P249	P250	DDP
Melaka	5252	5251	1984	P2858	P2854	DDP
Petaling Jaya	5096		Ho Coy Choke	H2000		HCC
Rantau Panjang	8151	8150	J. Leslie	P4611	P4610	BCT
Seremban	5246	5245	1984	P2809	P2808	DDP
Subang	5233	5234	1984	P2731	P2733	DDP
Sungai Ara	5356	5357	Penang 1984	P2666	P2670	DDP
Sungai Pinang	5228	5227	Penang 1984	P2713	P2712	DDP
Sungai Rasau	8152	8153	J. Leslie	P4629	P4630	BCT
Sungai Terap	8171	8170	J. Leslie	P4677	P4671	BCT
Sunge Way-Subang	5239	5240	1984	P2750	P2753	DDP
Sunshine Beach	5223	5224	Penang 1984	P2694	P2696	DDP
Tanjung Asam	5351	5352	Penang 1984	P2646	P2648	DDP
Telok Bahang	5225	5226	Penang 1984	P2699	P2704	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. intermedia						
MALAYA, continued from previous page						
Telok Kumbar	5231	5232	Penang 1984	P2721	P2722	DDP
Ulu Gombak-1	5242	5241	1984	P2785	P2784	DDP
MOOREA-TAHITI						
Arue	6593		Tahiti 1983	P2362		DDP
Arue	8796		Single conidium isolate from P2362	D36		DJJ
Baie D'Opunohu	5128	5127	Moorea 1983	P2480	P2479	DDP
Bali Hai Region		5129	Moorea 1983		P2489	DDP
Haapiti-1	5124	5125	Moorea 1983	P2456	P2459	DDP
Mataiva		8972			W545	DJJ
South Coast	6595	5123	Tahiti 1983	P2427	P2421	DDP
Tahiti	8977			W552		DJJ
Tautira	6594		Tahiti 1983	P2402		DDP
Viaire		5126	Moorea 1983		P2473	DDP
NEW ZEALAND						
Ahipara	5116	5117	North Island 1983	P2264	P2269	DDP
Cornwallis Beach	5120	5119	North Island 1983	P2306	P2301	DDP
Mangere	7829	7830	Aukland greenhouse	P4428	P4432	BCT
Miner's Cove	6795	6796	1988 (R. Beever)	P4221	P4224	DDP
Mt. Albert		5118	North Island 1983		P2295	DDP
Waipu	5122	5121	North Island 1983	P2341	P2339	DDP
PAPUA NEW GUINEA						
Baiyer River-1	4857	4858	1983	P1786	P1789	DDP
Baiyer River		8794	Single conidium isolate from P1794		D34	DJJ
Brown River Highway		4859	1983		P1985	DDP
Bubia-1f$_1$	1937	1938	Markham Valley 1968,	P358	P359	DDP
Depo-Sogeri	4860	4861	1983	P1970	P1972	DDP
Goroka-1	4862	4863	1983	P1705	P1710	DDP
Goroka Area	5340	5339	corn cobs, yellow ecotype, 1983	P1758	P1737	DDP
Goroka		8793	Single conidium isolate from P1737		D33	DJJ
Highlands Highway		4838	1983		P1558	DDP
Hiri		4864	1983		P1987	DDP
Kaindi Road	4839	4840	1983	P1672	P1670	DDP
Lae-Unitech	4841	4842	1983	P1618	P1617	DDP
Lae f$_1$-12;Lae f$_1$-1	1786	1787	Lae, from ascospores, 1968	P64	P65	DDP
Leron-1	4843	4844	1983	P1701	P1702	DDP
Mt. Hagen	5342	5341	corn cobs, yellow ecotype, 1983	P1856	P1855	DDP
Mumeng	4845	4846	1983	P1600	P1597	DDP
Munum-1	4847	4848	1983	P1569	P1570	DDP
Marinville	4865	4866	1983	P1860	P1861	DDP
Nadzap	4849	4850	1983	P1582	P1588	DDP
Narikubun-1	4851	4852	1983	P1630	P1632	DDP
Pt. Moresby-Hohola-1	4867	4868	1983	P1873	P1874	DDP
Rouna-3; -4	1784	1785	Rouna Rd, near Pt. Moresby, 1968	P39	P41	DDP
Rouna-6	4869	4870	1983	P1927	P1921	DDP
Rouna-8	4871	4872	1983	P1957	P1968	DDP
Sogeri Rd-1	4873	4874	1983	P1916	P1917	DDP
Tiaba	4875	4876	1983	P1880	P1878	DDP
Tiaba		8795	Single conidium isolate from P1878		D35	DJJ
Wau-2	4853	4854	1983	P1656	P1651	DDP
Yalu	4855	4856	1983	P1561	P1560	DDP

Strain designation	FGSC # and mating type A	FGSC # and mating type a	Comments	Number in other culture collection A	Number in other culture collection a	Obtained from
N. intermedia, continued from previous page						
PHILIPPINES						
Manila	5641		yellow ecotype, 1968	P27		DDP
Manila-1; -1c	1762	1763	1968	P23	P25	DDP
Manila-8; -7	1782	1783	yellow ecotype, 1968	P30	P29	DDP
Manila		8763	Single conidium isolate from P25		D3	DJJ
Manila	8764		Single conidium isolate from P27	D4		DJJ
Philippine Islands 4		433	PI-4 Srb (from Everett?)			NHH
X	629		E. Quisumbling	11513		ATCC
X-1		630	E. Quisumbling		11514	ATCC
X-2	631		E. Quisumbling	11515		ATCC
PUERTO RICO						
Aguada	3702	3703	1979	P1194	P1195	DDP
Aguadilla	3700	3701	1979	P1175	P1174	DDP
Betances	3724	3725	1979	P1216	P1215	DDP
Colonia Paraiso		3706	1979		P1304	DDP
Garrochales	3697		1979	P1143		DDP
Indiera Alta	3728	3729	1979	P1245	P1246	DDP
La Prada	3698	3699	1979	P1149	P1150	DDP
Lago de Yauco	3726	3727	1979	P1225	P1233	DDP
Playa Cortada	3711	3712	1979	P1250	P1251	DDP
Salinas	3709	3710	1979	P1272	P1270	DDP
San Felipe	3708	3707	1979	P1286	P1281	DDP
San German	3704	3705	1979	P1199	P1200	DDP
SINGAPORE						
Singapore-1b; -1	1812	1813	1969	P278	P277	DDP
Singapore-2		436	A. Thompson			NHH
Singapore-3	5253	5254	1984	P2862	P2863	DDP
Singapore-5	5256	5255	1984	P2870	P2868	DDP
SOUTH PACIFIC						
Fiji N6-6; -	435	432	Fiji (L.S. Olive→Ryan→Horowitz)			NHH
Kolonia-1	5402	5403	Kolonia, Ponape 1984	P3310	P3313	DDP
Kolonia-2	5405	5404	Kolonia, Ponape 1984	P3319	P3315	DDP
Moen-4	5389	5388	Moen, Truk 1984	P3253	P3250	DDP
Moen-6	5391	5390	Moen, Truk 1984	P3262	P3261	DDP
Moen-7	5392		Moen, Truk 1984, yellow ecotype	P3266		DDP
Moen-7		5393	Moen, Truk 1984		P3268	DDP
Moen-8	5395	5394	Moen, Truk 1984	P3275	P3273	DDP
Moen-9	5396	5397	Moen, Truk 1984	P3282	P3285	DDP
Moen-10	5398	5399	Moen, Truk 1984	P3286	P3287	DDP
Moen-14	5400	5401	Moen, Truk 1984	P3302	P3304	DDP
Palau		6623	West Carolines 1983 (R. Levin)		P1556	DDP
Ponape-1	5407	5406	Ponape 1984	P3329	P3327	DDP
Ponape-2	5408	5409	Ponape 1984	P3334	P3335	DDP
Rota-1		6216	Rota 1984	P3168		DDP
Rota-3	5387	5386	Rota 1984	P3175	P3174	DDP
Songsong-1	6214		Rota 1984	P3151		DDP
Songsong-3	6215		Rota 1984	P3166		DDP
SWAZILAND						
Enzulini		7832	near Happy Valley Motel (J. Leslie)		P4439	BCT

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. intermedia, continued from previous page						
TAIWAN						
Chia-i-1; -i-2	1788	5642	yellow ecotype, 1968 (via H.W. Li)	P56	P62	DDP
Fua-Lian-1	1818		1968 (via H.W. Li)	P58		DDP
Fua-Lian-2 f_1		1819	1969 (via H.W. Li)		P77	DDP
Fu-wei-1	1789		yellow ecotype, 1968 (via H.W. Li)	P57		DDP
Kao-shong-1	1790		yellow ecotype, 1968 (via H.W. Li)	P60		DDP
Sing-in-1	1791		yellow ecotype, 1968 (via H.W. Li)	P61		DDP
Sing-in	8766		Single conidium isolate from P61	D6		DJJ
Tapei-1c; -1g	1766	1767	1968	P13	P17	DDP
Taipei	8761		Single conidium isolate from P13	D1		DJJ
Taipei		8762	Single conidium isolate from P17		D2	DJJ
THAILAND						
Bangkok-5	5257	5258	1984	P2880	P2883	DDP
Bangkok Airport 5260	5259	1984		P2892	P2887	DDP
Ban Khao Yai	8812		Single conidium isolate from P2938	D52		DJJ
Ban Phru Mao	6806		1989 (J. Leslie)	P4344		DDP
Ban Phru Mao	8862		Single conidium isolate from P4344	D102		DJJ
Khao Eto	5365	5364	1984	P2923	P2921	DDP
Khao Yai-1	5369	5368	1984	P2938	P2936	DDP
Khao Yai-2	5370	5371	1984	P2942	P2948	DDP
Klong Rangsit no. 4	5262	5261	1984	P2898	P2896	DDP
Klong Rangsit no. 5	5360	5361	1984	P2902	P2904	DDP
Klong Rangsit km57	5363	5362	1984	P2914	P2910	DDP
Nakhon Nayok	5367	5366	1984	P2932	P2926	DDP
Prabart Sarabur	8094	8093	J. Leslie	P4201	P4198	BCT
Tarkfa Nahorn Sawan	8091	8092	J. Leslie	P4195	P4196	BCT
TRINIDAD						
Caroni Swamp	7550	7549	1992 (N. Giles)	P4584	P4583	BCT
Walter AFB	7548		1992 (N. Giles)	P4582		BCT
UNKNOWN ORIGIN						
cocobean		589	From Dodge			BBG

Neurospora intermedia mutants

(see Shew, H.W. 1978. Neurospora Newsl. **25**:25)

Strain designation	FGSC # A	FGSC # a	Linkage group	Obtained from
ACRIFLAVINE RESISTANT				
acr-A	3406	3407	I	HWS
acr-2(KH5*)	8743	8742		
ALBINO				
al-A		3410	I	HWS
al-3(RP100)*	6567	6568	V	DDP
ASPARAGINE				
asn-A	4280	4281	V	BCT
ARGININE				
arg-A	3370	3371	I	HWS
arg-B	3372	3373	IV	HWS
arg-C	3374	3375	I	HWS
arg-E	3376	3377	II	HWS
arg-F	3378	3379	I	HWS
COLONIAL				
col-A	3412		III	HWS
col-B	3413		III	HWS
col-C	3414	3415	IV	HWS
CYSTEINE				
cys-A	3389	3390	IV	HWS
cys-B	3533	3534	IV	HWS
DELAYED GROWTH				
deg	3408	3409	V	HWS
HISTIDINE				
his-A	3391	3392	I	HWS
his-B	3393	3394	V	HWS
his-C	3395	3396	IV	HWS
his-D	3397	3398	I	HWS
his-E	3399	3400	III	HWS
LEUCINE				
leu-A		3401	I	HWS
METHIONINE				
met-A	3967	3380	III	BCT/HWS
met-B	3381	3382	IV	HWS
met-E	3383	3384	IV	HWS
met-F	3385	3386	IV	HWS
met-G	3387	3388	V	HWS
ORANGE AGAR				
ora	3411	4282	IV	BCT/HWS
PYRIDOXINE				
pdx-A	3404	3405	IV	HWS
RESISTANT TO SPORE-KILLER				
r(Sk-2)	1832	1833		DDP
r(Sk-3)	1786			DDP

* Progeny of 6th backcross into *N. intermedia* from *N. crassa*

Strain designation	FGSC # and mating type A	FGSC # and mating type a	Comments	Number in other culture collection A	Number in other culture collection a	Obtained from
NEUROSPORA LINEOLATA						
A-236	1910 homothallic		near Lahore, Pakistan	18966		ATCC
NEUROSPORA PANNONICA						
TRTC 51327	7221 homothallic		near Hortobagyi, Hungary	CBS 270.91		JCK
Spain		10032	W-1293			DJJ
NEUROSPORA SITOPHILA						
Reference strains, derived wild types, and mutants						
P8085;P8086	2216	2217	sitophila reference strain	P8085	P8086	DDP
fl(P1012);Sk-1^K	4762	4763	fluffy reference stocks (Sk-1^K)	8222	8223	DDP
fl^P;Sk-1^S	4887	4888	fluffy reference stocks (Sk-1^S)	8226	8227	DDP
P8097 *acon*;P8098 *acon*	2664	2665		P8097	P8098	DDP
56.1-aPc		581				BBG
56.8;56.4	2019	2020		P8066	P8067	DDP
56.6-Apc	583			CU108		BBG
56.7-APC	584					BBG
112.19	2539		W. Herter → CBS 1919	112.19		CBS
173.25		2538			173.25	CBS
Arlington APC	417			CU104		BBG
B		964	f$_1$ from FGSC 963 X standard Dodge isolate			JW
Beale APC	415			CU110		BBG
HSS	586					BBG
HSSf$_1$22aPC		412			CU101	BBG
HSSf$_1$32APC	414			CU103		BBG

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. sitophila, Reference strains, derived wild types, and mutants continued						
MNHN504	1137		From Museum Natural History, Paris no source data	QM#8194		EGS
WA;Wa	2983	2984	Whitehouse wild types	P8106	P8107	DDP
no#	346					MBM
pdx(299)		348	pyridoxine mutant 299			MBM
rg-2 thi(1090)	3886			SFT-5		NCM
rg-1(B53) pdx(299)	3888			M-17		NCM
rg-2	4643	4644		8221	8220	DDP
rg-2		3887			SFT-9	NCM
rg-2 su-2	3891	3892		NSA	Nsa	NCM
rg-2 su-2		3889			15-6	NCM
rg-2 su-2 cr-1	3890			15-7		NCM
$Sk\text{-}1^{S}$	5940	5941		P2443	P2444	DDP
Sk-1		7866			P4689	BCT
thi(1090)	3959	347		P504		DDP
(rg-2 thi(1090) + rg-1(B53) pdx(299))	3895		Heterokaryon of 3886 + 3888			NCM
Original collected *N. sitophila* strains						
AUSTRALIA						
Kilcoy		8173	Queensland		P4689	BCT
Robina	6802		1989 (J. Tierney via D. Shaw)	P4328		DDP
BRITISH WEST INDIES						
Old Man Bay-1	8176	8174	Grand Cayman, J. Leslie	P4696	P4691	BCT
Old Man Bay-2	8177	8178	Grand Cayman, J. Leslie	P4711	P4712	BCT
Old Man Bay-3	8180	8179	Grand Cayman, J. Leslie	P4736	P4735	BCT
CENTRAL AND SOUTH AMERICA						
Brazil		6673	from fermented cassava (Y.K. Park)		46892	ATTC
Coba	6646		Quintana Roo, Mexico (M. Bojko)	P4140		DDP
Isla Mujeres	6640	6639	Quintana Roo, Mexico (RLM)	P4135	P4132	DDP
Panama (UP203)	1134		Canal Zone 1945 (Jump)	QM#5082		EGS
Panama 4NHB6B	1135		Jaques, Panama 1944 (Jump)	QM#5692		EGS
Panama 52B6CI	1136		1945 (Barghoorn)	QM#6444		EGS
Piracununga-1	3355		Brazil 1978	P1039		DDP
Todos Santos	6851		Mexico 1986 (R. Metzenberg)	P4043		DDP
Todos Santos	6852		Mexico 1986 (R. Metzenberg)	P4044		DDP
Urbano Santos	8118		Northeast Brazil (YK Park)	P8267		DDP
CHINA						
Harbin	3987		Heilongjiang 1980 via N. Giles P1527		DDP	
CONGO						
Bouanza	6558		1985	P3856		DDP
Kinkala-1	6559		1985	P3889		DDP
Port du Djoue-1	6555		1985	P3792		DDP
Port du Djoue-2	6556	6557	1985	P3797	P3799	DDP
Port du Djoue-2		6849	1985		P3800	DDP
CONTINENTAL UNITED STATES						
Arlington	1843		Rosslyn, Virginia 1927 ($Sk\text{-}1^{K}$)	178.27		CBS
Bayou Chicot-2		3215	Louisiana 1977 ($Sk\text{-}1^{K}$)		P871	DDP
Belen	8580		New Mexico	W684		DJJ
Coon-9		3216	Louisiana 1977 ($Sk\text{-}1^{K}$)		P887	DDP
Elizabeth-2	3214		Louisiana 1977 ($Sk\text{-}1^{K}$)	P862		DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. sitophila						
CONTINENTAL UNITED STATES, continued						
El Paso		4201	Texas 1980 (H. Luscombe) (*Sk-1*^{K})		P1502	DDP
Everglades		4202	Florida 1980		P1503	DDP
Ithaca, N.Y.	3999		1979 (O. Yoder) (*Sk-1*^{K})	P1501		DDP
LaBelle-1h		2371	Florida 1970		P411	DDP
Los Alamos #1	8590		New Mexico	W775		DJJ
Los Lunas	8575	8574	New Mexico	W643	W632	DJJ
Marrero-1	2234	2235	Louisiana 1972 (*Sk-1*^{K})	P472	P475	DDP
Palo Alto-1		2494	(*Sk-1*^{K}) California 1973 (M.R. Smith)	P653^{SK}		DDP
Palo Alto-2	2684		California 1973 (M.R. Smith)	P756		DDP
Ravenswood-2		3217	Louisiana 1977 (*Sk-1*^{K})		P889	DDP
Rexford	8559		Montana	W491		DJJ
San Jose		8181	Coffee maker, California		P4779	BCT
Syracuse	6220		New York 1984 (M. Schechtman)	P3516		DDP
J1131X	1128		Philadelphia, PA 1949 (Reese)	Q.M. #909		EGS
EUROPE						
no#	963		France 1958			JW
2		1779	Chichester, England 1933 (W.H. Wilkins)			RLM
GABON						
Ekowong	6224	6225	1985	P3921	P3923	DDP
Makokou-1	6222	6223	1985	P3912	P3913	DDP
Makokou-1	6850		1985, *r(Sk-1)*	P3914		DDP
Makokou-1		6886	1985		P4427	DDP
Makokou-7		6227	1985		P3933	DDP
HAITI						
Anse-A-Galets-2; -1	4782	4781	1984	P3499	P3497	DDP
Au Borgne-1	4783	4784	1984	P3459	P3458	DDP
Au Borgne-2	4785	4786	1984	P3463	P3464	DDP
Bas Quartier	4787	4788	1984	P3476	P3470	DDP
Berard	4789	4790	1984	P3481	P3483	DDP
Carrefour Mme. Gras	4791	4792	1984	P3494	P3492	DDP
Carrefour Mme. Gras	8823		Single conidium isolate from P3494	D63		DJJ
Gran Sous	4793	4794	1984	P3510	P3506	DDP
Haut Diquini	4795	4796	1984	P3414	P3413	DDP
Haut du Cap	4797	4798	1984	P3485	P3484	DDP
Merger		4799	1984		P3440	DDP
HAWAII						
Hanalei-2f		2368	Kauai 1972		P569	DDP
Hanalei-3		2370	Kauai 1972		P575	DDP
Hanalei-3j-1	6676		Separated from Hanalei-3j			JWT
Hanalei-3j-2	6689		(FGSC 2369)		JWT	
INDIA						
Golur-1e; -2	2491	2492	Karnataka 1969;1974	P333	P708	DDP
Golur	8770		Single conidium isolate from P333	D10		DJJ
Mercara	4800		from soil 1975 (R. Maheshwari)	P2515		DDP
ITALY						
Turchino Est.	10035		2003	W-1309		DJJ
Turchino Est.		10039	2003		W-1326	DJJ
Turchino Est.		10041	2003 *Sk-1*		W-1329	DJJ
Genoa	10053		2003 *Sk-1*	W-1396		DJJ

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. sitophila						
ITALY, continued						
Genoa		10052	2003 *Sk-1*		W-1394	DJJ
Genoa		10055	2003		W-1416	DJJ
IVORY COAST						
Adiopodoume-1	6295	6294	1985	P3760	P3759	DDP
Adiopodoume-4	6297	6296	1985	P3775	P3774	DDP
Adiopodoume-5		6798	1989 (D. Le Pierres)		P4261	DDP
Adiopodoume-5	6855	6856	Ivory Coast 1989 (D. Le Pierres)	P4257	P4260	DDP
Adiopodoume-6	6799	6800	1989 (D. Le Pierres)	P4279	P4283	DDP
Adiopodoume-6	6862	6863	Ivory Coast 1989 (D. Le Pierres)	P4375	P4376	DDP
Adiopodoume-8	6859		Ivory Coast 1989 (D. Le Pierres)	P4312		DDP
Adiopodoume-8	6801		1989 (D. Le Pierres)	P4313		DDP
Adiopodoume-9	6860	6861	Ivory Coast 1989 (D. Le Pierres)	P4314	P4318	DDP
Adiopodoume	8832		Single conidium isolate from P4314	D72		DJJ
Ahanoui-2	6198	6199	1985	P3588	P3589	DDP
Balayo	6285	6284	1985	P3615	P3612	DDP
Brabadogou		6858	Ivory Coast 1989 (D. Le Pierres)		P4289	DDP
Divo-6	6297	6296	1985	P3583	P3581	DDP
Duekoue	6289	6288	1985	P3626	P3625	DDP
Grabiokoko	6200	6283	1985	P3592	P3593	DDP
Issia	6287	6286	1985	P3623	P3620	DDP
Loguale	6290	6291	1985	P3629	P3630	DDP
Man-2	6293	6292	1985	P3666	P3665	DDP
Tiassole	6194	6195	1985	P3566	P3567	DDP
Yopougon-2	6857		Ivory Coast 1989 (D. Le Pierres)	P4270		DDP
JAPAN						
Obama-1; -1b	1764	1765	Kyushu 1968 ($Sk\text{-}1^{K}$)	P1	P2	DDP
173.25		2538	Y. Nishiwaki → CBS 1925			
MALAYA and SINGAPORE						
Ipoh Road	6847		Malaysia 1984	P2766		DDP
Kampang Pengakalan	8167	8168	J. Leslie	P4661	P4668	BCT
Kenaboi		4801	10-71 (C.C. Ho)		P3401	DDP
Klang-6f		2493	1969		P268	DDP
Ladang Glengowrie	4802		1984	P2830		DDP
Mantin-1	4803		1984	P2835		DDP
Mantin-2	4804		1984	P2839		DDP
Singapore-5	4807		1984	P2869		DDP
Singapore-9		6848	Singapore 1983		P3075	DDP
Sungai Terap		8169	J. Leslie		P4670	BCT
Telok Kumbar	4805		Penang 1984	P2637		DDP
MOOREA and TAHITI						
Afareaitu	4731	4732	Moorea 1983 ($Sk\text{-}1^{K}$)	P2500	P2502	DDP
Baie D'O Punohu		4733	Moorea 1983		P2476	DDP
Haapape	4745		Tahiti 1983	P2377		DDP
Haapiti-1	5936		Tahiti 1983 ($Sk\text{-}1^{K}$)	P2454		DDP
Haapiti-2	5937	4734	Moorea 1983 (5937 is $Sk\text{-}1^{K}$)	P2466	P2461	DDP
Hitiaa	4746	4747	Tahiti 1983	P2400	P2394	DDP
Moorea		8974			W548	DJJ
Musee Gauguin		4748	Tahiti 1983		P2430	DDP
North Road	4749	4750	Tahiti 1983 (4750 is $Sk\text{-}1^{K}$)	P2372	P2374	DDP
Papenoo	4751	4752	Tahiti 1983	P2380	P2379	DDP
Papetoia	5939	5938	Moorea 1983 ($Sk\text{-}1^{K}$)	P2483	P2482	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
N. sitophila,						
MOOREA and TAHITI, continued from previous page						
Plateau de Taravao		4753	Tahiti 1983		P2408	DDP
Plateau de Taravao	5934	5933	Tahiti 1983 ($Sk\text{-}1^{K}$)	P2412	P2410	DDP
Potii		4754	Tahiti 1983		P2415	DDP
Punaauia	5940	5941	Tahiti 1983	P2443	P2444	DDP
Tautira	4757		Tahiti 1983	P2407		DDP
Teavaro	4736	4737	Moorea 1983 (4737 is $Sk\text{-}1^{K}$)	P2495	P2492	DDP
Temae		4738	Moorea 1983 ($Sk\text{-}1^{K}$)		P2451	DDP
Teoharoa		4739	Moorea 1983 ($Sk\text{-}1^{K}$)		P2490	DDP
Tahiti	8976		From N. Giles, 1997	W551		DJJ
Tiarei-1	4758	4759	Tahiti 1983	P2387	P2386	DDP
Tiarei-1	4758	4759	Tahiti 1983	P2387	P2386	DDP
NIGERIA						
Nigeria 243; 112	2009	2010	Nsukka, Eastern Nigeria 1965	P8064	P8065	DDP
Nigeria	8883		Single conidium isolate from P8064 D123			DJJ
PAPUA NEW GUINEA						
Brown River	4740		Teak Plantation, 1983	P2004		DDP
Brown River Area		4741	1983		P2028	DDP
Hiri	4742		1983	P1989		DDP
Kanusia		4743	1983		P2018	DDP
Munum-1		4744	1983		P1573	DDP
PORTUGAL						
Tapada de Mafra	10022		2003 *Sk-1*	W-1249		DJJ
Monchique		10026	2003		W-1262	DJJ
PUERTO RICO						
Garrochales	3695		Garrochales, 1979	P1142		DDP
Playa Cortada	3696		Playa Cortada 1979	P1259		DDP
Playa Cortada		6846	1979		P1269	DDP
SOUTH PACIFIC						
Matavera		6235	Rarotonga, R. Beever 1987		P4091	DDP
Matavera	6853	6854	Rarotonga 1987 (R. Beever)	P4090	P4092	DDP
Merizo	6549		Guam 1984	P3218		DDP
Moen-3	6553		Moen, Truk ($Sk\text{-}1^{K}$)	P3245		DDP
Moen-4	6554		Moen, Truk ($Sk\text{-}1^{K}$)	P3249		DDP
Songsong-1		6213	Rota, 1984		P3150	DDP
Tonga	4203	4204	Tonga 1981 (L. Olive) ($Sk\text{-}1^{K}$)	P1544	P1543	DDP
Vanuatu		4806	1975 (R.E. Beever)		P3409	DDP
SPAIN						
Macanet de la Selva		10030	2003		W-1290	DJJ
Macanet de la Selva	10031		2003 *Sk-1*	W-1291		DJJ
Macanet de la Selva		10032	2003 *Sk-1*		W-1293	DJJ
SWITZERLAND						
Leuk	10034		2003 *Sk-1*	W-1300		DJJ
THAILAND						
Bangkok		6807	1989 (J. Leslie)		P4351	DDP
Ban Phru Mao	6806	6805	1989 (J. Leslie)	P4344	P4342	DDP
Hat Yai	6803	6804	1989 (J. Leslie)	P4337	P4339	DDP
Khao Yai-4	6489		1984	P2998		DDP

Strain designation	FGSC # and mating type A	FGSC # and mating type a	Comments	Number in other culture collection A	Number in other culture collection a	Obtained from
N. sitophila,						
THAILAND, continued from previous page						
Khao Yai	8813		Single conidium isolate from P2998	D53		DJJ
TURKEY						
Gebze		6232	1984 (Ali Sazci)		P3957	DDP
Other *N. sitophila* wild types:						
NRRL 1275		848	A. McCrea, 1932, culture media		1275	NRRL
NRRL 2884		2685	ontjom strain, 1948, A.K. Smith		2884	CWH
NRRL 2884		3299	ontjom strain (Ellis→Perkins)		P8125	DDP
***NEUROSPORA SUBLINEOLATA* Furuya et Udagawa**						
(=*Anixiella sublineolata*)						
SANK 17876	5508 homothallic		From soil, Iriomote Island, Okinawa pref., Japan, March 1973 (K. Furuya)			KF
NEUROSPORA TERRICOLA						
WFS 5000	1889 homothallic		Spring Green, Wisconsin 1961		14941	ATCC
NEUROSPORA TETRASPERMA						
Reference strains; derived wild types						
85A; 85a	1270	1271	Recommended tetrasperma reference strains			HBH
87	614^{PS}		Columbia Univ. (Dodge)	87		BBG
4		350	A. Sussman (Dodge)		4	MBM
5		349	A. Sussman (Dodge)		5	MBM
1396		640	J.A. Stevenson		6484	ATCC
180.27	1842^{PS}		An original C.L. Shear stock	180.27		CBS
NRRL 2164	849^{PS}		Same as Dodge 204	2164		NRRL
***N. tetrasperma* wild-collected strains**						
AFRICA						
Liberia	965^{PS}		1957 (Harbel),			JW
Makokou-8	6228^{PS}		Gabon, 1985	P3936		DDP
Mt. Tonkgui	6577^{PS}		Ivory Coast	P3671		DDP
AUSTRALIA						
Beerburrum	8172^{PS}		Queensland	P4687		BCT
South Beach	7828^{PS}		Queensland	P1557		BCT
Narrabeen	7850^{PS}		New South Wales	P4605		BCT
BORNEO						
Menggatal	6573^{PS}		Sabah	P3124		DDP
Warcup-derived	7323		Alpha	T220-10-5a		RLM
Warcup	7324^{PS}		Zeta	T220-89-A/a		RLM
Warcup-derived	7325		Iota	T220-7A		RLM
BRAZIL						
Serra Arcara	8998		Via G. Samuels, +	W1088		DJJ
CARIBBEAN						
Berard	6576^{PS}		Haiti	P3480		DDP
Indiera Alta	3731^{PS}		Puerto Rico 1979	P1244		DDP
Pescail	6574^{PS}		Haiti	P3449		DDP
San Felipe	3730^{PS}		Puerto Rico 1979	P1289		DDP

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. tetrasperma,						
CARIBBEAN, continued from previous page						
Thebaudiere	6575^{PS}		Haiti	P3456		DDP
CENTRAL and SOUTH AMERICA						
Campinas-2	3356^{PS}		Brazil	P981		DDP
Chemax	6635^{PS}		Yucatan, Mex. 1988 (RLM)	P4114		DDP
Chichen Itza	6641^{PS}		Quintana Roo, Mex. 1988 (RLM)	P4164		DDP
Coba-2	6643	6644	Mexico 1988 (RLM)	P4177	P4178	DDP
Coba 131	7585	7586		78-02	78-03	RLM
Ekwarun	5913^{PS}		Guyana, 1984 (G. Samuels)	P4071		DDP
G248	4500^{PS}		Isla Santa Cruz, Galapagos Islands (D.P. Mahoney)	8210		DDP
G281	4501^{PS}		Zamora, Ecuador (D.P. Mahoney)	8215		DDP
G354	4502^{PS}		Isla Santa Cruz, Galapagos Islands (D.P. Mahoney)	8211		DDP
Imbaima Dai	5909^{PS}		Guyana, 1984 (G. Samuels)	P4057		DDP
Jaboticabal-3	3357^{PS}		Brazil	P1067		DDP
Orinoco Delta-1	7551^{PS}		Venezuela, 1992 (N. Giles)	P4587		BCT
Todos Santos	6234^{PS}		Mexico, 1986 (R. Metzenberg)	P4045		DDP
UFC-200	850^{PS}		La Lima Honduras 1958	UFC #220		RDG
9457	637		Argentina (K. Raper → Dodge)	9457		ATCC
N. tetrasperma						
CONTINENTAL UNITED STATES						
Chapin	3329^{PS}		South Carolina 1978	P1132		DDP
Chiquita Loma Rd.	8999		CA a+A	W1098		DJJ
Columbia	3330^{PS}		South Carolina 1978	P1133		DDP
Elizabeth-5	3203^{PS}		Louisiana 1977	P865		DDP
Empire-1v2; -1ba	2501	2502	Louisiana 1972	P665	P471	DDP
Franklin	8102^{PS}		Louisiana	P4458		BCT
Franklin	9024	9025	Louisiana Burned cane	W1	W2	DJJ
Franklin	9026	9027	Louisiana Burned cane	W3	W4	DJJ
Franklin	9028	9029	Louisiana Burned cane	W5	W6	DJJ
Franklin	9030	9031	Louisiana Burned cane	W7	W8	DJJ
Franklin	9032		Louisiana Burned cane	W9		DJJ
Franklin	9033	9037	Louisiana Burned cane	W11	W12	DJJ
Franklin	9035	9036	Louisiana Soil	W19	W20	DJJ
Franklin	9037	9038	Louisiana Burned cane	W25	W26	DJJ
Franklin	9039	9040	Louisiana Soil	W27	W28	DJJ
Franklin	9041	9042	Louisiana Burned cane	W30	W31	DJJ
Franklin	9043	9044	Louisiana Soil	W431	W432	DJJ
Franklin	9045	9046	Louisiana Soil	W435	W436	DJJ
Franklin	9047	9048	Louisiana Soil	W437	W438	DJJ
Franklin	9049	9050	Louisiana Soil	W439	W440	DJJ
Welsh	9051	9052	Burned grass Single conidium isolates from P510	P4379	P4380	DJJ
Welsh	9053	9054	Burned grass Single conidium isolates from P514	P4381	P4382	DJJ
Georgia Plantation	8105^{PS}		Louisiana	P4511		BCT
Groveland-1	1942^{PS}		Florida 1970	P436		DDP
Homestead-1f	1943^{PS}		Florida 1970	P388		DDP
Jakes Branch		8997	New Jersey		W1007	DJJ
LaBelle-1	1941^{PS}		Florida 1970	P404		DDP
Lake Alfred-1b	1944^{PS}		Florida 1970	P425		DDP
Moss Hill-5	3205^{PS}		Texas 1977	P815		DDP

Strain designation	FGSC # and mating type A	a	Comments	Number in other culture collection A	a	Obtained from
N. tetrasperma						
CONTINENTAL UNITED STATES, continued from previous page						
Northside Planting	8139^{PS}		Louisiana	P4516		BCT
Perkins Colony-1	3327^{PS}		Georgia 1978	P1130		DDP
Perkins Colony-2	3328^{PS}		Georgia 1978	P1131		DDP
Perkins-1v2	2505		Louisiana 1972	P654		DDP
Raleigh	3998	4245	North Carolina 1981	P1534	P1535	DDP
Sugartown-5	3204^{PS}		Louisiana 1977	P856		DDP
Sweetwater-1m		2507	Florida 1970		P403	DDP
Welsh-1bv1; -1bv2	2503	2504	Louisiana 1972	P658	P663	DDP
Welsh	8773		Louisiana Single conidium isolate from P658	D13		DJJ
FRANCE						
France	10029^{PS}			W-1273		DJJ
HAWAII						
Hanalei-1bv1; -1bv3	2510	2511	Kauai, 1972	P664	P659	DDP
Lihue-1v1; -1v2	2508	2509	Kauai, 1972	P657	P656	DDP
Waimea Falls-2	3296^{PS}		Oahu, 1976	P771		DDP
INDONESIA						
Gianjor-1	1794^{PS}		Bali 1969	P202		DDP
MALAYA						
Batu Ferringi-2	6578^{PS}		Penang	P2687		DDP
MOOREA-TAHITI						
Arue	6582^{PS}		Tahiti 1983	P2362		DDP
Haapiti-1	6590^{PS}		Moorea 1983	P2455		DDP
Hitiaa	6584^{PS}		Tahiti 1983	P2392		DDP
Musee Gauguin	6588^{PS}		Tahiti 1983	P2434		DDP
Plateau de Taravao	6586^{PS}		Tahiti 1983	P2411		DDP
South Coast	6587^{PS}		Tahiti 1983	P2422		DDP
Tautira	6585^{PS}		Tahiti 1983	P2401		DDP
Temae	6589^{PS}		Tahiti 1983	P2447		DDP
Teovare	6592^{PS}		Moorea 1983	P2494		DDP
Tiarei-1	6583^{PS}		Tahiti 1983	P2383		DDP
Viaire	6591^{PS}		Moorea 1983	P2468		DDP
NEW ZEALAND						
Ahipara	6474^{PS}		1983	P2265		DDP
Ahipara-Shipwreck Bay	6485^{PS}		1983	P2356		DDP
Auckland City	6581^{PS}			P3958		DDP
Brookby	6479^{PS}		1983	P2316		DDP
Clevedon	6480^{PS}		1983	P2328		DDP
Cornwallis Beach	6478^{PS}		1983	P2302		DDP
Dargaville	6473^{PS}		1983	P2250		DDP
Fox Glacier	6218^{PS}		1984 (R. Beever)	P3403		DDP
Herekino	6475^{PS}		1983	P2272		DDP
Hillcrest	7831^{PS}		D. Rainey, from soil	P4435		BCT
Kawakawa	6481^{PS}		1983	P2329		DDP
Mt. Albert	6579^{PS}			P2293		DDP
New Zealand S-4		642	(J.H. Warcup)			MJM
Okaihu	6484^{PS}		1983	P2353		DDP
Omapere	6476^{PS}		1983	P2283		DDP
Pirongia	6580^{PS}			P3357		DDP
Hana	6482^{PS}		1983	P2330		DDP

NEW ZEALAND, continued from previous page

Waipu	6483^{PS}	1983	P2338	DDP
Waitakere	6477^{PS}	1983, (R. Beever)	P2298	DDP
PAPUA NEW GUINEA				
Baiyer River-5	6486^{PS}	1983	P1793	DDP
Mt. Hagen-5	6487^{PS}	1983	P1835	DDP
PORTUGAL				
Portugal	10057^{PS}	2006	W-1530	DJJ
Portugal	10023^{PS}	2006	W-1251	DJJ
Portugal	10019^{PS}	2006	W-1245	DJJ
Portugal	10016^{PS}	2006	W-1240	DJJ
Portugal	10015^{PS}	2006	W-1238	DJJ

PS Pseudohomothallic (A+a)

Miscellaneous N. tetrasperma from Dodge collection

(via New York Botanical Garden)
see Metzenberg and Ahlgren 1969. Neurospora Newsl. 15:9-10;
1971. Genetics 68:369-381.

	FGSC # and mating type	
Strain designation	A	a
86.9	615^{PS}	
NS-130	425	
394.4-Ae	608	
394.5-ae	609^{PS}	
616-Ae	616	
2521.12-ae		604
J3C3		617
343.6-AE		606
N-aD-wild type	590	
ND=dwarf		596
S1-aD		593
10-Ade	602	
16-ade		595
C4-Ad	591	
C8-ad		592
D6-AI	600	

Bisexual heterokaryons	FGSC #
Dwarf 16-ade	597
H3-aI	599
Dwarf 16-aDP+C4-Ad	598
H3-aI+D4-AI	601
16-ade + 10-Ade	603
343.6AE + 340.6-a	607
394.4-Ae+ 394.5-ae	610
343.6-AE + 394.5-ae	611
343.6-AE + 2521.12-ae	612
343.6-AE + 395.-ae	613
2521.12-ae + 87.11-AE	619

N. tetrasperma mutants

(See Howe, H.B, Jr. and P. Haysman 1966 Genetics 54:293-302) Most of the mutant markers were described and mapped to linkage groups by Howe and Haysman, 1966 Genetics 54:293-302. The *E* gene is useful for obtaining homokaryotic ascospores. *E/e* gives moistly 8spored asci; *E/E* gives very few asci, all 8-spored. Mating type is tagged by *al(102)*, which shows no recombination with *A*. This section contains mainly single mutants (with or without *al(102)* or *E*)

Locus	FGSC # A	FGSC # a	L.G.	Allele	Obtained from
ACRIFLAVINE RESISTANCE					
acr(111)	1251		I	111	HBH
acr(112)	1252	7858	III	112	HBH/DDP
acr(112); E	7292	7293			DDP
ADENINE					
ad(101)	1255		V	101	HBH
ALBINO					
al(102)	1256		I	102	HBH
al(102);E	7234				DDP
al-2; lys-1	8605		IR; VL	102; 33933*	DDP
al-2; cys-10; E	8607		IR; IVL	102; 39816*	DDP
* from *N. crassa*					
BUDDED ASCOSPORES					
bud	9593	9594		R300-1	NBR
COLONIAL					
col(105)	1260		IV	105	HBH
col(118)	1261		V	118	HBH
col(119)	1262		VII	119	HBH
col(119);E	7480				DDP
CYCLOHEXIMIDE RESISTANCE					
cyh(113)	1253	6691	V	113	HBH/DDP
cyh(113);E		7235			DDP
cyh(114)	1254		I	114	HBH
cyh(114);E	7233				DDP
CYSTEINE*					
cys(123)	1265	6707	VI	123	HBH/DDP
cys(123);E	7236				DDP
cys-10		8606	IVL	39816#	DDP
*Responds to cysteine or methionine, not to sulfite. Formerly called *met(123)*					
#from *N. crassa*					
EIGHT SPORE					
E	7502	7503	VI	E	DDP
$E(f_8)$*	8114	8115			DDP
* Progeny of eight sib-matings. Asci with eight viable spores more frequent but still low.					
ERGOSTEROL					
erg-3	9077			Te-4	DK
HYG *erg-3* duplication	9078			121	DK
HYG *erg-3* duplication	9079			122	DK
HYG *erg-3* duplication	9080			123	DK
HYG *erg-3* duplication	9081			131	DK
HYG *erg-3* duplication	9082			132	DK
HYG *erg-3* duplication	9083			133	DK

Locus	FGSC # A	a	L.G.	Allele	Obtained from
LAWN					
lwn(P2612)		7282	VII	P2612	DDP
lwn;al(102)	7281				DDP
lwn;E		7284			DDP
lwn;al(102);E	7283				DDP
LYSINE					
lys(122)	1264			122	HBH
lys(122);E		7237			DDP
lys-1		8606	V	33933*	DDP
* from *N. crassa*					
NITRATE NON-UTILIZER					
nit(VP1)		7877	IV	VP1	DDP
nit(VP1);al(102)		7876	I;IV		DDP
nit(VP1);E		7865			DDP
nit(VP1);al(102);E	7864				DDP
OSMOTIC					
os(P2610)	6692		I	P2610	DDP
os;E	8116	8117	I;VI	P4519	DDP
PANTOTHENATE					
pan(124)	1266	7859	IV	124	HBH/DDP
pan(124);E	7860	7861			DDP
SELF STERILE					
ss	9354			16s	DK
TRYPTOPHAN					
trp(126)	1268		II	126	HBH
UNKNOWN					
un(127)	1269		IV	127	HBH

Strains for testing linkage *

(al(102);pan(124);col(119) A + met(123) E A) FGSC # 7568 DDP (Tests I, IV, VII)

(*pan(124);col(119) a + lys(112) E a*) FGSC # 7569 DDP (Tests IV, VII)

* If both parents contain E, only the first listed component of the heterokaryon will produce progeny. See Perkins 1994 FGN **41**:71.

Markers introduced from *N. crassa*

Locus	FGSC # A	a	L.G.	Allele	Obtained from
T(IR;IIR)4637al-1	7878		IR,IIR		DDP
FLUFFY					
fl^{P}	7084	7085	IIR		DDP
$fl^{P};E$	7136	7087			DDP
PEACH					
pe;E	7862	7863	IIR		DDP
PEAK					
pk		7879	VR		DDP

NEUROSPORA TOROI = *N. tetrasperma*

Strain designation	FGSC # A	a	Collection date, comments	Number in other collection A	a	Obtained from
259.35		688^{PS}	Puerto Rico (R.A. Toro) (Dodge → CBS → Howe)	CBS 259.35		HBH
259.35		2541^{PS}	B.O. Dodge → CBS	CBS 259.35		CBS

PS Pseudohomothallic (A+a)

NEUROSPORA COLLECTED FROM NATURE, SPECIES UNCERTAIN

Strain designation	FGSC # A	a	Collection date, comments	Number in other collection A	a	Obtained from
New Zealand M-1		643	J.H. Warcup (*N. discreta*?)			MJM
New Zealand S-3		644	J.H. Warcup			MJM
N2798		588	Beadle (1943) → Dodge			BBG
Tiaba-8		3269	Tiaba, Papua New Guinea 1968		P47	DDP (D5 *N. discreta*)
Carrefour Dufort	8225		DDP, 1984, Haiti	P3426		BCT (D58 PS1)
Leogane	8226		DDP, 1984, Haiti	P3431		BCT
Fougbesso	8227		DDP, 1984, Ivory Coast	P3653		BCT
N'Douci	8227		DDP, 1984, Ivory Coast	P3694		BCT
Hiri		8229	DDP, 1983,Papua New Guinea		P4025	BCT
Crouching Lion	8230		DDP, Hawaii		P4102	BCT
Rondon		8231	Gary Samuels, 1984 Brazil		P4249	BCT
Tucamanduba	8232	8233	Norman Giles, 1992 Brazil	P4604	P4608	BCT
Swaziland	8234		John Leslie, 1990 Swaziland	P4769		BCT
Madurai		8235	DDP, 1984 India		P4770	BCT
Brabadougou	8317		Ivory Coast. *N. discreta*?	P4297		DDP
Fougbesso		8318	Ivory Coast.		P3660	DDP (67 *N. discreta*)
Fougbesso		8334	Ivory Coast. *N. discreta?*		P3655	BCT
Agbanou	8335		Ivory Coast. *N. discreta?*		P3748	BCT
Asikro	8336		Ivory Coast . *N. discreta?*		P3750	BCT
Brabadougou	8338	8337	Ivory Coast. *N. discreta*?	P4527	P4288	BCT
Brabadougou	8339		Ivory Coast. *N. discreta*?	P4528		BCT
Bora Bora		8973			W546	DJJ

GENES TRANSFERRED AMONG NEUROSPORA SPECIES

Strain designation	FGSC # A	a	Source of gene(s)	Obtained from
'Foreign' genes now in *N. crassa*				
ars 343		2052	N. *tetrasperma*	RLM
ars UFC-220		1909	*N. tetrasperma*	RLM
gin 637/3.4		647	*N. sitophila* (*os-1* allele?)	MJM
nit-2 K31	33		*N. sitophila*	DDP
nit-4;Sk-2^{K}	1170	1171	*N. intermedia*	AMS
nit-4	2993	2994	*N. intermedia* (free of *Sk-2*^{K})	DDP
per-1 P760	6708	6709	*N. intermedia*	DDP
rg-2	4238	4239	*N. sitophila*, 3rd BC	DDP
Sk-2^{K}	6648	6647	*N. intermedia*→*N. crassa* 10th BC	BCT
Sk-2^{K}	3114	3115	*intermedia*→*crassa* OR inbreds, 10th BC	DDP
Sk-2^{K} *dow*	4260	4261	*Sk* from *N. intermedia*	DDP
Sk-2^{K} *phe-2 dow*	4538	4539	Sk from *N. intermedia*	DDP
Sk-2^{K}*;fl*^{P}	3297	3298	Sk from *N. intermedia*, 9th BC	DDP
Sk-3^{K}	3577	3578	Sk from *N. intermedia*, 10th BC	DDP
Sk-3^{K}*;fl*^{P}	3579	3580	Sk from *N. intermedia*, 10th BC	DDP
Sk-2^{K} *acr-2*	6928	6929	Sk from *N. intermedia*	BCT
Sk-2^{K} *acr-7*	6930		Sk from *N. intermedia*	BCT
acr-7 Sk-3^{K}	6931	6932	Sk from *N. intermedia*	BCT
$A^{S(E)};a^{S(E)}$	2995	2996	*N. sitophila* mt from Whitehouse wt, 4th BC	DDP
$A^{S(V)};a^{S(V)}$	3054	3010	*N. sitophila* mt from Dodge wt, 4th BC	DDP
A^{T} a^{T}	3070	3071	*N. tetrasperma* mating type genes in Oak Ridge *N. crassa*	RLM

'Foreign' genes now in *N. intermedia*

fl^{P}	5798	5799	from *N. crassa*, 7th BC	DDP
A^{C}	1755		m.t. from *N. crassa*, 10th BC	AMS
al-3 RP100	6567	6568	from *N. crassa*, 6th BC	DDP
acr-2 KH5	8743	8742	from *N. crassa*, 6th BC	DDP
acr-2 his-7 KH5 Y152M31		8962	from *N. crassa,* 7th BC	DDP
cum; acr-2 P5241; KH5	8963		from *N. crassa,* 7th BC	DDP

'Foreign' genes now in *N. sitophila*

rg-2 su-2 cr-1	3890		*cr-1* from *N. crassa*	NCM
rg-1; pdx(299)	3888		*rg-1* from *N. crassa*	NCM
fl^{P}	4887	4888	*fl*^{P} from *N. crassa*, 5th BC	DDP

'Foreign' genes now in *N. tetrasperma*

cys-10		8608	from *N. crassa*, 7th BC	DDP
fl^{P}	7084	7085	from *N. crassa*	DDP
fl^{P}*;E*	7136	7087	*fl*^{P} from *N. crassa*	DDP
lys-1		8606	from *N. crassa*, 7th BC	DDP
pe;E	7862	7863	*pe(Y8743m)* from *N. crassa*	DDP
pk		7879	*pk(29-044-5*) from *N. crassa*	DDP
Sk-2^{K} *acr-2*	6934	6935	*Sk-2*^{K} from *N. intermedia* via *N. crassa* *acr-2* from *N. crassa*	DDP
Sk-2^{K} *acr-2;E*	6936	6937	*Sk-2*^{K} from *N. intermedia* via *N. crassa* *acr-2* from *N. crassa*	DDP
Sk-3^{K} *acr-7*	6938	6939	*Sk-2*^{K} from *N. intermedia* via *N. crassa* *acr-7* from *N. crassa*	DDP
Sk-3^{K} *acr-7;E*	6940	6941	*Sk-2*^{K} from *N. intermedia* via *N. crassa* *acr-7* from *N. crassa*	DDP
tol^{c} *trp-4*	7359	7360	from *N. crassa*, 7th BC	DJJ
tol^{c} *trp-4;cys(123)*	7357	7358	*tol*^{c} *trp-4* from *N. crassa*, 7th BC	DJJ
tol^{c} *trp-4;lys(122)*		7361	*tol*^{c} *trp-4* from *N. crassa*, 7th BC	DJJ
T(IR;IIR)4637 al-1		7878	from *N. crassa*	DDP

HYBRID STRAINS USEFUL FOR INTERSPECIFIC GENE TRANSFER

see Metzenberg and Ahlgren 1969 NN 15:9-10
Metzenberg and Ahlgren 1973 Can. J. Genet. Cytol. 15:571-576
Perkins 1991 FGN 38:84

	FGSC #		
Strain designation	A	a	Comments
C1,T1	1770		*N. crassa* (FGSC 987) X *N. tetrasperma* (FGSC 606)
C1,T3	1771	1772	1 grandparent *N. crassa*, (987), 3 *N. tetrasperma*
C3,T1	1773	1774	3 grandparents *N. crassa*, (987), 1*N. tetrasperma*
C4,T4		1778	cross of C1,T3 A X C3,T1 a
C2049,I2047	1775	1776	*N. intermedia* (FGSC 1755) X *N. crassa* (FGSC 988)
C1,S15	1769		3rd backcross of *N. sitophila-crassa* hybrid to *N. sitophila*
C17,S15		1777	cross *N. sitophila* (FGSC 1769) X *N. crassa* (FGSC 988)

APPARENTLY HYBRID STRAINS

	FGSC #		
Strain designation	A	a	Comments
Madurai		8198	Possible hybrid of *N. crassa* and *N. intermedia,* Tamil Nadu India (D42 *N. crassa*)
Georgetown-8	8199		Possible hybrid of *N. crassa* and *N. intermedia* (D51 *N. intermedia*)
Carrefour Dufort	8200		Possible hybrid of *N. crassa* and *N. intermedia* (D57 *PS1*)
Merida-1		8201	P4157, Possible hybrid of *N. crassa* and *N. intermedia* (D92 *PS2*)
Merida-1		8202	P4158, Possible hybrid of *N. crassa* and *N. intermedia* (D93 *PS2*)
Mallilinatham		8203	Possible hybrid of *N. crassa* and *N. intermedia* (D100 *N. crassa*)
Nosy Be	8204	8205	Possible hybrid of *N. crassa* and *N. intermedia* (D120-121 *PS2*)

OTHER GENERA RELATED TO NEUROSPORA

Strain designation	Mating type	FGSC #	Collection place (collector:comments)	Other number
Apiosordaria verruculosa		8744	D.P. Mahoney	A40
Coniochaeta tetrasperma		8311	D.P. Mahoney, 1975 So. California soil	SA451
Coniochaeta tetrasperma		8312	D.P. Mahoney, 1975 So. California soil	SA42
Coniochaeta tetrasperma		8313	D.P. Mahoney, 1965, Galapagos Island soil	G218
Chromocrea spinulosa		4896	From M.J. Mathieson	8216(DDP)
Gelasinspora sp. (S23)	H	6877	R. Maheshwari → Perkins	8259(DDP)
Gelasinospora brevispora	H	7795	Tanzania (J.C.Krug)	
Gelasinospora calospora	H	958	Dowding collection (Keeping)	
Gelasinospora cerealis	H	959	Dowding collection	
Gelasinospora cratophora	H	7796	Tanzania (J.C.Krug)	
Gelasinospora dictyophora	H	7798	Tanzania (J.C.Krug)	
Gelasinospora hapsidophora	H	7797	Tanzania (J.C.Krug)	
Gelasinospora hapsidophora		8332	Karnataka India (J.C.Krug)	TRTC 51609
Gelasinospora hapsidophora		8333	Hyderabad India (J.C.Krug)	TRTC 51570
Gelasinospora hippopotama	H	7794	Egypt (J.C.Krug)	TRTC 51352
Gelasinospora indica	H	7793	Australia (J.C.Krug)	TRTC 51332
Gelasinospora reticulospora	H	960	Dowding collection	
Gelasinospora tetrasperma	PS	966	Dowding standard type	
Gelasinospora tetrasperma	PS	7033	E.S. Keeping → ATCC	ATCC 11345
Gelasinospora sp.	A	8238	Sauk Co, WI (R. Metzenberg)	Otter creek 1422A
Gelasinospora sp.	a	8239	Sauk Co, WI (R. Metzenberg)	Otter creek 1422a
Gelasinospora sp.	A	8240	Sauk Co, WI (R. Metzenberg)	Otter creek 1423A
Gelasinospora sp.	A	8241	Sauk Co, WI (R. Metzenberg)	Otter creek 1423a
Gelasinospora sp.	A	8242	Sauk Co, WI (R. Metzenberg)	Otter creek 14234A
Gelasinospora sp.	A	8243	Wilmington DE (R. Metzenberg)	14261A
Gelasinospora santi-flori		8330	Mulanje Mt. Malawi (J.C.Krug)	TRTC 51861
Gelasinospora santi-flori		8331	Ksar Haddada Tunisia (J.C. Krug)	TRTC 51663
Podospora anserina	+	6710	wild type s (L. Belcour)	
Podospora anserina	-	6711	wild type s (L. Belcour)	
Podospora anserina	+	6712	*cap*^{R}-1 (L. Belcour)	
Podospora anserina	-	6713	*cap*^{R}-1 (L. Belcour)	
P. austrohemisphaerica	A	8314	D. P. Mahoney, 1990 New Zealand	185
P. austrohemisphaerica	a	8315	D. P. Mahoney, 1993 New Zealand	250-8
Podospora tetraspora	H	7436	France (D. Marcou → N. Raju)	8231 (DDP)
Sordaria brevicollis	A	1903	wild type (L.S. Olive	ATCC 14519
Sordaria brevicollis	a	1904	wild type (L.S. Olive)	ATCC 14520
Sordaria brevicollis	A	7139	backcrossed strain (D.J. Bond)	SC28-R4A
Sordaria brevicollis	A	7140	backcrossed strain (D.J. Bond)	SC28-R5
Sordaria brevicollis	a	7141	backcrossed strain (D.J. Bond)	SC28-R3a
Sordaria brevicollis	a	7142	backcrossed strain (D.J. Bond)	SC28-R9a
Sordaria brevicollis b4	A	1906	beige spores (Olive)	ATCC 16101
Sordaria brevicollis y10	a	1905	yellow spores (Olive)	ATCC 16100
Sordaria brevicollis mo-c 70	A	3576	D.J. Bond → M.D. Shelby	ATCC 32495
Sordaria fimicola	H	2918	wild type (L.S. Olive)	A1
Sordaria heterothallis	-	2738	W.G. Fields JM333E	ATCC 14965
Sordaria heterothallis	+	2739	W.G. Fields JM333B	ATCC 14966
Sordaria macrospora	H	4818	wild type (G. Leblon)	0000GL
Sordaria sclerogenia	A	2740	W.G. Fields F314A. Soil	ATCC 16510
Sordaria sclerogenia	a	2741	W.G. Fields F314a. Soil	ATCC 16511
Chaetomium globosum	-	10151	K. O'Donnell	NRRL 1870

Mating Type Notes PS - Pseudohomothallic H - Homothallic

ASCOBOLUS

Strain designation	Genotype	FGSC #	Mating type	Collection place (collector:comments)
Ascobolus stercorarius	C^1D^1	7799	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2	7800	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1	7801	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2	7802	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^1	7803	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2	7804	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1	7805	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2	7806	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^1 $meth^-$	7807	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2 $meth^-$	7808	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1 $meth^-$	7809	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2 $meth^-$	7810	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^1 $meth^-$	7811	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2 $meth^-$	7812	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1 $meth^-$	7813	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2 $meth^-$	7814	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^1 nic^-	7815	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2 nic^-	7816	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1 nic^-	7817	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2 nic^-	7818	a	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^1 nic^-	7819	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^1D^2 nic^-	7820	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^1 nic^-	7821	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	C^2D^2 nic^-	7822	A	GNB, NY-NJ, Herbivore Dung
Ascobolus stercorarius	*st I*	9915	a	GNB
Ascobolus stercorarius	*StI*	9916	A	GNB
Ascobolus furfuraceus	*foII 21*	9917	A	GNB
Ascobolus furfuraceus	*fo II 24*	9918	a	GNB

PART V. Aberration Stocks

Each aberration is identified by a symbol specifying the type of aberration (*T*= translocation, *In*=inversion, *Dp*=duplication, *Tp*=intrachromosomal transposition). This is followed by Roman numerals in parentheses, specifying the linkage group(or groups), where known, and finally by the original isolation number (an integral part of the symbol).

For reciprocal translocations, linkage groups are separated by a semicolon. For insertional translocations and other rearrangements that generate viable duplications, an arrow indicates the direction of transfer of the transposed segment (which will contribute the duplicated segment).

Symbols of markers known to be distinct and separable from the aberration are set off by a comma e.g. *T(IV;VI)45502,pyr-4*. The isolation number of such separable markers are given in parentheses. Mutant phenotypes not known to be separable from the aberration are symbolized without a comma, and no isolation number is given for them e.g. *T(I;VII)17084 thi-1*.

In some cases more than one separable aberration may be recovered from the same initial strain. These bear the same isolation number, but to avoid confusion, a lower case letter (other than a) is appended to the isolation number of each component aberration, or of each aberration after the first -- e.g. *T(I;V)36703* and *T(II;III)36703b*, both of which were present in the original strain 36703.

All aberration stocks were deposited by D.D. Perkins except as follows:

AJG:	2957	DNP:	1160,1161,1563,1564	MEC:	670
AMK:	917	EGB:	2946	PSL:	766,767
AMS:	3418	ELT:	870	RLM:	2533,2537,3158-3169, 8320
BCT:	3134,3135,3156	IB:	4433,4434,6699,6700	RWB:	484,509,529
DAS:	2272	JFL:	3948-3951,4629-4635, 7406-7413	SB:	7504

A majority of the listed rearrangements are described as to origin, phenotype, fertility, genetics and cytology, and published references are cited, in Perkins and Barry. 1976. Adv. Genet. 19: 133-285 (1977) and Neurospora Newsletter 24:12-13. Also see "Chromosome Rearrangements in Neurospora and other Filamentous Fungi", Advances in Genetics, 236:239-398(1997). For information on rearrangements analyzed subsequently, contact D. Perkins. Strains are listed in ascending order according to the first non-interupted arabic numeral following the parentheses. Digits subsequent to an interuption or letter are ignored unless needed for secondary ordering.

Genotype (isolation numbers of separable markers)	FGSC stock # matin type		Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a		A	a
A. Reciprocal Translocations. Single Translocation stocks.					
T(IIIR;VI)1	976	975	*T(IR;VIL)UK9-13*	7285	7286
T(III;VI);V1M44n	4255	4256	*T(II;III)UK9-15*	6816	6817
T(IVR;VI)V1M44o os-2	4286	4287	*T(II;V)UK9-17*	7070	8258
T(IIIR;IVR)RLM02 pho-5^{C}	7869		*T(I;VR)UK9-18 am*	6871	6872
T(III;IVR)RLM04 pho-5^{C}		7870	*T(II;III)UK9-25*	6818	6819
T(IIR;VL)UK4-22	7129	7130	*T(I;IV)UK9-30*	6873	6874
T(II;IV)UK4-33	6864	6865	*T(IVR;VIIR)AR10*	2007	2008
T(II;IV)D5	2393	1554	*T(IR;IVR)Z10*	5808	5809
T(IL:IIR)KH5-9 eas	7143	7144	*T(IVR;VR)AR11r*	2093	2094
T(III;VII)UK5-20	6836	6837	*T(IL;VR)AR12*	2006	1462
T(IR;VI)UK5-27	6912	6913	*T(IR;VIL)AR13*	1913	1914
T(II;V)UK5-31	6916	6917	*T(II;VR)UK14-3*	7038	7039
T(VI.VII)UK5-32	6866	6867	*T(I;II;VI)UK14-7*	7031	7032
T(I;IVR)RLM06 pho-5^{C}		7871	*T(I;V)UK15-1*	7082	7083
T(VIR;VIIR)ALS7	1993	2016	*T(IV;VII)UK19-4*	7047	7048
T(I;VI)UK7-11	6838	6839	*T(IL;VI)UK19-37*		7051
T(IV;VI)B8	2394	2395	*T(VI;VII)UK19-65*	7049	7050
T(III;IVR)RLM08 pho-5^{C}	7872	7873	*T(VR;VII)17-088 Pk*	3672	3418
T(IVR;VII)RLM09 pho-5^{C}		7874	*T(I;VI)UK17-51*		7073
T(IIR;VIL)AR9r	2131	2132	*T(I;VI)UK17-51,al-1*^{S}		7072
T(IVR;VIL)MN9 cpc-1 (MN9)	6700	6699	*T(III;VII)AR19*	1915	1916
T(I;IV)TLd9-2	5804	5805	*T(IL;IVR)MEP24 arg-2*	3170	3171
T(IV;V)TLd9-6	5806	5807	*T(IVR;VR)RLM25 pho-5*^{C}		7875

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a
T(IL;V)T27M9	2095	
T(IIL;VL)AR30	2004	2005
T(IIL;VL)AR30,caf-1 at	3950	3951
T(IIL;VL)AR30,fl(P)	3948	3949
T(V->IV)AR33, acon-3	8603	8604
T(IV;V)T33M8	2397	2398
T(IVR;VR)MEP35d	4526	4527
T(III;IV)T42M36	2443	2444
T(III;VII)LO44	5789	5790
T(VL;VII)AR45	1760	1761
T(IV;V)L046	4639	4640
T(IIR;VIIR)T51M143	2399	2400
T(I;VI)T51M158	2759	2760
T(I;VI)T51M166	2401	2402
T(IIIR;VR)Z52,inl(89601)	5810	5111
T(I;IVL)HK53 cut	2272	2068
T(I;IVL)HK53 cut,mei-1	176	
T(IR;VI)P54	2445	2446
T(IR;IVR)T54M19	2135	2136
T(VR;VI)T54M117 un	3055	3056
T(II;III)T54M140b	2941	2942
T(IIR;IIIR)AR62	1545	1546
T(I;II)B66	1464	1465
T(IV;VIL)P73B12	2623	2624
T(IR;IIIR)P73B101	2645	2646
T(IIR;VIIR)P73B169	2625	2626
T(IR;IIR)STL76	2096	2097
T(I;VIIR)K79 met-7	2297	2298
T(II;IV)SG81 mb	4532	4533
T(I;VI)C84	3437	3438
T(VIL;VII)MN86	3185	3186
T(VI;VII)NCRL91 plm	4243	4244
T(I;II)UK93D1	7566	7567
T(IIIR;VI)UK93 D3	8112	8113
T(I;V)UK93E1	7660	7661
T(II;VI)Z99,aro-9(Y325M6)	5812	5813
T(III;V)NM101	1879	1880
T(I;III)NM107	2058	2059
T(III;VII)JL108	6632	6633
T(IL;IIIR)NM109	2627	*2628*
T(IR;VR)ALS111	2629	2630
T(III;VII)Y112M4r	2631	2632
T(IV;VII)NM113	1917	1918
T(III;IV)NM118	2403	2404
T(IR;IVR)NM119	1447	1334
T(I;III)Z119	5870	5871
T(I;VII)Z121	6570	6571
T(IV;VII)ALS122	2986	2987
T(VI;VII)NM124	2214	1472
T(IVR;VR)NM125	2447	2448
T(IIR;IVR)NM126	1611	1612
T(I;III)NM127	2405	2406
T(I;IVR)NM128	7338	
T(I;II)NM129	2330	2331
T(I;VL)NM130	2407	2408
T(III;IV)NM131	2409	2410
T(IIR;IIIR)ALS132	3041	3042
T(IR;IV)NM132	7339	
T(II;VII)NM134	1919	1920
T(I;II)NM135	2023	2024

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a
T(I;IV)Z135	5814	
T(I;III)NM136	2639	2588
T(I;IV)NM137	1874	1875
T(IR;IVR)NM139 bs	1565	1566
T(IR;IVR)NM140	1759	1548
T(IVR;VR)NM141	2025	1479
T(IR;VR)NM143	1549	1550
T(IR;IVR)NM144	1336	1335
T(IVR;VR)NM145	2098	2099
T(I;III)NM146	2449	2450
T(I;IIIR)NM150	2060	2061
T(I;VIR)NM152d	4697	4698
T(IIR;VR)ALS154,mei-3(JL102)		2062
T(IIR;VR)ALS154		2063
T(IIR;VR)ALS154,mei-3;fl(JL102;P)		4629
T(IR;VIIR)NM155	1877	1878
T(IV;VII)NM156	1921	1922
T(VR;VIR)NM157	2648	2649
T(IVR;VIIR)NM158	2026	2027
T(V;VII)NM159	2411	2412
T(IR;IVR)NM160	1338	1337
T(IIR;IIIR)C161 aro(C161)	2106	2107
T(IIR;IIIR)NM161	2028	2029
T(VR;VI)NM162b	2591	2592
T(IR;VIL)NM163	2030	2756
T(IR;IVR)NM164	1341	1340
T(I;VII)ALS167,rg-1 cr-1(B53,B123)	2413	2529
T(I;IIR)NM168	1923	1924
T(IIIR;VIIR)NM169r	1816	1817
T(I;IV)NM170		1489
T(I;IV)P170	4497	4498
T(V;VI)NM171	2451	2452
T(IR;IIL)ALS172	3035	3036
T(IR;IVR)NM172	1345	1518
T(VR;VI)AR174	2678	2679
T(I;VR)AR175	2593	2594
T(VIR;VIR)NM175	2295	2293
T(IV;V)Y175M253	3521	3522
T(VR;VII)Z175	5902	5903
T(V;VII)Z175,inl(89601)	5815	5816
T(IIIR;VL)AR177	2680	2681
T(I;IVR)AR180b	2754	2755
T(IR;IIIR)AR180r	2939	2940
T(IIR;VR)NM180	2031	1491
T(IIR;VI)AR181	2453	2454
T(I;IVR)NM181	2933	2934
T(I;VI)AR182	2597	2598
T(IIIL;VL)NM183	2633	2634
T(V;VI)AR184	2416	2417
T(III;VI)AR186	1925	1926
T(I;IV)AR193	2470	2471
T(IIL;VI)Z194	5862	5863
T(IVR;VI)AR207	1927	1928
T(IR;III)AR208	1929	1930
T(III;IV)AR211	1933	1934
T(IR;IVR)AR212	1521	1522
T(IR;IIL)AR216	1950	
T(IR;IIL)AR216,al(AR216)	1606	1607
T(IVR;VR)AR221	2034	2035
T(I;VI)Y234M419	2635	2636

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	*a*
T(I;VIL)Y234M470	6019	6020
T(I;VR)Z252	5920	5921
T(II;IV)Y256M230	1556	
T(II;IV)Y256M230;ylo-2(Y256M230)	917	
T(I;IV)D304	1443	1444
T(I;II)OY324	3835	3836
T(VL;VIL)OY325 ser-6	3737	3738
T(II;VI)OY326	3676	3677
T(IR;VR)OY327	3663	
T(IR;VR)OY327,al-2(15300)		3664
T(I;VI)OY328	3678	3679
T(I;VI)OY331	3680	3681
T(I;II)OY332		3682
T(IL;VIIR)SB332 cla-1;bd		7504
T(II;IV)OY334	3683	3684
T(I;III)OY335		3686
T(I;III)OY335;ylo-1 (Y30539y)	3685	
T(II;V)OY336	3797	3798
T(IL;IIR)OY338 arg/lys	3837	3838
T(IIIL;VR)OY339	3687	3688
T(II;IV)OY340	3689	3690
T(IR;IIR)OY341		3692
T(IR;IIR)OY341,al-2 (15300)	3691	
T(III;IV)OY342d	7492	7493
T(I;III)OY344	3748	3749
T(I;III)OY345	3799	3800
T(IV;VI)P347	4258	4259
T(III;VI)OY352	5791	5792
T(I;II)OY353		5793
T(III;VI)OY354	5895	5896
T(I;III)OY355	5866	5867
T(VI;VII)OY356	5904	5905
T(I;IIIR)OY357	6138	6139
T(I;VI)OY358	6021	6022
T(IIL;VIL)B362r	3011	3012
T(IVR;VIIR)STL384b	2421	2422
T(IVR;VIL)STL384r	2419	2420
T(IIIL;VL)MB412	5794	5795
T(III;VII)MB414	7134	7135
T(V;VI)A420	2334	2335
T(IR;VII)TM429 his-3	2530	2531
T(IR;VIL)P649	1608	1609
T(IL;VII)MB727	3944	3945
T(I;VI)RLM940, ylo-1 (30539y)	7494	7495
T(I;VII)S1007	227	224
T(I;VII)S1007,asn (S1007)		484
T(III;IV)S1302 col-6		1400
T(IR;VR)C-1670 pk	483	2761
T(I;VII)P1676	1935	1936
T(II;III)P1831	5930	5931
T(V;VI)JH2003	2423	2424
T(I;II)P2006	7496	7497
T(III;IV)P2089	6781	6782
T(I;II)P2117	6300	6668
T(III;VI)P2190	6491	6492
T(IVR;VR)R2355		222
T(IVR;VR)R2355;ylo-1;wc-1 (Y30539y;P829)	221	
T(II;V)R2497	4290	4291
T(I;II)EB2501	3047	3048
T(IR;III)P2648	1492	2032
T(II;VI)P3340	3123	3124
T(IR;VR)P3427	5796	5797
T(I;IIIR)3717 vis	2682	2683
T(I;VR)P4038`	5872	5873
T(IR;IIR)4637 al-1	253	252
T(IR;IIR)4637 al-1;pan-1;het-I (4637;5531;no#)	7342	
T(I;IIR)P4704	2425	2426
T(IR;VR)P5166	2185	2186
T(IL;IIL)P5390	2455	2456
T(IL;VR)P5401	2427	2428
T(IIIR;VI)P6070	2601	2602
T(IR;IIL)P7889	3316	3317
T(I;VR)P7987	3221	3222
T(III;VII)P8804	6684	6685
T(V;VII)P9103	4699	4700
T(IR;IVR)P9329	3851	3852
T(III;IV)P9673	3828	3829
T(IR;VIIL)17084 thi-1	216	509
T(IR;VR)36703	1445	1446
T(IR;VR)36703,arg-1 (36703)	273	529
T(IIL;III)36703b	1552	1553
T(IVR;VIR)45502	1067	1876
T(IVR;VIR)45502,pyr-3 (45502)	208	207
T(VR;VIL)46802 inl	670	1199
T(VR;VIL)46802 inl,his-1,pk;chol-2,ad-8 (C84,B6;47904,Y226M58)	1283	1284
T(IL;VR)47711	226	223
T(II;IV)P50391	7591	7592
T(IV;VII)P50392	7531	7532

	FGSC stock # mating type		
Genotype	*A*	*a*	(isolation numbers of separable markers)
Stocks with two or more reciprocal translocations			
T(IIL;VL)AR30 T(IIR;VR)ALS154, acr-3;arg-5 fl;ilv	4633	4634	KH24(r),27947,P,STL3
T(IIL;VL)AR30 T(IIR;VR)ALS154 fl		4635	P
T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1 (=alcoy linkage tester)	997	998	C102(t);Y30539y
T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1;csp-2 (alcoy;csp-2)	3661	3434	C102(t);Y30539y;UCLA101
T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1;inl;csp-2 (alcoy;csp-2)		3717	C102(t);Y30539y;37401;UCLA101
T(I;II)4637 al-1;T(IV;VI)45502,pyr-3		2196	45502
T(I;VII)17084 thi-1; T(IV;VI)45002,pyr-3	1079	1080	45502
T(I;VII)S1007,un-3;T(V;VI)46802		1071	55701(t)
T(I;II)4637 al-1; T(IV;V)R 2355; T(VI;VII)MN 86		8610	
B. Complex translocations involving more than two linkage groups			
In(IL;IR)T(IL;IIIR)SLm-1	5413	5414	
T(III;IV;VI)TLd4-4	5924	5925	
T(VI;VII)TLd5-7	5802	5803	
T(I;IV;VR)UK8-21	7068		
T(I;IV;VR)UK8-21,at		7069	M111
T(III;IV;VII)UK14-5	7080	7081	
T(IIIR→[IR;IIR])AR17	2442	1463	
T(IL;IVR;IVR;VR)MEP35 arg-3	3844	3845	
T(III;VR;VII)ALS169	3197	3198	
T(IR→VII;IR;V;VII)AR173	2468	2469	
T(IVR;VIL;VIIR)ALS175	2931	2932	
T(I;III;VI;VII)AR176	2708	2709	
T(I;III;VR;VI)ALS178,rg-1 cr-1		7501	B53 B123
T(IIL→[;IV;V])AR179	2595	2596	
T(I;IVR;IR;IIIR)AR180	7491		
T(IR→II;I;VII)AR217	3033	3034	
T(IR→II;I;VII)AR217,ad-9 cyh-1		3149	Y154M37,KH52(r)
T(IIIR→ ;IIIR;VIL)D305	2139	2140	
T(IIIR→ ;IIIR;VIL)D305,dow	3150	3151	P616
T(IIIR;V;VIIR)P1156	2599	2600	
T(IVR→VIIL;IL;IIR;IVR)S1229 arg-14,pe	2946	268	Y16329,Y8743m
T(VIL→[I;IIIR])Y16329	2710	2711	
T(VIL→[I;III]R)Y16329,phe-2	870		
C. Inversions that do not generate viable duplications see Barry and Leslie, 1982; Turner and Perkins, 1982			
In(IL;IR)OY323	3793	3794	
In(IL;IR)OY323,al-2	4257	3796	15300
In(IL;IR)OY323,arg-1,al-2	3795		B369,15300
ro-10 In(IL;IR)OY323,al-2,arg-13	7481	7482	AR7,15300
In(IL;IR)OY348	3839	3840	
In(IIR)UCLA191 eas	2960	2961	
In(IIR)UCLA191 eas	9472	9473	
rid-1; In(IIR)UCLA191 eas	9996	9997	rip1 or rip4; UCLA191
In(IIR)UCLA191 eas trp-3	9998	9999	UCLA191 td24
arg-12 In(IIR)UCLA191 eas trp-3		10000	UM107 UCLA191 td24
arg-12 In(IIR)UCLA191 eas		10002	UM107 UCLA191
(*ace-1 In(IIR)UCLA191 eas* + helper 1)		10001	T2492 UCLA191 + helper
(un-20 *In(IIR)UCLA191 eas trp-3* + helper 1)	10003		P2402 UCLA191 td24 + helper

D. Insertional translocations that do not generate viable duplications

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	*a*
T(IR↔IV)Y112M15 ad-3A	2957	
T(IR↔VR)S1325 nic-2	1558	1557

E. Rearrangements that produce viable duplications when crossed by normal

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	*a*
T(VIR→IVR)CJS1	2676	2677
T(IR→VL)UK1-35	6881	6882
T(IR→IIR)MD2	3826	3827
T(VR→VL)UK2-y,am	7245	7246
T(VR→VL)UK2-y,am al-3 inl UK2-y,RP100 89601	7589	7590
T(IR→VII)UK2-26,al-1(34508)		7030
T(IVR→VL)UK2-32	7294	7295
T(VR→VIL)UK3-41,inl (37401)	6869	6870
T(VR→VII)EB4	3046	2180
T(VIL→IR)IBj5 cpc-1	4433	4434
T(IIIR→IL)UK8-18	7037	7131
T(IIIR→IL)UK8-18,ro-2 (B20)		7133
T(VR→IIIR)DBL9	5926	5927
T(VR→IIIR)DBL9,inv (DBL9)	5928	5929
T(IR→VIR)UKT12	6926	6927
T(IR→VIR)UKT12,un-1 (44409)	7036	
In(IL→IR)AR16	3315	1614
In(IL→IR)AR16,leu-3 (R156)		3129
T(IIIR→[IR,IIR])AR17	2442	1463
T(IIL→IIIR)AR18	2643	2644
T(VL→IVL)AR33	2021	2396
T(VL→IVL)AR33,caf-1 (KH101)	5220	5221
T(IL;IVR;IVR;VR) MEP35 arg-3	3844	3845
T(VIL→IR)T39M777	2133	2134
T(VIL→IR)T39M777,ad-8 (Y112M343)	3187	3188
T(VIL→IR)T39M777,chol-2 (47904)		3131
T(VIL→IR)T39M777,chol-2;arg-13 (47404;RU3)	3130	
T(VIL→IR)T39M777 het-8^{HO}	7411	7410
T(VIL→IR)T39M777 het-8^{PA}	7413	7412
T(VIL→IR)T39M777,nit-6,het-8^{OR} *(OP4)*	7409	7408
T(VIL→IR)T39M777,ser-6,het-8^{OR} *(DK42)*	7406	7407
T(IL→VIL)T51M156 un	2270	2271
T(VIIL→IVR)T54M50,het-e (no#)	2466	2467
T(VIIL→IVR)T54M50,het-E (no#)	2603	2604
T(VIIL→IVR)T54M50,het-e nic-3 (no#,Y31881)	3132	3133
Tp(IR→IR)T54M94		2928
Tp(IR→IR)T54M94,al-2 cyh-1 (RIP-15300 KH52)		7565
Tp(IR→IR)T54M94,un-18 (T54M94(t))	2943	
T(I;III;III;II)T54M140 un	4528	
T(VL→)MB67	6714	6715

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	*a*
T(II→VIIR)P73B159 wc-1	3039	3040
T(VIIR→IR)Z88	6298	6299
T(IR→VIR)NM103	2137	2138
T(IR→VIR)NM103 het-5^{PA}	7346	7347
T(IR→VIR)NM103,ad-9 cyh-1 al-2 (Y154M36,KH52(r),15300)		3134
T(IR→VIR)NM103,cyh-1 al-1^{Y} *arg-13 R (KH52(r),ALS4,RU3,35408)*		3135
T(IR→IIIR)Y112M4i ad-3B	2637	2638
T(I→IV)Y112M115 ad-3A	2957	
T(IIL→VR)NM149,het-c (no#)	1483	1482
T(IIL→VR)NM149,het-C (no#)	3879	3880
T(IIL→VR)NM149,het-c^{PA} *(no#)*	2647	2188
T(IIL→VR)NM149,het-6^{PA} *(no#)*	7352	7353
T(IIL→VR)NM149,het-c^{AD} *(no#)*	2191	2192
T(IIL→VR)NM149,het-c^{AD} *pyr-4 (no# 36601)*	7314	7315
T(IIL→VR)NM149,het-c^{GR} *(no#)*	2193	2194
T(IIL→VR)NM149,het-C pyr-4 (no#,36601)		3136
T(IIL→VR)NM149,het-C ro-3 (no#,R2354)	2011	2012
T(IVR→I)NM152	1752	1753
T(IVR→I)NM152, trp-4		8957
T(IR;IIR;III)Y155M64 ad-3A	3037	3038
T(IVR→VIR)ALS159	2100	2101
T(IVR→VIR)ALS159,cot-1 cys-4;ylo-1 (C102(t),K7,Y3053)		3138
T(IVR→VIR)ALS159,cys-4;ylo-1 (K7,Y30539y)	3137	
T(IVR→VIR)ALS159,met-2 pan-1;ylo-1 (P159,5531,Y30539)		3189
T(IVR→VIR)ALS159,trp-4 met-2; ylo-1 (Y2198,K43,Y30539)	3190	
T(IR→VL)NM169d	2279	2280
T(IR→VII;IR;V;VII)AR173	2468	2469
T(IVR;VIL;VIIR)ALS175	2931	2932
T(IIR→VL)ALS176	2102	2103
T(IIR→VL)ALS176,het-C het-D	2414	3014
T(IIR→VL)ALS176 ,het-C het-d	3013	2415
T(IIR→VL)ALS176,fl (L)		3139
T(IIR→VL)ALS176,pe (Y8743m)		3140
T(IIR→VL)ALS176,pe fl (Y8743m,L)	3141	3142
T(I;III;VI;VII)AR176	2708	2709
In(IL→IR)NM176	3267	1613
In(IL→IR)NM176,ser-3 (47903)		3143
T(IIR→IL)NM177	1610	2003

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a
T(IIR→IL)NM177,aro-1 (Y7655)	3158	
T(IIR→IL)NM177,cys-11 (85518)	3159	3160
T(IIR→IL)NM177,leu-3 (R156)		3161
T(IIR→IL)NM177,leu-3 leu-4 (R156,R108)	3162	
T(IIR→IL)NM177,nuc-2 (RLM38)	3165	
T(IIR→IL)NM177,pcon^{c-2} *nuc-2*$^{(t)35}$ *(c-2,35(t))*	3166	
T(IIR→IL)NM177,pcon^{c} *(c-2)*	2533	3163
T(IIR→IL)NM177,preg^{c} *(c-1)*	2537	3164
T(VIIL→IVR)ALS179	2264	2265
T(VIIL→IVR)ALS179,cya-8A + a^{m1} *ad-3B cyh-1 (P9178 + 1,B114,KH52)*	4557	
T(IIL→[IV;V])AR17	2595	2596
T(IR→VL)ALS182	2973	2974
T(IR→VL)ALS182,al-2 (15300)		3929
T(IR→VL)ALS182,met-6 (35809)		3146
T(IR→VL)ALS182,thi-1 cyh-1 aur (56501,KH52(r),34508)	3144	
T(IR→VL)AR190	1951	1952
T(IR→VL)AR190,lys-1 (66202)	3174	3175
T(IR→VL)AR190,met-6 al-1^{Y} *(35809,ALS4)*		3167
T(IR→VL)AR190,nic-2 (43002)	3172	3173
T(IR→VL)AR190,nic-2 cyh-1 al-1 (43002,KH52(r),JH216)	3176	3177
T(IR→VL)AR190,nic-2 ad-9 cyh-1 al-2 (43002,Y154M37,KH52(r),MN58p)	3180	3181
T(IR→VL)AR190,nic-2 al-2 lys-1 (43002,MN58,66202)	3178	3179
T(IR→VL)AR190,thi-1 (56501)	3169	3168
T(VIR→IVR)AR209	1931	1932
T(VIR→IVR)AR209,pan-2 (Y154M64)	3147	3148
T(IR→II;I;VII)AR217	3033	3034
T(IR→II;I;VII)AR217,ad-9 cyh-1 (Y154M37,KH52(r))		3149
T(IIIR→ ;IIIR;VIL)D305	2139	2140
T(IIIR→ ;IIIR;VIL)D305,dow (P616)	3150	3151
T(VIR→IIIR)OY320	3635	3636
T(IL→VL)OY321	3746	3747
T(IL→VL)OY321,nit-2 leu-3 (nr37,R156)	4288	4289
Dp(VL→IL)QNS-1 (OY321)	5380	
Dp(VL→IL)QNS-2 (OY321)	6572	
Dp(VL→IL)QNS-6 (OY321),nit-2 leu-3; caf-1 at (nr37,R156;KH101,M111)	5381	
T(IL→IVR)OY322	3662	
T(VIR→IIIR)OY329	3670	3671
T(IL→VR)OY330	3665	
T(IVR→IL)OY333 met	3666	3667
T(IIR→IVR)OY337	3669	
T(IIR→IVR)OY337;al-2 (15300)	3668	
T(IIR→IVR)OY337,fl trp-3 (P,td24)		4886
T(IIR→IVR)OY337 het-D	7472	7473

Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a
T(IR→VIR)OY343	3881	3882
T(IR→VIR)OY343,al-2 arg-13 (15300,RU3)	6704	
T(IL→VIL)OY347		3870
T(VIL→IVR)OY349	5868	5869
T(VIL→IR)OY350	4641	4642
T(VIL→IR)OY350 chol-2	8277	8278
T(IVR→I)B362i	2935	2988
T(IIIR;VR;VII)P1156	2599	2600
(IVR→VIIL;IL;IIR;IVR)S1229 arg-14,pe (S1229,Y8743m)	2946	268
T(I→VIL)S1425	5011	5012
T(IIL→IV)R2394	2757	2758
T(IL→IIIR)R2472 pro	3284	3285
T(IIR;VIR)R2459	7287	7288
T(IIL→VI)P2869	1828	1829
T(IIL→VI)P2869,ylo-1 (Y30539y)	3125	3126
In(IL→IR)H4250	1563	1564
In(IL→IR)H4250,arg-1 (H4250)	1160	1161
In(IL→IR)H4250,aur R (34508,35408R)	3156	
In(IL→IR)H4250,leu-3;tol (R156;N83)	3253	3254
In(IL→IR)H4250;tol (N83)	1947	2975
T(IVR→IIIR)S4342	2064	2065
T(IVR→IIIR)S4342,pt (S4342)	109	
T(IR→IIIR)4540 nic-2	766	767
T(VIIR→IL)5936	2104	2105
T(VIIR→IL)5936,arg-10 (B317)	3152	3153
T(VIIR→IL)5936,leu-3 (5936)	217	
T(VIIR→IL)5936,nt (65001)	3154	
T(IR→VII)P7442 mo	3208	3209
T(VIL→[I;IIIR])Y16329	2710	2711
T(VIL→[I;IIIR])Y16329,phe-2	870	
T(IL→IIR)39311	1245	1246
T(IL→IIR)39311 a^{m33}		6705
T(IL→IIR)39311,ser-3 arg-1;tol (47903,B369,N83)		3220
T(IL→IIR)39311,suc (39311)		41
T(IL→IIR)39311,suc (39311)		1247
T(IL→IIR)39311;tol trp-4 (N83,Y2198)	2985	2976

Genotype			FGSC stock # *A*	 *a*	(isolation numbers of separable markers)

F. Heteromorphic chromosome stocks

SATELLITE-LESS

sat	no #	VL	944	945

G. Mini-chromosome stocks

T(VIL→IR)T39M777, T(VIR→IIIR)OY329, ad-8A(Y112M343)	8320	8404

Part VI. Testers and Stocks for Special Purposes

Information on special purpose stocks has been presented at several times in Neurospora Newsletter, including 9:11, 1966; 18:11, 1971; 19:30, 1972; 20:40, 1973; 21:22, 1974; 24:14, 1977; 26:9, 1979; 29:41, 1982; 31:35, 41, 1984.

A. *N. crassa* Linkage Testers

Testers to determine linkage group

1. alcoy - *T(I;II)4637 al-1;T(IV;V)R2355,cot-1;T(III;VI)1,ylo-1*

	A	a		A	a
alcoy	997	998	alcoy;*csp-2* (VII marked)	3661	3434

Follow-up testers for use with alcoy

	A	a		A	a
al-1;pe (I;II)	1203	1204	*trp-1;ylo-1* (III;VI)	6808	1208
al-1;arg-5	1205	1206	*trp-1;ylo-1;csp-2*	6680	6681
al-1;arg-5;csp-2	6664	6665	*al-1;arg-5;cot-1;inl*	1885	1886
cot-1;inl *(IV;V)*	1243	1244	*al-1;arg-5;trp-1;ylo-1*	2124	1888
cot-1;al-3	3612	3613	*trp-1;cot-1;inl;ylo-1*	1987	1988
cot-1;al-3;csp-2	6666	6667	*trp-1;cot-1;al-3;ylo-1*	4321	4322

2. Multiply marked centromere testers

multicent-1 (Perkins NN 19:30)			*multicent-2* (Metzenberg *et al.* NN 31:35)		
acr-2;pdx-1;at;ylo-1;wc-1	1985	1986	*un-2;arg-5;thi-4;pyr-1;*		
bal;acr-2;pdx-1;at;ylo-1;wc-1	2014	2015	*lys-1 inl;nic-3 ars-1;*		4488
multicent-3 (Perkins FGN 37:31)			*multicent-4* (Perkins FGN 37:31)		
In(IL;IR)OY323;arg-5;acr-2;			*arg-5;acr-2;psi;at;ylo-1;wc-1*	6828	6829
pdx-1;at;ylo-1;wc-1	6824	6825			

multicent-5 (Perkins FGN 37:31) *In(IL;IR)OY323;arg-5;acr-2;psi;at;ylo-1;wc-1*	6832	6833

3. Pairs of strains used as prototrophic heterokaryons in crosses X unmapped mutants (E. Käfer)

Mt	Strain designation	FGSC#
a	+ + ; *rip-1* + ; *acr-2 dow* ; + + ; *ylo-1* ;*nic-3 arg-10*	5200
a	cyh-1 al-2 ; + *ro-7* ; + + ; *pan-1 cys-4* ; + ; + +	5201
A	+ + ; *rip-1* + ; *acr-2 dow* ; + + ;*ylo-1* ;*nic-3 arg-10*	5199
A	*un-5* + ; *cys-10 uvs-2* ;*al-3 inl*^{t} + *his-6* ; + + +	5202
a	*un-5* + ; *cys-10 uvs-2* ;*al-3 inl*^{t} + *his-6* ; + + +	5203
a	+ *un-18* ; + + ; + + *cyh-2* + ;*chol-2 ylo-1 trp-2*	5204
A	*arg-5* ;*acr-2* ; *mtr* ; + + *al-3 inl*^{t} ; + + *rib-1* + ; *met-7*	5205
A	+ ; + ; + ;*lys-1 cyh-2* + + ;*chol-2 ylo-1* + *trp-2;* +	5207
a	*arg-5* ;*acr-2* ; *mtr* ; + + *al-3 inl*^{t} ; + + *rib-1* +; *met-7*	5206
a	+ ; + ; + ;*lys-1 cyh-2* + + ;*chol-2 ylo-1* + *trp-2;* +	5208

A + ; + ; + +; + ; lys-1 *+ +; ylo-1 pan-2; nic-3 met-7* 5210
Aarg-5 ;acr-2 ;pdx-1 mtr; pan-1; + al-3 inl^t*; + + ; + +* 5209

A sn cr-1 ; + ; + ; +; lys-1 cyh-2 + + ;ylo-1 + pan-2 ;nic-3 + 5211
A + + ; arg-5 ; acr-2 ; mtr ; + + al-3 inl^t *; + rib-1 + ; + met-7* 5205

a sn cr-1 ; + ; + ; + ; lys-1 cyh-2 + + ;chol-2 ylo-1 trp-2; + 5213
a sn cr-1 ; arg-5 ; acr-2 ; mtr ; + + al-3 inl^t *; + + + ;met-7* 5212

A *sn cr-1 ; + ; + ; + + ; + ;lys-1 + + ;ylo-1 pan-2 ;nic-3 met-7* 5215
A *sn cr-1 ;arg-5 ;acr-2 ;pdx-1 mtr;pan-1 ; + al-3 inl*^{t} *; + + ; + +* 5214

4. Testers for linkage in distal regions

Linkage Group I

	A	a		A	a
ro-10	3618	3619	*un-5 al-2 arg-13*	2282	2283
ro-10 un-5	7222	7223	*un-5 al-1 R*	2177	2178
ro-10 al-2 un-18	3789	3790	*In(IL;IR)OY323 al-2*		3796
ro-10 nit-2 leu-3	7224	7225	*al-2 R un-18*	7232	
fr al-1 un-18	2617	2618	*R un-18*	7242	

Linkage Group II

	A	a		A	a
ro-7 arg-5 rip-1	6563	6564	*trp-3 un-15*	7201	7202
ro-7 rip-1	3467	3468			

Linkage Group III

	A	a		A	a
cum cyt-22 r(Sk-2)-1	7154		*Sk-2*^{K} *phe-2 dow*	4538	4539
cum r(Sk-2)-1 acr-7	7155		*Sk-2*^{K} *dow*	4260	4261
cum acr-7	7156	7157	*acr-2 trp-1 dow*	4119	4120
cum acr-7 dow	4540	4541	*nit-7 dow*	7163	
cum dow	4542	4543	*nit-7 erg-3*	7247	7248
			dow erg-3	7243	7244

Linkage Group IV

	A	a		A	a
cys-10 pdx-1 pan-1 uvs-2	4123	4124	*cys-10 mat*	2615	2616
cys-10 cot-1 uvs-2	2017	2018	*cys-10 uvs-2*	1989	2266

Linkage Group V

	A	a		A	a
dgr-1 lys-1	7238	7239	*caf-1 al-3 his-6*	3752	3753
dgr-1 at al-3 his-6	7152	7560	*un-9 his-6*		7189
dgr-1 al-3 his-6	7150	7151			

Linkage Group VI

	A	a		A	a
chol-2 ylo-1 ws-1	3519	3520	*chol-2 ylo-1 trp-2*	4137	4138
chol-2 nit-6	7212		*nit-6 ylo-1 un-23*	7563	7564

Linkage Group VII

	A	a		A	a
(cya-8A)+(a^{m1} *ad-3B cyh-1)*	4524	4525	*nic-3 wc-1 arg-10*	157	
spco-4 wc-1 nt	2284	2285	*nic-3 wc-1 sk*	2073	2074
nic-3 met-7 arg-10	4141	4142	*arg-10 nt*	7217	

Linkage Groups IIIL R;VIL R

	A	a		A	a
acr-2 dow;chol-2 ylo-1 trp-2	4153		*acr-2 dow;chol-2 trp-2*		4154
*T(III;VI)1 acr-2 leu-1 dow;ylo-*1	4145				

Linkage Groups IL R;IIL;IVL	A	a	Linkage Groups IR;IVR;VR	A	a
un-5 al-2;pi;cys-10	2922	2923	*un-18;mat;his-6*	2944	2945

Linkage Groups IIR;IIIR;VIR	A	a	Linkage Groups VIL;VIIL R R	A	a
rip-1;dow;trp-2	3313	3314	*chol-2;spco-4 wc-1 nt*	2924	2925

5. Multiply marked mapping strains containing *sn cr-1* for replication (E. Käfer)

mt	Strain designation	Linkage groups	FGSC #
A	*un-5 leu-3 sn cr-1 cyh-1 al-2 nic-1*	IL L C R R R R	5160
A	*leu-3 sn cr-1 cyh-1 al-2 nic-1*	IL C R R R R	5161
a	*sn cr-1;arg-5 pe fl;acr-2*	IC R;IIR R R;III	5168
A	*sn cr-1;acr-2 chol-2 ylo-1 trp-2*	IC R;III;VIL L R	5172
a	*sn cr-1;acr-2 chol-2 ylo-1 trp-2*	IC R;III;VIL L R	5173
A	*sn cr-1;acr-2 leu-1 trp-1 dow*	IC R;III R R R	5174
a	*sn cr-1;acr-2 leu-1 trp-1 dow*	IC R;III R R R	5175
A	*sn cr-1;acr-2 trp-1 dow*	IC R;III R R	5176
A	*sn cr-1;acr-2 leu-1 dow*	IC R;III R R	5177
a	*sn cr-1;acr-2 leu-1 dow*	IC R;III R R	5178
A	*sn cr-1;chol-2 lys-5 ylo-1 pan-2 trp-2*	IC R;VIL L L R R	5182
A	*sn cr-1;cys-10 pdx-1 pan-1 uvs-2*	IC R;IVL R R R	5186
a	*sn cr-1;cys-10 pdx-1 pan-1 uvs-2*	IC R;IVL R R R	5187
a	*sn cr-1;acr-2;cys-10 pdx-1 pan-1 uvs-2*	IC R;III;IVL R R R	5188
A	*sn cr-1;lys-1 cyh-2 al-3 inl pab-2 his-6*	IC R;VL R R R R R	5189
a	*sn cr-1;lys-1 cyh-2 al-3 inl pab-2 his-6*	IC R;VL R R R R R	5190
a	*sn cr-1;cyh-2 al-3 inl his-6*	IC R;VL R R R R R	5191
A	*sn cr-1;lys-1 cyh-2 al-3 inl pab-2*	IC R;VL R R R R	5192
a	*sn cr-1;lys-1 cyh-2 al-3 inl pab-2*	IC R;VL R R R R	5193
a	*sn cr-1;cyh-2 al-3 inl;nic-3 met-7 arg-10*	IC R;VR R R;VIIL R R	5196
A	*sn cr-1;lys-1 cyh-2;ylo-1 pan-2;nic-3*	IC R;VL R;VIL R;VIIL	5211
a	*sn cr-1;lys-1 cyh-2;chol-2 ylo-1 trp-2*	IC R;VL R;VIL L R	5213
A	*sn cr-1;arg-5;acr-2;pdx-1 mtr pan-2 al-3 inl*	IC R;IIR;III;IVR R R;VR R	5214
A	*sn cr-1;lys-1;ylo-1 pan-2;nic-3 met-7*	IC R;VL;VIL R;VIIL R	5215
A	*sn cr-1;lys-1 cyh-2;ylo-1 pan-2*	IC R;VL R;VIL R	5216
A	*sn cr-1;mtr met-2 pan-1;al-3 inl*	IC R;IVR R R;VR R	5218

B. Standard *N. crassa* wild types and mating type testers

St. Lawrence (Oak Ridge) background - *het-C d e*
See Perkins, Fungal Genet. Newsl. 51:7-8

	A		a		A	a
OR23-1VA	2489	ORS-6a	4200	*fl*	4317	4347

C. Species testers and reference strains

See Perkins and Turner 1988. Exp. Mycol. 12:91-131, Table 5

Neurospora crassa	A	a
fl^P (OR)	4317	4347
OR23-1VA	2489	
ORS-6a		4200
Neurospora discreta		
P851A	3228	
P8127a	4378	
Neurospora tetrasperma		
85A	1270	
85a		1271

Neurospora intermedia	A	a
Shp-1A/-1a	3416	3417
P13A	1766	
P17a		1767
P420A	2316	
P405a		1940

Neurospora sitophila	A	a
fl^P;*Sk-1*^{K}	4762	4763
P8085A (*Sk-1*^{K})	2216	
P8086a (Sk-1^K)	2217	
fl^P;*Sk-1*^{S}	4887	4888
P2443A (*Sk-1*^{S})	5940	
P2444a (*Sk-1*^{S})		5941

D. Heterokaryon Incompatibility Testers and Reference Strains

1. Normal sequence tester for *het-c*, *het-d*, *het-e* (Wilson-Garnjobst testers) For brevity and legibility genotype symbols are abbreviated in the list so that *het-c*, *het-d het-e* is given as *c,d,e*, etc. *het-c* is in IIL, *het-d* in IIR and *het-e* in VIIL. These strains contain *scot* and probably other genes in their background that affect both growth of heterokaryons and segregation of markers in crosses. Caution should be exercised when using these strains for genetic studies. See Jacobson et al. 1995, Fungal Genetics Newsletter 42. Other references are cited in Perkins 1988, Fungal Genetics Newsletter 35:44-46.

		FGSC #		
Genotype		A	a	Source
het-C D E				
pan-1;al-2	5531;15300	1423	1427	JFW
rib-2	Y30539r	478		LG
het-C D e				
inl	37401	1454	1439	JFW
pan-1;al-2	5531;15300	2656	2661	JFW
het-C d e				
inl	37401	1453	1438	JFW
pan-1;al-2	5531;15300	2658	2657	JFW
arg-12	UM107		1527	DDP
het-C d E				
inl	37401	538	477	LG
pan-1;al-2	5531;15300	1424	1428	JFW
het-c D E				
inl;al-2	34701;15300	476		LG
inl	34701		1572	JFW
pan-1;al-2	5531;15300	1425	1429	JFW
het-c D e				
inl	37401	1455	1437	JFW
pan-1;al-2	5531;15300	2727	2659	DRG
het-c d E				
inl	37401	474	473	LG
pan-1;al-2	5531;15300	1426	1430	JFW
rib-2	Y30539r	475		LG
het-c d e				
inl	3740	1422	1436	JFW
pan-1;al-2	5531;15300	2662	2660	JFW

Other strains	A	a	Source
het-c^{PA}*de arg-5; pan-2*	9062		NLG
het-c^{PA}*de arg-5; pan-2*		9063	NLG
het-c^{OR}*de pyr-4; vib-1*	9064		NLG
het-c^{OR}*de; vib-1*	9065		NLG
het-c^{PA}*de thr-2; vib-1*	9066		NLG
Δ*het-c arg-5 pan-2*	9068		NLG
Δ*het-c thr-2*	9069		NLG
het-6^{or} *het-c*^{pa} *thr-2*		9074	NLG

2. Testers for het-incompatibility in duplications. See Perkins 1975, 1977; Perkins *et al.* 1993. FGN 40:69-73; Mylyk 1975, 1976. All translocations with an arrow in the symbol regularly produce inhibited duplication progeny when crossed with a normal sequence strain that contains a different allele of the het gene that is specified. Oak Ridge wild types contain OR alleles of het-6, -7, -8, -9 and -10, by definition.

	FGSC #	
Genotype	A	a
het-c (IIL) (all are *het-6*^{OR})		
het-C (OR wild types)	2489	4200
het-c	7335	7336
het-C pyr-4	4030	4031
het-c pyr-4	7145	7146
cot-5 het-C	3560	3561
cot-5 het-c	7447	—
cot-5 het-C pyr-4 thr-2	7355	7356
T(IIL→VR)NM149 het-C	3879	3880
T(IIL→VR)NM149 het-c	1483	1482
T(IIL→VR)NM149 het-C pyr-4	—	3136
T(IIL→VR)NM149 het-C ro-3	2011	2012
het-c^{AD}	430	2614
het-c^{AD} *pyr-4 thr-2*	7313	—
T(IIL→VR)NM149 het-c^{AD}	2191	2192
T(IIL→VR)NM149 het-c^{AD} *pyr-4*	7314	7315
het-d (IIR) (all are *het-C*)		
het-D (RL wild types)	2218	2219
het-d (OR wild types)	2489	4200
T(IIR→VL)ALS176 het-D	2414	3014
T(IIR→VL)ALS176 het-d	3013	2415
T(IIR→IVR)OY337 het-D	7472	7473
T(IIR→IVR)OY337 het-d	3666	3667
het-e (VIIL)		
het-E (RL wild types)	2218	2219
het-e (OR wild types)	2489	4200
T(VIIL→IVR)T54M50 het-E	2603	2604
T(VIIL→IVR)T54M50 het-e	2466	2467
T(VIIL→IVR)T54M50 het-e nic-3	3132	3133
het-i (I or II by linkage to translocation 4637 *al-1*)		
het-I al-2 nic-1	7343	—
het-i al-2 nic-1	—	7344
het-I T(I;II)4637 al-1; pan-1	7342	—
het-i (ST74A, 8-1a)	262	988
het-5 (IR)		
het-5^{PA} (Panama CZ30.6)	1131	—
arg-13 het-5^{PA} (b$_{11}$ × OR)	7345	—
thi-1 ad-9 nit-1 het-5^{PA} *(b*$_{10}$ *× OR)*	7348	7349
T(IR→VIR)NM103 het-5^{PA} *(b*$_{4}$ *× OR)*	7346	7347
het-5^{OR} (OR wild types)	2489	4200
T(IR→II)MD2 het-5^{OR}	3826	3827
T(IR→VIR)NM103 cyh-1 al-1 arg-13 R het-5^{OR}	—	3135

het-6 (IIL)

Where not specified, the strain is *het-C*. Duplications from translocation NM149 include both the *het-c* locus and the *het-6* locus. Whether *het-6* heterozygosity contributes to an incompatible phenotype detected using NM149 can be determined by progeny-testing with AR18 or P2869.

	FGSC#	
Genotype	A	a
het-6^{PA} (Panama CZ30.6, CZ30.4) *(het-C*?)	1131	1130
het-6^{PA} (Probably *het-C*)	2189	2190
het-6^{PA} *arg-12* (b$_9$ from Spurger P836)	7350	7351
het-6^{PA} *thr-2*	8236	8237
T(IIL→VR)NM149 het-6^{PA} (b$_7$ from P836)	7352	7353
T(IIL→VR)NM149 het-6^{PA} *(Probably het-C*)	2647	2188
het-6^{OR} (OR wild types)	2489	4200
un-24 het-6^{OR}	7354	—
T(IIL→IIIR)AR18 het-6^{OR}	1561	1562
T(IIL→VI)P2869 het-6^{OR}	1828	1829
T(IIL→VR)NM149 het-6^{OR}	3879	3880
T(IIL→VR)NM149 het-6^{OR} (*het-c*)	1483	1482
T(IIL→VR)NM149 het-6^{OR} *pyr-4*	—	3136
T(IIL→VR)NM149 het-6^{OR} *ro-3*	2011	2012
het-7 (IIIR)		
het-7^{LI} (Liberia UA-1)	961	—
het-7^{OR} (OR wild types)	2489	4200
T(IIIR→X;IIIR;VIIL)D305 het-7^{OR}	2139	2140
T(IIIR→X;IIIR;VIIL)D305 het-7^{OR} *dow*	3150	3151
het-8 (VIL)		
het-8^{PA} (Panama CZ30.6, Marrero-1d)	1131	2224
T(VIL→IR)T39M777 het-8^{PA}	7413	7412
het-8^{OR} (OR wild types)	2489	4200
chol-2 nit-6 het-8^{OR}	7212	—
ser-6 het-8^{OR} *ad-8*	—	7213
T(VIL→IR)T39M777 het-8^{OR}	2133	2134
T(VIL→IR)T39M777 nit-6 het-8^{OR}	7409	7408
T(VIL→IR)T39M777 ser-6 het-8^{OR}	7406	7407
T(VIL→IR)T39M777 ad-8 het-8^{OR}	3187	3188
het-8^{HO} (Houma-1n, 1ℓ)	2220	3943
chol-2 nit-6 ser-6 het-8^{HO}	7485	7486
T(VIL→IR)T39M777 het-8^{HO}	7411	—

Genotype	FGSC # A	FGSC # a
het-9 (VIR)		
het-9^{PA} (Panama CZ30.6)	1131	—
het-9^{OR} (OR wild types)	2489	4200
T(VIR→IVR)AR209 het-9^{OR}	1931	1932
het-10 (VIIR)		
het-10^{CR} (Costa Rica UFC205a)	851	—
het-10^{OR} (OR wild types)	2489	4200
T(VIIR→IL)5936 het-10^{OR}	2104	2105

mating type (IL)

(In *a*^{m1}, the mating and *het*-incompatibility functions of *a* are both inactive; in *a*^{m33}, the *het* function is inactive but the *a* mating function remains intact. (Griffiths and DeLange 1978 Genetics **88**:239-254). *tol* is an unlinked suppressor of *A*/*a het*-incompatibility.)

Genotype	FGSC # A	FGSC # a
a^{m1} *ad-3B cyh-1*	—	4564
a^{m33}	—	5382
a^{m33} *arg-3*	—	5383
a^{m33} *ad-3B*	—	4568
tol (N83)	2338	1946
tol trp-4	2336	2337
leu-3 suc; tol pan-1	—	7322
leu-3 cyt-1 arg-3; tol	7337	—
T(IL→IIR)39311	1245	1246
T(IL→IIR)39311 a^{m33}	—	6705
T(IL→IIR)39311; tol trp-4	2985	2976
T(IL→IIR)39311 ser-3 arg-1; tol	—	3220
In(IL→IR)H4250	1563	1564
In(IL→IR)H4250; tol	1947	2975
In(IL→IR)H4250 leu-3; tol	3253	3254

E. Strains for mutant enrichment and replication

Strains for selective enrichment of mutants

	FGSC # A	FGSC # a		FGSC # A	FGSC # a
al-3 inl (89601)	2308	2301	*al-3 inl (83201t)*	2309	2310
sn cr-1;al-3 inl (89601)	2303	2306	*sn cr-1;al-3 inl (83201t)*	4160	4161

Strains for replica-plating

	FGSC # A	FGSC # a		FGSC # A	FGSC # a
sn cr-1	4158	4159	*rg-1 cr-1*	624	418
sn cr-1;csp-2	4157		*rg-1 cr-1;pe fl*	331	
sn cr-1;pe fl	4162	4163	*cr-1;pe fl*	4167	4168
sn cr-1;al-3 inl(t)	4160	4161	*cr-1;pe fl;al-3 inl(t)*	4166	
sn cr-1;pe fl al-3 inl(t)	4164	4165	*cr-1*	4008	4009
cot-1	4065	4066			

F. Cross for Molecular Mapping

To be used as kits. FGSC 4411 and 4416 are parent strains RLM 1-33 and Mauriceville 1c-a, respectively. All others are progeny from this cross. Reference: Metzenberg et al. 1984. Neurospora Newsletter 31:35-40. The genotype of RLM 1-33 is as follows:

Marked loci	Alleles	MT
al-2;arg-12 nuc-2;cot-1;inl	15300;UM3 T28-M2;C102(t);89601	a

FGSC#	*mt*	*al-2*	*arg-12*	*nuc-2*	*cot-1*	*in*l	FGSC#	*mt*	*al-2*	*arg-12*	*nuc-2*	*cot-1*	*inl*
4411	a	−	−	−	−	−	4421	A	+	+	+	−	+
4412	A	+	−	−	+	−	4422	A	+	−	+	−	+
4413	A	+	−	−	+	−	4423	a	+	+	+	−	+
4414	A	+	+	+	+	+	4424	a	−	−	−	−	+
4415	A	+	+	+	−	−	4425	a	−	−	−	−	−
4416	A	+	+	+	+	+	4426	a	−	+	+	−	+
4417	a	−	+	+	+	+	4427	a	−	−	−	−	−
4418	a	−	+	+	+	+	4428	a	−	−	−	−	+
4419	a	−	−	−	+	+	4429	a	−	+	+	−	+
4420	A	−	−	−	+	+	4430	a	−	+	+	−	+

G. Multicent-2 cross for molecular mapping

Multicent-2 cross kit of centromere testers. Progeny from the cross Mauriceville 1c-A (FGSC 2225) X multicent-2a. Ref: Metzenberg et al. 1984. Neurospora Newsletter 31:35-40

Multicent-2: *un-2 ; arg-5 ; thi-4 ; pyr-1;lys-1 inl ; nic-3 ars*

(FGSC 4488) 46006(t);24947;85902; ? ;33933 89601;Y31881 101

FGSC	I	I	II	III	IV	V	VR	VIIL	VII
no.	*mt*	*un-2*	*arg-5*	*thi-4*	*pyr-1*	*lys-1*	*inl*	*nic-3*	*ars*
4450	A	+	+	−	+	+	+	+	−
4451	a	+	+	−	+	+	+	−	−
4452	A	+	−	−	+	−	−	−	−
4453	A	+	−	−	−	−	−	−	−
4454	a	−	+	+	+	−	+	+	+
4455	a	−	+	+	+	−	−	+	+
4456	A	+	−	+	−	−	−	+	+
4457	A	+	−	−	−	−	+	+	+
4458	A	+	+	−	+	−	−	−	−
4459	A	+	+	−	+	−	−	−	−
4460	a	−	−	+	−	+	+	+	+
4461	a	−	−	+	−	+	+	+	+
4462	A	+	−	+	−	+	+	−	−
4463	A	+	−	+	−	+	−	−	−
4464	A	+	+	+	+	−	−	−	−
4465	A	+	+	+	+	−	−	+	−
4466	a	+	+	+	−	+	+	−	−
4467	A	+	+	+	−	+	+	−	−
4468	a	+	+	−	+	−	−	+	−
4469	A	+	+	−	+	−	+	−	−
4470	A	+	+	+	+	+	−	−	−
4471	A	+	+	+	+	+	+	−	−
4472	a	−	+	−	+	+	+	−	−
4473	a	−	+	−	+	+	−	−	−
4474	a	−	+	−	+	−	−	−	+
4475	a	−	+	−	+	−	+	+	+
4476	a	−	+	−	+	+	+	+	+
4477	a	−	+	−	+	+	+	−	+
4478	a	−	−	+	−	−	−	−	−
4479	a	−	−	+	−	−	+	−	−
4480	a	−	−	+	−	+	−	+	+
4481	A	+	−	+	−	+	+	+	+
4482	a	−	−	+	+	+	+	−	−
4483	A	−	−	−	−	+	+	−	−
4484	a	−	+	+	+	+	−	+	+
4485	a	−	+	+	−	+	+	+	+
4486	A	+	−	−	+	−	+	−	−
4487	A	+	−	−	+	−	−	−	−
4488	a	−	−	−	−	−	−	−	−

H. Strains for obtaining protoplasts or spheroplasts

	A	a	
slime in heterokaryon A/A		327	Emerson 1963 Genetica 34:162; Nelson et al. 1975 NN 23:15.
slime-like	1118		Scarborough 1978 Meth. Cell. Biol. 20:117
slime-like (fast variant)	4761		Scarborough 1985 Exp. Mycol. 9:275
inl (allele 37401)	3659	3660	Wooton et al. 1980 Neurospora Newsl. 27:33
os-1 (allele E11200)	47	34	Emerson and Emerson 1958 PNAS 44:668
os-1 (allele M16)	812	813	Hamilton and Calvet 1964 J. Bact. 88:1084
os-1 (allele NM233t)	4493	4494	Selitrennikoff et al. 1981 Exp. Mycol 5:155

I. Strains for disruption of essential genes

(Metzenberg and Grotelueschen 1992 Fungal Genetics Newsletter 39:37-49)

7251-7260 are Host (H) strains for transformation. They should be carried on Vogel + vitamins + maltose (VVM); glucose may be used instead of maltose. Other supplements needed are as indicated.

FGSC#	Strain	M.t.	Genotype	Carrying medium
7251	I H	a^{m33}	*nic-2 cyh-1; inl inv mei-2*	VVM
7252	II H	*a*	*thr-3 arg-12*^{s}*; pyr-3; inl inv* *me*i-2	VVM + thr + urid
7253	III H	*a*	*acr-2 trp-1; inl inv mei-2*	VVM + trp
7254	IV H	*a*	*pan-1 mtr; inl inv mei-2*	VVM
7255	V H	*a*	*cyh-2 lys-2 leu-5 mei-2*	VVM + lys + leu
7256	VI H	*a*	*pan-2 Bml; inl inv mei-2*	VVM
7257	VII H	*a*	*nic-3 oli; inl inv mei-2*	VVM
7258	II H, alt	*a*	*pyr-4; inl inv mei-2*	VVM + urid
7259	V H, alt	*a*	*cyh-2* am_{132} *inl inv mei-2*	VVM + leu
7260	VI H, alt	*a*	*pan-2 fpr-6; inl inv mei-2*	VVM
7270	IV H, alt	*a*	*pyr-1 mtr;inl inv mei-2*	VVM + urid

7261-7269 are forced heterokaryons with the sterile helper strain, a^{m1} *ad-3B cyh-1* (FGSC 4564), so that the functional mating type is that of the partner listed below. These should be carried on minimal medium.

FGSC#	Strain	M.t.	Genotype	Carrying medium
7261	I M	*A*	*ad-3A;* am_{132} *inl inv mei-2*	min
7262	II M	*A*	*pyr-3; trp-3;* am_{132} *inl inv mei-2*	min
7263	III M	*A*	*ad-2;* am_{132} *inl inv mei-2*	min
7264	IV M	*A*	*trp-4;* am_{132} *inl inv mei-2*	min
7265	V M	*A*	am_{132} *inl inv mei-2*	min
7266	VI M	*A*	*ad-1;* am_{132} *inl inv mei-2*	min
7267	VII M	*A*	*met-7;* am_{132} *inl inv mei-2*	min
7268	II M, alt.	*A*	*arg-12;* am_{132} *inl inv mei-2*	min
7269	V M, alt.	*A*	*inl met-3 inv mei-2*	min

7271-7280 are Control (C) nutritionally-forced heterokaryon strains for studying how to optimize the decomposition of heterokaryons when no inviable nucleus has been created by RIP. The heterokaryons are between strains FGSC 7251-7260 and the a mating type derivatives corresponding to 7261-7270, taken pairwise. For example, FGSC 7271 = FGSC 7251 + a derivative corresponding to the *A* partner in FGSC 7261; etc.) The functional mating type is, of course, *A*. These heterokaryons should be carried Vogel minimal medium + inositol + maltose (VIM).

FGSC#	Strain	M.t.	Genotype of one component	Other component FGSC#
7271	I C	*a*	*ad-3A;* am_{132} *inl inv mei-2*	7251
7272	II C	*a*	*pyr-3; trp-3;* am_{132} *inl inv mei-2*	7252
7273	III C	*a*	*ad-2;* am_{132} *inl inv mei-2*	7253
7274	IV C	*a*	*trp-4;* am_{132} *inl inv mei-2*	7254
7275	V C	*a*	am_{132} *inl inv mei-2*	7255
7276	VI C	*a*	*ad-1;* am_{132} *inl inv mei-2*	7256
7277	VII C	*a*	*met-7;* am_{132} *inl inv mei-2*	7257
7278	II C, alt. *a*	*arg-12;*	am_{132} *inl inv mei-2*	7258
7279	VC, alt. *a*	*inl*	*met-3 inv mei-2*	7259
7280	VIC, alt.	*a*	*ad-1;* am_{132} *inl inv mei-2*	7260

Alleles used in this work

acr-2	KH5	*Bml*	511r	*met-7*	4894	*pyr-3*	37301(p)
ad-1	3254	*cyh-1*	KH52r	*mtr*	15r	*pyr-4*	36601
ad-2	Y175M256	*cyh-2*	KH53r	*nic-2*	43002	*thr-3*	T42M59(t)
ad-3A	68306	*inl*	89601	*nic-3*	Y31881	*trp-1*	25
am	132	*lys-2*	37101	*oli*	1616	*trp-3*	td37
arg-12	UM3	*mei-2*	ALS181	*pan-1*	5531	*trp-4*	Y2198
arg-12^{s}	37301s	*met-3*	36104	*pan-2*	Y153M96		

Strains for disruption of essential genes by vegetative eviction

mep his-3;mtr;pan-2 (7505 A, 7506 a) *his-3 cyh-1 al-1;mtr;inl* (7507A, 7508 a)

J. Strains that produce only microconidia (See also "Strains for replication")

	A	a		A	a
fl;dn	3517	3518	*pe fl*	4169	4170

K. Special Teaching Strains

ad-3A (FGSC 3917) *ad-3A* (FGSC 3916) *his-3 nic-2 al-2;pan-2* (FGSC 3918)
see Griffiths, A.J.F. 1981 Neurospora Newsletter 28:5
nic-1; nic-2 (FGSC 8304) *nic-1; nic-3 ars-1; a* (FGSC 8305) *nic-1; nic-2 ars-1; A*(FGSC 8306)

Set of strains for demonstration of intragenic complementation. See Selitrennikoff and Bailey 1974. Neurospora Newsl 21:22.

nic-2	2527	*csp-1 nic-2*	2513	*csp-2(FS590);nic-2*	2515
nic-3	2528	*csp-1;nic-3*	2514	*csp-2(FS590) nic-3*	2516
		*csp-2(FS591);*nic-2	2517	*csp-2(UCLA101);nic-2*	2519
		csp-2(FS591) nic-3	2518	*csp-2(UCLA101) nic-3*	2520

eas^{UCLA191} strains containing markers useful in the classroom (Sargent, 1985)

Conidia do not become airborne in strains containing the mutations *easily wettable* (*eas*) or *conidial separation* (*csp*), making them attractive for use in teaching. For this reason, M.L. Sargent (Neurospora Newslett. 32:12-13, 1985) combined a variety of representative markers with *eas* allele UCLA191, the only mutant allele then available. *eas*^{UCLA191} is present in each of the strains listed below, in addition to the mutant gene that is shown. Allele UCLA191 has since been shown to be inseparable from a within-arm (paracentric) inversion *In(IIR)UCLA191 eas* (Perkins, Freitag et al., in preparation). When heterozygous, the inversion eliminates crossovers right of *eas* in LG IIR. The UCLA191 inversion is cryptic, with no apparent effect on marker phenotype or on fertility, and its presence does not impair the usefulness of Sargent's strains for experiments with marker phenotypes or with recombination of markers other than those in IIR. Additional *eas*^{UCLA191}-linked markers are listed with inversions in Part V C.

		FGSC #	
Locus	Allele	A	a
Easily Scorable			
ad-3A	38701	4651	4642
cot-2	R1006(t)	4653	4654
fl	DE1	8601	8602
trp-4	Y2198	4655	4656
Color mutants			
White			
al-1	JP45-2	4657	4658
al-1	34508	4663	4664
al-3	P7775	4661	4662
Aurescent			
aur (*al-1*)			
Yellow			
al-1 (pale)	80-96	4665	4666
al-1(lemon)	RWT-ylo	4667	4668
ylo-1	P1193	4669	4670
ylo-2	Y256M230	4671	4672
Rosy			
al-2	Y254M165	4659	4660
al-2	MN58p	4673	4674
al-3^{ros}	Y234M470	4675	4676
Nutritional mutants			
arg-1	B369	4677	4678
arg-2	CD80	4679	4680
arg-5	CD6	4681	4682
arg-6	CD25	4683	4684
inl	37401	4685	4686
pan-2	B2(Y153M66)	4687	4688
Sexual development			
cys-3	NM27(t)	4689	4690
Cytoplasmic inheritance			
[mi-3]	3754	4691	4692
[poky]	3627-4	4693	4694

L. Strains for photobiology and circadian rhythms

Strain designation	FGSC # A	FGSC # a	Strain designation	FGSC # A	FGSC # a
bd	1858	1859	*csp-1;cel bd*	3485	
csp-1;bd	2948	4547			
bd;csp-2	4548	4549	*al-2 al-1;al-3*	4552	
csp-1;bd;oli	3483		*cyh-1 al-2 al-1;al-3*		4553
frq^{1}*;bd*	2670	2671	*cyh-1 al-2 al-1;al-3 inl;bd;csp-2*		4554
frq^{2}*;bd*	2672	2673	*bd cel*		2947
frq^{3}*;bd*	2674	2675	*chr;bd*	4908	
frq^{4}*;bd*	2958	2959	*prd-1;bd*		4902
frq^{6}*;bd*	4897		*prd-2;bd*	4903	4904
frq^{7}*;bd*	4898	4899	*prd-3;bd*	4905	4906
frq^{8}*;bd*	4900	4901	*prd-4;bd*		4907
frq^{10} *bd*	7490		*wc-1 al-2 al-1(aur);al-3*	5140	5141
bd;rib-1		7543	*bd rib-2*		7544
cyh-1 al-2 al-1	4550	4551	*bd his-3 wc-1*^{ko}		9001

M. Spore-killer tester strains

In heterozygous crosses of *Sk*^{K} X *Sk*^{S}, four ascospores are usually killed in each ascus, and the survivors are almost all *Sk*^{K}. Superscript letters signify: Killer(K), Sensitive (S). r(Sk-) signifies nonkiller strains that are resistant to killing. pr(sk-) signifies partially resistant strains. The strains listed in column 1 are currently used for reference and testing. Oak Ridge and other common wild-type laboratory strains of *N. crassa* are *Sk-2*^{S} *Sk-3*^{S}. *Sk-2* and *Sk-3* are in linkage group III. See Turner and Perkins 1991, Am. Nat. <u>137</u>:416-429; Turner and Perkins 1993, Fungal Genet. Newsletter <u>40</u>:76-78.

Species and genotype	Origin of allele*	FGSC # *A*	FGSC # *a*	Comment†
Neurospora crassa				
Sk-2^{K}	B	6648	6647	10th backcross to *N. crassa*, mixed background
Sk-2^{K}	B	3114	3115	10th backcross to *N. crassa*, inbred to OR wild type
cum Sk-2^{K} *acr-7*	B	—	7432	
Sk-2^{K} *acr-7*	B	6930	—	10th backcross to *N. crassa*
Sk-2^{K} *acr-7 leu-1 his-7*	B	—	7373	
Sk-2^{K} *acr-2 leu-1 his-7*	B	7387	7388	
Sk-2^{K} *acr-2 leu-1*	B	7375	7374	
Sk-2^{K} *acr-2 his-7*	B	7376	—	
Sk-2^{K} *leu-1*	B	7371	—	
Sk-2^{K} *his-7*	B	7378	—	
Sk-2^{K} *phe-2 dow*	B	4538	4539	
Sk-2^{K} *dow*	B	4260	4261	
Sk-2^{K}*; fl*	B	3297	3298	9th backcross to *N. crassa*
Sk-2^{K}	P	7368	7367	12th backcross to *N. crassa*
Sk-2^{K} *acr-2*	P	7385	7386	
Sk-2^{K}	J	7369	7370	12th backcross to *N. crassa*
cum Sk-2^{K} *acr-2*	J	7383	7384	
Sk-2^{K} *acr-2*	J	6928	6929	15th backcross to *N. crassa*
Sk-2^{K}	J	7392	7393	Used for testing *N. crassa* from India
r(Sk-2)-1	-	2222	—	Iowa-1, LA (P527)
r(Sk-2)-1 cum	-	7379	7380	
cum r(Sk-2)-1 acr-7		—	7389	
r(Sk-2)-2	-	—	7398	Derived from *N. crassa* P2604, Georgetown, Malaya. See 8275
Sk-3^{K}	P	3577	3578	10th backcross to *N. crassa*
cum Sk-3^{K}	P	7382	7381	
cum Sk-3^{K} *his-7*	P	7390	7391	
Sk-3^{K} *acr-2*	P	—	7077	
Sk-3^{K} *acr-7*	P	6931	6932	15th backcross to *N. crassa*
Sk-3^{K} *fl*	P	3579	3580	10th backcross to *N. crassa*

Spore Killer strains, continued

Species and genotype	Origin of allele*	FGSC # *A*	FGSC # *a*	Comment†
Sk-2^{S} Sk-3^{S} *fl*§		6682	6683	*fl*^{P} (RL) testers
r(Sk-3)		7395	—	6th backcross to *N. crassa*
cum r(Sk-3)		—	7396	6th backcross to *N. crassa*
cum r(Sk-3) leu-1		—	7394	9th backcross to *N. crassa*
r(Sk-3) acr-7 ser-1		7397	—	6th backcross to *N. crassa*
mod(pr) ad-4		8272		
pr(sk-2) ser-1			8273	
pr(sk-2) mod(pr) ser-1		8274		
pr(sk-2) mod(pr)		8276	8275	Combined loci formerly called r(sk-2)-2. See 7398
leu-3 Sk^{S}	R156		9588	IL
Sk-3; arg-1	-; B369		9591	III; IL
Sk-2; arg-1	Java; B369		9589	III; IL
Sk-2; leu-3	Java; R156		9590	III; IL
Sk-3; leu-3	-; R156		9592	III; IL
arg-1 Sk^{S}	B369		9587	IL
arg-1 Sk-2^{K}			9920	
leu-3 Sk-2^{K}			9921	
leu-3 Sk-2^{K}			9922	
Neurospora intermedia				
Sk-2^{K}	B	7401	7402	3rd and 4th backcross to Taipei background
Sk-2^{K}	P	7429	—	3rd backcross to Taipei background
Sk-2^{K}	J	7399	7400	f_1 of Tjiawi-2d (P162) × Taipei-1c (P13)
Sk-2^{K}	SA	7426	—	Menggatal, Sabah (P3126)
r(Sk-2)		1832	1833	Townsville-1b (P113), Townsville-1 (P112)
Sk-3^{K}	P	3193	3194	Derived from Rouna-1 (P32)
r(Sk-3)		6595	5123	Tahiti (P2427, P2421)
Sk-2^{S} *Sk-3*^{S‡}		3416	3417	Shew wild types (Taipei background)
Sk-2^{S} *Sk-3*^{S} *fl*‡		5798	5799	7th backcross of *fl*^{P} from *N. crassa* to Shew wild types
Neurospora sitophila				
Sk-1^{K}		2216	2217	Derived from Dodge's Arlington stocks
Sk-1^{K}			7866	Purified from mixed collection near Brisbane Australia
Sk-1^{K}; *fl*		4762	4763	*fl* P(1012) from Whitehouse *N. sitophila*, 3rd backcross to Dodge stocks
Sk-1^{S}		5940	5941	Tahiti (P2443, P2444)
Sk-1^{S}; *fl*		4887	4888	5th backcross of *fl*^{P} from *N. crassa* to Panama VP203 or derivative
r(Sk-1)		6850	—	Makokou-1 (P3914)
Neurospora tetrasperma				
(See Raju and Perkins 1991 Genetics <u>129</u>: 25-37. *E:* 8-spored ascus.)				
Sk-2^{K} *acr-2*	J	6934	6935	8th-9th backcross to *N. tetrasperma*
Sk-2^{K} *acr-2*; *E*	J	6936	6937	4th backcross to *N. tetrasperma*
Sk-3^{K} *acr-7*	P	6938	6939	7th-8th backcross to *N. tetrasperma*
Sk-3^{K} *acr-7*; *E*	P	6940	6941	8th backcross to *N. tetrasperma*
Sk-2^{S}		1270	1271	Wild types 85A, 85a (also *Sk-3*^{S})
Sk-2^{S}; *E*		5897	5901	85A, 85a background (also *Sk-3*^{S})

* B: Brunei (Borneo); J: Java; P: Papua New Guinea; SA: Sabah (Borneo).

† "nth backcross" Indicates progeny from the *nth* backcross of *Sk*^{K} into the alien genetic background. Introgressed killer strains with markers, for which there is no comment, are all from well backcrossed parents. Stock numbers prefixed with P are given for strains that originated from nature. For origins of stocks designated by place names, see Part V.

‡ These strains are sensitive to killing both by *Sk-2*^{K} and by *Sk-3*^{K}. The double symbol is used to specify phenotype, and does not imply that *Sk-2*^{K} and *Sk-3*^{K} necessarily represent two genes at separate loci. It has not been determined how many loci are involved in determining sensitivity vs. resistance to either or both Spore killers.

N. Transport Mutants

Amino Acid Transport

Strain designation	FGSC number A	FGSC number a
pmb	4814	4815
*mtr**	4812	4813
pmb mtr		2276
mtr pmb pmg	4607	4608

Strain designation	FGSC number A	FGSC number a
pmg	4613	4614
pmb pmg	4810	4811
pmg mtr	4808	4809

* Many other *mtr* (=*pmn*) mutants available. Refer to single mutant entries in Part I

Other mutants that may involve amino acid transport
fpr-1; fpr-2; hlp-1; hlp-2; su(mtr). See Part 1

Transport or putative transport mutants for other metabolites

metabolite	mutant	metabolite	mutant	metabolite	mutant
acetate	*acp^{i}*	oligopeptides	*glt*	pyrimidine bases	*uc-5*
ammonium	*mea-1*	phosphate	*pho-4*	pyrimidine nucleotides	*ud-1*
glucose	*car*	potassium	*trk*	siderophores	*sit*
isopropylmalate	*ipm-1, -2*	sulfate	*cys-13, 14*	sorbose	*sor*

Mutants possibly affecting more than one transport system
fpr-6; hgu-4; mod-5; nap; un-3

General regulatory mutants controlling related enzymes that include permeases
cys-3; nit-2; nuc-1; nuc-2 (=pcon); pgov; preg

O. Tester sets of strains to determine the genotype of ad-3 mutants induced in homokaryons or two-component heterokaryons

Mating type A			Mating type a		
ad-3B			*ad-3B*		
Genotype and mutant number	Complon coverage	FGSC #	Genotype and mutant number	Complon coverage	FGSC #
ad-3B (2-17-118)	1	4936	*ad-3B (2-17-258)*	1	5853
ad-3B (2-17-128)	2	4765	*ad-3B (2-17-128)*	2	885
ad-3B (2-31-8)	10-11	4926	*ad-3B (2-31-8)*	10-11	6501
ad-3B (2-32-3)	15	4766	*ad-3B (2-32-3)*	15	6506
ad-3B (2-32-5)	16-17	4767	*ad-3B (2-32-5)*	16-17	6507
ad-3A (1-68-13)	-	4764	*ad-3A (1-68-13)*	-	5041
ad-3B (1-112-2)	NC	4937	*ad-3B (1-112-2)*	NC	677
his-2 nic-2 al-2	-	4933	*his-2 nic-2 al-2*	-	5509
ad-2 inl		4768	*ad-2 inl*	-	5042

P. Strains used to study the genetic structure of the *ad-3region and impaired complementation between non-allelic mutations in Neurospora**[†]

Stock number	Genotype	FGSC #
11-1-11	*ad-3A*^{R}	5016
11-1-5	*ad-3A*^{IR}	5017
11-1-6	*ad-3A*^{IR}	5018
11-1-8	*ad-3A*^{IR}	5019
11-1-13	*ad-3A*^{IR}	5020
11-1-122	*ad-3A*^{IR}	5021
11-1-121	*ad-3B*^{IR}	5026
11-1-1	*ad-3B*^{R}	5022
11-1-2	*ad-3B*^{IR}	5023
11-1-7	*ad-3B*^{IR}	5024
11-1-10	*ad-3B*^{IR}	5025
11-1-121	*ad-3B*^{IR}	5026
11-1-123	*ad-3B*^{IR}	5027

*F.J. de Serres 1964 Genetics 50:21-30

† F.J. de Serres 1965 Natl. Cancer Inst.Monograph no 18:33-50

Q. Set of tester strains to determine the extent and type of functional damage in individual *ad-3*^{IR} mutations [‡]

Stock number	Genotype	FGSC #
11-1-13	*ad-3A*^{IR}	5020
12-5-194	*ad-3A*^{IR}	5028
12-7-215**	*ad-3A*^{IR}	5029
12-7-104	*ad-3AR + RL*^{CL}	5030
12-7-108	*ad-3AR + RL*^{CL}	5031
12-7-294	*ad-3B*^{IR}	5032
12-5-182	*ad-3B*^{IR}	5033
12-4-330	*ad-3B*^{R} *+ RL*^{CL}	5034
12-4-1059	*ad-3B*^{R} *+ RL*^{CL}	5035
12-6-141	*(ad-3A ad-3B)*^{IR}	5036
12-1-18	*(ad-3A ad-3B nic-2)*^{IR}	5037

‡F.J. de Serres 1968 Genetics 58:69-72

** Strains used as testers in trikaryon to characterize new *ad*-3 mutants

R. Strains for testing reverse mutation rates

Reversion by base substitution:

Genotype	FGSC #
ad-3A(N23) al-2 cot-1 pan-2 A	3331[A]
ad-8(E193) al-2 cot-1 pan-2 a	5072[B]

Reversion by frameshift

Genotype	
ad-3A(N24) al-2 cot-1 pan-2 a	3332[A]
ad-8(E146) al-2 cot-1 pan-2 a	5071[B]

A see Ong 1978 Mutat. Res. 53:297-308

B see Kimura et al. 1986 Fungal Genet. Newsl. 33:28

S. Strains used as testers to determine the extent and type of genetic damage in the *ad-3* and immediately adjacent regions

Genotype	FGSC #
his-2 nic-2 al-2 pan-2 inl cot-1	
lys-4 al-2 pan-2 inl cot-1	5039
his-3 al-2 pan-2 inl cot-1	5040
ad-3B + RL^{CL}	5035
ad-3A + RL^{CL}	5031
ad-3B + RL^{CL}	5053
ad-3A + RL^{CL}	5054
ad-3A + RL^{CL}	5030
ad-3B + RL^{CL}	5055
ad-3A + RL^{CL}	5056
ad-3B + RL^{CL}	5034

F.J. de Serres 1969 Mutat. Res. 8:43-50

T. Wild type (wt) and repair-deficient strains with genetic markers identical to those used in component II of Heterokaryon 12 (F.J. de Serres)

Repair allele	Markers	FGSC#
wt	*al-2;pan-2;cot-1 A*	2583
wt	*al-2;pan-2;cot-1 a*	4934
uvs-1	*al-2;pan-2;cot-1;uvs-1 A*	4581
	al-2;pan-2;cot-1;uvs-1 a	4582
uvs-2	*al-2;pan-2;cot-1;uvs-2 A*	4583
	al-2;pan-2;cot-1;uvs-2 a	4584
uvs-3	*al-2;pan-2;cot-1;uvs-3 A*	4778
	al-2;pan-2;cot-1;uvs-3 a	4779

Repair allele	Markers	FGSC#
uvs-4	*al-2;pan-2;cot-1;uvs-4 A*	4585
	al-2;pan-2;cot-1;uvs-4 a	4586
uvs-5	*al-2;pan-2;cot-1;uvs-5 A*	4587
	al-2;pan-2;cot-1;uvs-5 a	4588
uvs-6	*al-2;pan-2;cot-1;uvs-6 A*	4776
	al-2;pan-2;cot-1;uvs-6 a	4777
upr-1	*al-2;pan-2;cot-1;upr-1 A*	4935

Strains used as heterokaryon testers

74-OR24 *a*	*his-2(C94) nic-2(43002)*	5058
74-OR17-69*A*	*his-2(C94) nic-2(43002)*	5059

U. Mutant strains used as a tester set in trikaryon tests to distinguish between point mutations and multilocus deletions in the *ad-3* region

Mutant number	Tester number	Genotype	FGSC#
12-1-18	308	*(ad-3A ad-3B nic-2*^{IR}*)*	5037
12-7-215	21	*(ad-3A)*^{IR}	5029
12-5-182	38	*(ad-3B)*^{IR}	5033

V. Strains used as heterokaryon testers in crosses of various strains to obtain stocks heterokaryon compatible with 74A and derivatives

Stock number	Genotype	FGSC #
74-OR17-24*a*	*his-2 nic-2*	5058
74-OR17-69*A*	*his-2 nic-2*	5059
68306-OR6-5*a*	*ad-3A*	5043
68306-OR6-6*A*	*ad-3A*	5044

W. Two component heterokaryons of *Neurospora crassa* for studying the effects of various repair deficient mutations on mutation induction in the *ad-3* region

Heterokaryon number	Genotype	FGSC number
12	*his-2 ad-3A ad-3B nic-2;ad-2;inl A*	2582
(FGSC 2581)	*al-2;pan-2;cot-1 A*	2583
59	*his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-2 A*	4773
	al-2;pan-2;cot-1;uvs-2 A	4583
72	*his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-3 A*	4959
	al-2;pan-2;cot-1;uvs-3 A	4778
57	*his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-4 A*	4774
	al-2;pan-2;cot-1;uvs-4 A	4585
73	*his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-5 A*	4775
	al-2;pan-2;cot-1;uvs-5 A	4587
63	*upr-1 his-2 ad-3A ad-3B nic-2;ad-2;inl A*	4772
	upr-1 al-2;pan-2;cot-1;uvs-2 A	4935
71	*his-2 ad-3A ad-3B nic-2;ad-2;inl A*	2582
	al-2;pan-2;cot-1;uvs-2 A	4583
70	*his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-2 A*	4773
	al-2;pan-2;cot-1 A	2583

X. 2-17 series *ad-3* mutants induced with nitrous acid by F.J. de Serres

Complon coverage is listed where known

* marks *ad-3A* mutants, remainder are *ad-3B*   + marks mating type *a*, remainder are *A*

Allele	FGSC#	Complons	Allele	FGSC #	Complons	Allele	FGSC#	Complons
2-17-2	5741	2-7	2-17-63	5755	3-14	2-17-147	4994	1-14
2-17-3	5742	18	2-17-65*	5736		2-17-149	5489$^+$	1-17
2-17-4	5599		2-17-67*	5737		2-17-153	5006	1-15
2-17-5	5743	2-7	2-17-68	4925	10-11	2-17-158	4995	1
2-17-7	4966	1-17	2-17-69*	4975		2-17-159	5496	1-17
2-17-9	4967	2-11	2-17-71	4976	2-7	2-17-166*	4991	1-17
2-17-11	5744	18	2-17-72	5005	2-4	2-17-170*	4992	
2-17-12	4998	1-14	2-17-73	5468	2	2-17-173	5498	1-17
2-17-13	5745	1-17	2-17-74	4977	2-7	2-17-181	5763	1-12
2-17-14	5491$^+$	1-17	2-17-75	5757	12-16	2-17-186*	4996	
2-17-15*	4968		2-17-76	4978	2	2-17-190	5499	1-17
2-17-16	5746	1-14	2-17-77*	4979		2-17-200	5765	1-14
2-17-17	4969	9-11	2-17-78	4980	1-12	2-17-211	5766	1-17
2-17-18	4970	1-17	2-17-79	4924	9-11	2-17-212	5557	
2-17-19*	4971		2-17-80	5758	2	2-17-214	5767	1-14
2-17-21	4972	2-11	2-17-81	5759	3-14	2-17-217	5768	1-17
2-17-22	5747	9-11	2-17-82	4932$^+$	17	2-17-218	5769	1-17
2-17-25	5547$^+$	12-16	2-17-84*	4981		2-17-220	5770	1-17
2-17-26	5493$^+$	1-17	2-17-85	5760	2	2-17-221	5771	1-17
2-17-28*	5733		2-17-91	5469$^+$	2	2-17-228	5772	1-17
2-17-30	4929$^+$	12-16	2-17-93*	4984		2-17-230	5773	1-17
2-17-31	5750	2-4	2-17-94	4930$^+$	14-17	2-17-232*	4993	
2-17-34	4927$^+$	10-13	2-17-95	5487	2-5	2-17-233*	4997	
2-17-35	5751	12-16	2-17-105	5494$^+$	1-17	2-17-258	4936$^+$	1
2-17-36	5752	1-17	2-17-107	4982		2-17-366	5774	1
2-17-37	4921$^+$	6-7	2-17-108*	5738		2-17-371	5775	1
2-17-39	4999	2-5	2-17-110*	4985		2-17-387	5776	1-15
2-17-40	4973	1-12	2-17-114	4922$^+$	7-9	2-17-398	5777	1
2-17-41*	5734		2-17-117	4918$^+$	3-12	2-17-433	5778	1-14
2-17-44*	5735		2-17-118	4917$^+$	1	2-17-441	5779	5-14
2-17-45	5000	1-17	2-17-121*	5739		2-17-448	5780	3-10
2-17-47	4931$^+$	16-17	2-17-122	4986	3-11	2-17-478	5781	1
2-17-51	4919$^+$	4-7	2-17-124*	4987		2-17-496	5497	1-17
2-17-52*	886		2-17-125*	5740		2-17-793	5007	2
2-17-53	5001	18	2-17-126	5495$^+$	1-17	2-17-794	5782	1
2-17-54	5002	10-11	2-17-127	4988	1-17	2-17-799	5008	1
2-17-55	884	1-17	2-17-128	885	2	2-17-814*	2458	
2-17-56	575	3-14	2-17-129	4920$^+$	5-8	2-17-825*	5038	
2-17-57	497	1-17	2-17-130	4923	8-14	2-17-906	5009	2-3
2-17-58	5754	3-12	2-17-135*	4989		2-17-912	5010	2-3
2-17-59	5030	1-13	2-17-137	3259	1-17	2-17-928	5783	1
2-17-61	5004	2-3	2-17-141*	4990		2-17-967	5784	1

2-17 series derivatives:

Genotype	Alleles	FGSC#	Genotype	Alleles	FGSC#
ad-3B nic-2	2-17-17 43002	5316	*arg-3 ad-3B*	30300 2-17-124	5297$^+$
ad-3B nic-2	2-17-19 43002	5296	*arg-3 ad-3B*	30300 2-17-128	5337$^+$
ad-3B nic-2	2-17-37 43002	5286	*arg-3 ad-3B*	30300 2-17-158	5529$^+$
ad-3B;pe fl	2-17-51;Y8743m L	5536	*arg-3 ad-3B*	30300 2-17-17	5314$^+$
ad-3B;pe fl	2-17-74;Y8743m L	5535	*arg-3 ad-3B*	30300 2-17-19	5295$^+$
ad-3B;pe fl	2-17-75;Y8743m L	5534	*arg-3 ad-3B*	30300 2-17-233	5292$^+$
ad-3B nic-2	2-17-79 43002	5313	*arg-3 ad-3B*	30300 2-17-37	5284$^+$
ad-3B nic-2	2-17-124 43002	5298	*arg-3 ad-3B*	30300 2-17-79	5312$^+$
ad-3B nic-2	2-17-233 43002	5294	*arg-3 ad-3B*	30300 2-17-793	5308$^+$
ad-3B nic-2	2-17-793 43002	5310	*arg-3 ad-3B*	30300 2-17-799	5288$^+$
ad-3B nic-2	2-17-799 43002	5290	*arg-3 ad-3B*	30300 2-17-82	5283$^+$

Y. 2-15 series ad-3 mutants induced with diepoxybutane by F.J. de Serres

* marks *ad-3A* mutants, remainder are *ad-3* + marks mating type *a*, remainder are *A*

Allele	FGSC #	Allele	FGSC #	Allele	FGSC #
2-15-5*	5664	2-15-94*	5668	2-15-122	5701
2-15-8	5680	2-15-95*	5669	2-15-123	5051
2-15-9	5681	2-15-96	5692	2-15-124*	5676
2-15-15	5682	2-15-97	5693	2-15-125	5703
2-15-18*	5665	2-15-98*	5670	2-15-126	5704
2-15-20*	5666	2-15-102	5694	2-15-127	5725
2-15-24	5683	2-15-103*	5671	2-15-128	5705
2-15-47	5684	2-15-105	5719	2-15-129	5706
2-15-54	5716	2-15-106	5720	2-15-131	5707
2-15-58	5685	2-15-107*	5672	2-15-133	5708
2-15-64	5686	2-15-108	5695	2-15-134	5709
2-15-66	5687	2-15-109	5696	2-15-135	5710
2-15-72	5465$^+$	2-15-110	5697	2-15-137*	5677
2-15-86	5688	2-15-111	5698	2-15-138	5711
2-15-88*	5667	2-15-112	5699	2-15-140	5712
2-15-89	5689	2-15-114*	5673	2-15-142*	5678
2-15-90	5717	2-15-115*	5674	2-15-144	5713
2-15-91	5690	2-15-116	5722	2-15-145	5714
2-15-92	5691	2-15-117	5700	2-15-146	5638$^+$
2-15-93	5718	2-15-119*	5675	2-15-147*	5679
2-15-121	5723	2-15-148	5726		

Other *ad-3A* and *ad-3B* mutants from F.J. de Serres

	Allele	FGSC #			Allele	FGSC #	
		A	a			A	a
ad-3A	1-83-5	5657		*ad-3B*	1-112-9	5447	5446
ad-3A	1-83-10	5658		*ad-3B*	1-152-68	5659	5483
ad-3A	1-112-13	5648	5445	*ad-3B*	1-155-55	5660	
ad-3A	1-112-15	5649		*ad-3B*	1-155-55	5484	
ad-3A	1-152-36	5650		*ad-3B*	1-230-49	5485	
ad-3A	1-154-22	5651		*ad-3B*	1-230-83	5486	
ad-3A	1-154-28	5652		*ad-3B*	1-230-200	5460	
ad-3A	1-155-64	5653		*ad-3B*	1-234-148	5661	5461
ad-3A	1-155-314	5654		*ad-3B*	1-263-111	5662	
ad-3A	1-175-167	5655		*ad-3B*	2-11-6	5463	
ad-3A	1-230-47	5656		*ad-3B*	2-11-5	5462	
ad-3A	2-31-2	5628		*ad-3B*	2-11-163	5464	
ad-3A	2-32-10	5637		*ad-3B*	2-16-18	5727	
				ad-3B	2-16-22	5728	

Z. Additional *ad-8* alleles

FGSC#	Allele	Mutagen	FGSC#	Allele	Mutagen
3489	1-112-165 (E2)	X	5421	1-251-3 (ES3)	UV
451	1-112-343 (E5)	X	5422	1-251-4 (ES4)	
3490	1-155-56 (E10)	X	3505	1-252-12 (ES16)	UV
3491	1-175-28 (E14)	X	5423	1-253-1 (E134)	S
3494	1-224-42 (E35)	S	5424	1-253-11 (E143)	UV
3495	1-224-43 (E36)	X	5425	1-253-14 (E145)	UV
3496	1-226-3 (E42)	S	5426	1-256-21 (ES61)	UV
447	1-226-58 (E80)	UV	5427	1-263-45 (E216)	
3500	1-230-17 (E96)	S	5428	1-263-57 (E226)	EMS
3501	1-234-24 (E110)	UV	5429	1-263-58 (E227)	EMS
3502	1-234-31 (E115)	UV	5430	1-264-11 (E255)	BUDR
3503	1-234-32 (E116)	UV	5431	1-264-29 (E271)	UV
5419	1-234-34 (E118)	UV	5432	1-K5-9 (E157)	NA
3504	1-234-42 (E121)	UV	5433	1-K5-35 (E163)	NA
5420	1-250-1 (E128)	UV	5434	E326	

AA. Dikaryons and Trikaryons

Components: Each homokaryon has the genotype *ad-3*(A or B) *al-2;cot-1;pan-2*

11-1-6, 11-1-11, 11-1-13 and 11-1-122 are *ad-3A*: 11-1-1, 11-1-7, 11-1-10, 11-1-121 and 11-1-123 are *ad-3B*

Other alleles: *al-2(1-112-38); cot-1(C102(t); pan-2(1-153-96)*

74-OR152-7A - *ad-3A(1-112-13) ad-3B(35203);nic-2(43002);cot-1(C102(t)*)

All strains are mating type *A*

FGSC #	Composition	FGSC #	Composition
5817	11-1-11 + 11-1-1	5832	11-1-11 + 11-1-1 + 74-OR152-7A
5818	11-1-11 + 11-1-7	5833	11-1-11 + 11-1-7 + 74-OR152-7A
5819	11-1-11 + 11-1-10	5834	11-1-11 + 11-1-10 + 74-OR152-7A
5820	11-1-11 + 11-1-121	5835	11-1-11 + 11-1-121 + 74-OR152-7A
5821	11-1-11 + 11-1-123	5836	11-1-11 + 11-1-123 + 74-OR152-7A
5822	11-1-6 + 11-1-7	5837	11-1-6 + 11-1-7 + 74-OR152-7A
5823	11-1-6 + 11-1-10	5838	11-1-6 + 11-1-10 + 74-OR152-7A
5824	11-1-6 + 11-1-121	5839	11-1-6 + 11-1-121 + 74-OR152-7A
5825	11-1-6 + 11-1-123	5840	11-1-6 + 11-1-123 + 74-OR152-7A
5826	11-1-13 + 11-1-123	5841	11-1-13 + 11-1-7 + 74-OR152-7A
5827	11-1-122 + 11-1-7	5842	11-1-122 + 11-1-7 + 74-OR152-7A
5828	11-1-122 + 11-1-121	5843	11-1-122 + 11-1-121 + 74-OR152-7A
5829	11-1-122 + 11-1-123		

BB. *his-3* alleles from Yale. Most strains obtained from M.E. Case or F.J. de Serres.

	FGSC#				FGSC#				FGSC #		
Allele	A	a	Mutagen	Allele	A	a	Mutagen	Allele	A	a	Mutagen
1-152-16	6032	6510	X	1-226-123	6074		UV	1-234-1435	6105		UV
1-152-66	6511			1-226-171	6075		UV	1-234-1438	6106	6524	UV
1-152-111	455		X	1-226-216	6076	6517	UV	1-234-1439	6107		UV
1-155-245	6033		X	1-226-408	6077		UV	1-263-315	6126		EMS
1-155-261	462	6512	X	1-226-430	6078	6518	UV	1-269-248	6127		EMS
1-155-270	6045		X	1-226-433	6079		UV	1-269-276	6128		EMS
1-155-275	6046		X	1-226-437	6080		UV	1-269-357	6129		EMS
1-155-276	6047		X	1-226-471	6081		UV	1-269-358	6130		EMS
1-155-278	6048		X	1-226-496	6034		UV	1-269-363	6131		EMS
1-155-280	6049	6513	X	1-226-497	6082		UV	1-269-371	6132		EMS
1-175-167 *ylo*	6050			1-226-498	6083		UV	1-269-399	6133		EMS
1-175-265	6051			1-226-500	6084		UV	1-306-107[&]	6108		UV
1-175-614	4495	4496	S	1-226-503	6085		UV	1-306-119[&]	6109		UV
1-189-83	6053	6514	X	1-226-514	6086		UV	1-306-120[&]	6110		UV
1-189-85	6054		X	1-226-534	6087		UV	1-306-124[&]	6111		UV
1-189-93	6055		X	1-226-548	6035		UV	1-306-125	6527		UV
1-189-95	6056		X	1-226-551	6088		UV	1-306-127	6533	6525	UV
1-193-8	6057		UV	1-226-565	6089		UV	1-306-128[&]	6114		UV
1-193-14	6058		UV	1-226-566	6090	6519	UV	1-306-134[&]	6115		UV
1-193-16	6059		UV	1-226-573	6091		UV	1-306-136[&]	6116		UV
1-193-17	6060		UV	1-226-579	6092		UV	1-306-139	6528		UV
1-224-15	6061		X	1-226-585	6093		UV	1-306-143	6529		UV
1-224-24	6062		X	1-226-589	6094		UV	1-306-144[&]	6119		UV
1-224-26	6063	6515	X	1-226-606	6095		UV	1-306-148	6530		UV
1-224-30	6064		X	1-234-524	6096		UV	1-306-149[&]	6121		UV
1-224-32	6065		X	1-234-563	6097		UV	1-306-151[&]	6122		UV
1-224-38	6066			1-234-566	6521	6520	UV	1-306-162[&]	6123		UV
1-226-61	6067		UV	1-234-567	6098		UV	1-306-168	6532	6531	UV
1-226-74	6068		UV	1-234-574	6099		UV	1-306-176[&]	6125		UV
1-226-77	6069	6516	UV	1-234-681	6100		UV	1-306-218	6526		UV
1-226-92	6070		UV	1-234-698	6101		UV				
1-226-94	6071		UV	1-234-707	6102		UV				
1-226-121	6072		UV	1-234-723	6103		UV				
1-226-122	6073		UV	1-234-1288	6104		UV				
				1-234-1352	6522	6523	UV				

[&] contain *ad-6* 1-175-30 (Y175M30)

CC. leu-2 mutants from S.R. Gross.

All UV induced

		FGSC #				FGSC #	
Locus	Allele	*A*	*a*	Locus	Allele	*A*	*a*
leu-2	D6	6964		*leu-2;inl*	D107;89601	6987	
leu-2;inl	D7;89601	6965		*leu-2;inl*	D112;89601	6988	
leu-2;inl	D15;89601	6966		*leu-2;inl*	D117;89601	6989	
leu-2;inl	D18;89601	6967		*leu-2;inl*	D119;89601	6990	
leu-2;inl	D19;89601	6968		*leu-2;inl*	D128;89601	6991	
leu-2	D22	6970	6969	*leu-2;inl*	D130;89601	6992	
leu-2;inl	D28;89601	6971		*leu-2;inl*	D136;89601	6993	
leu-2;inl	D30;89601	6972		*leu-2;inl*	D160;89601	6994	
leu-2;inl	D32;89601	6973		*leu-2;inl*	D166;89601	6995	
leu-2;inl	D42;89601	6975		*leu-2;inl*	D174;89601	6996	
leu-2	D44	6977	6978	*leu-2*	D176	6997	
leu-2;inl	D52;89601	6979		*leu-2;inl*	D201;89601	6998	
leu-2;inl	D69;89601	6980		*leu-2;inl*	D203;89601	6999	
leu-2	D72	6982	6981	*leu-2;inl*	D219;89601	7000	
leu-2;inl	D76;89601	6983		*leu-2;inl*	D220;89601	7001	
leu-2;inl	D82;89601	6984		*leu-2;inl*	D226;89601	7002	
leu-2;inl	D89;89601	6985		*leu-2;inl*	D228;89601	7003	
leu-2;inl	D96;89601	6986		*leu-2;inl*	D250;89601	7004	
				leu-2	R86	7006	7005

DD. Strains for Targetted transformation

	FGSC #		
Designation	A	a	Depositor
am target strain TEC39		8071	JAK
am target strain TEC41-1	8072		JAK
*mep1 his-3; in*l(SadI-BglII)::λ	8914		DJE
his-3::lpl $^{\triangle(5192-6046)}$ *::hph*$^{+}$*::tk*$^{+}$*; inl*	9096	9097	DWL

EE. Strains for Assaying Aneuploidy

Designation	A	a
mtr::hph, trp-2	8288	8289
mtr::hph, trp-2, al-2	8290	
trp-2, arg-3 a^{m33}		8291

From A. T. Hagemann, Described in Fungal Genetics Newsletter 44:15-18 (1997)

FF. Stocks Maintained as Heterokaryons on Minimal Medium

Loci	Alleles	FGSC # Mating type A	a	Obtained from
(his-2 ad-3A ad-3B nic-2;inl A + al-2;cot-1;pan-2 A)	C94 Y112M13 35203 43002;Y175M256;JH319 + Y112M38;C102(t);Y387-15.7a		2581	FJD
(fmf-1;pyr-3 A + ad-2;per-1 A)	PB-6;KS43 + STL2;AB-T8		3111	TEJ
(fmf-1;tol pan-1 A + tol trp-4 A)	PB-J6;N83 5531 + N83 Y2198		3112	TEJ
(fz;sg;arg-1 cr-1 al-1 os-1 A + al-2 nic-1 lys-3 os-1 A)	no#;no#;B369 B123 34508 B135 + 15300 1413 4545 E11200		327	SE
(fz;sg;os-1 A + arg-1 cr-1 al-1 os-1 A)	no#;no#;B135 + B369 B123 34508 B135		1119	SE
(fz;sg;arg-1 cr-1 al-1 os-1 A + tol pan-1 a)	no#;no#;B369 B123 34508 B135 + N83 5531		2713	REN
(nd al-2 a + lys-1 a)	no# 15300 + 4545		3572	KDM
(nd al-2 a + lys-1 a)	no# 15300 + 4545		3571	KDM
(nd al-2 a + lys-1 a)	no# 15300 + 4545		3570	KDM
(nd al-2 nic-1 a + pan-2 a)	no# 15300 S1413 + Y153M66	6868	BSR	
(cwl A + In(IL↔IR)H4250 arg-1 A)	R2441 + H4250 H4250	3842	DDP	
(T(VII→IV)ALS179,cya-8 + a^{m1} *ad-3B cyh-1)*	ALS179, P9178	4557		DDP
(cyt-7 wc-1 nt sk + a^{m1} *ad-3B cyh-1)*	21 P829 65001 P1718	7474	7475	DDP
(fr al-1^{Y} *un-18 +* a^{m1} *ad-3B cyh-1)*	B110 ALS4 T54M90		4499	DDP
(ro-7 arg-5 rip-1 + a^{m1} *ad-3B cyh-1)*	R2470 27947 4m(t)	6565	6566	DDP
(ro-10 al-2 un-18 + a^{m1} *ad-3B cyh-1)*	AR7 15300 T54M94	4619	4620	DDP
(ro-10 In(IR;IL)OY323 al-2 arg-13 + a^{m1} *ad-3B cyh-1)*		7483	7484	DDP
(ser-3 un-16 acr-3 + a^{m1} *ad-3B cyh-1)*	47903 T42M69 KH14		5095	DDP
(nic-3 wc-1 sk + a^{m1} *ad-3B cyh-1)*	Y31881 P829 B234		7220	DDP
(os-4;pan-2 + a^{m1} *ad-3B cyh-1)*	NM201o;Y153M96		5894	DDP
(acr-2 uvs-4 leu-1 + a^{m1} *ad-3B cyh-1)*	KH5(r) ALS12 33757	7445	7446	DDP
(uvs-5;al-3 inl + a^{m1} *ad-3B cyh-1)*	ALS13;RP100 89601	7316	7317	DDP
(dgr-1 at al-3 his-6 + a^{m1} *ad-3B cyh-1)*	KHY15 M111 RP100 Y152M105	7588	7562	DDP
(cyt-7 nic-3 + a^{m1} *ad-3B cyh-1)*	20 Y31881	7581		DDP
(fr nit-2 + a^{m1} *ad-3B cyh-1)*	B110 nr7	7868		DDP
(*fl trp-3 +* a^{m1} *ad-3B cyh*)	P, TD24	8597	8598	DDP
(T(III;IV)S1302 col-6 A + a^{m1} *ad-3B cyh-1)*	S1302	8414		DDP

GG. Strains for Forcing and Resolving Heterokaryons

Loci	Alleles	FGSC # Mating type A	a	Obtained from
his-3 cyh-1; Bml^{r}; *inl*	1-234-723, KH52(r); 511(r); 37401	8373		RLM
his-3 cyh-1; Bml^{r}; *inl a*^{m33}	1-234-723, KH52(r), 511(r); 37401		8374	RLM
his-3::tk^{+} *cyh-1*; Bml^{r}; *inl*	KH52(r);511(r); 37401		8375	RLM
his-3^{+}::tk^{+} *cyh-1*; Bml^{r} *pan-2 a*^{m33}	KH52(r); 511(r); Y153M96		8376	RLM
his-3^{+}::tk^{+} *cyh-1*; Bml^{r} *pan-2*; *inl a*^{m33}	KH52(r); 511(r); Y153M96;37401		8377	RLM
his-3^{+}::tk^{+} *cyh-1*; Bml^{r}; *inl*; *nic-3 a*^{m33}	KH52(r); 511(r); 37401;Y31881		8378	RLM
mat^D {tk^{+}(FUDR^{s})} *cyh-1*; *Bml pan-2; inl*	"helper 2"		8745	RLM
mat^D *his-2* {tk^{+}(FUDR^{s})} *cyh-1; Bml pan-2; inl*	"helper 4"		8746	RLM
mat^D *his-3* {tk^{+}(FUDR^{s})} Bml pan-2	"helper 5"		8747	RLM
mat^D his-3; *cyh-1*; *Bml pan-2; inl*	"helper 6"		8748	RLM

HH. Strains for studying MSUD

Loci	Alleles	FGSC # Mating type		Obtained from
		A	a	
pan-2; his-3::his-3$^+$	Y153M96	8749	8750	RLM
pan-2; his-3::his-3$^+$ act$^+$	Y153M96	8751	8752	RLM
pan-2; his-3::his-3$^+$H3H4	Y153M96	8753	8754	RLM
pan-2; his-3::his-3$^+$Bml^r	Y153M96	8755	8756	RLM
pan-2; his-3::his-3$^+$*pma*$^+$	Y153M96	8757	8758	RLM
pan-2; his-3::his-3$^+$*mei-3*$^+$	Y153M96	8759	8760	RLM

II. Multiple morphological-mutant stocks

Loci	FGSC #	Designation	Depositor
col-15;spco-9	9366	OG1	OG
smco-6;col-17	9367	OG2	OG
smco-5;col-17	9368	OG3	OG
spco-4;col-15	9369	OG4	OG
smco-6;col-15	9370	OG5	OG
smco-4;col-16	9371	OG6	OG
spco-4;fr	9372	OG7	OG
smco-6;fr	9373	OG8	OG
spco-4;pk	9374	OG9	OG
spco-11;col-17	9375	OG10	OG
smco-6;col-1	9376	OG11	OG
spco-11;col-1	9377	OG12	OG
spco-11;col-8	9378	OG13	OG
spco-4;col-1	9379	OG14	OG
smco-6;col-8	9380	OG15	OG
spco-11;col-15	9381	OG16	OG
col-15;spco-7	9382	OG17	OG
col-4;spco-11	9383	OG18	OG
col-4;spco-10	9384	OG19	OG
col-4;spco-9	9385	OG20	OG
col-4;spco-6	9386	OG21	OG
col-4;spco-5	9387	OG22	OG
spco-4;col-4	9388	OG23	OG
smco-7;col-4	9389	OG24	OG
smco-6;col-4	9390	OG25	OG
smco-7;col-17	9391	OG26	OG
smco-4;col-17	9392	OG27	OG
col-15;smco-7	9393	OG28	OG
col-16;fr	9394	OG29	OG
col-4;fr	9395	OG30	OG
spco-11;spco-10	9396	OG31	OG
smco-8;smco-6	9397	OG32	OG
col-8;col-17	9398	OG33	OG
col-16;spco-5	9399	OG34	OG
smco-6;col-16	9400	OG35	OG
col-16;smco-5	9401	OG36	OG
col-16;spco-10	9402	OG37	OG
smco-7;col-16	9403	OG38	OG
col-16;spco-6	9404	OG39	OG
col-4;spco-12	9405	OG40	OG
spco-11;gran	9406	OG41	OG
gran;col-1	9407	OG42	OG
gran;col-17	9408	OG43	OG
smco-7;fr	9409	OG44	OG
col-16;gran	9410	OG45	OG
spco-6;gran	9411	OG46	OG
spco-4;gran	9412	OG47	OG

Multiple morphological-mutant stocks, continued from previous page

gran;fr	9413	OG48	OG
smco-9;col-16	9414	OG49	OG
spco-6;smco-9	9415	OG50	OG
col-16;pk	9416	OG51	OG
sp;fr	9417	OG52	OG
spco-12 fr	9418	OG53	OG
col-4 cot-1	9419	OG54	OG
mcb;col-17	9420	OG55	OG
spco-4;cot-1	9421	OG56	OG
cot-1;gran	9422	OG57	OG
smco-7;cot-1	9423	OG58	OG
smco-7;col-17	9424	OG59	OG
spco-4;col-17	9425	OG60	OG
sn;fr	9426	OG61	OG
gran;spco-12	9427	OG62	OG
cot-1;gna-1	9428	OG63	OG
sn;col-15	9429	OG64	OG
smco-7;cnb-1	9430	OG65	OG
smco-6;sn	9431	OG66	OG
col-16;spco-7	9432	OG67	OG
smco-5;cnb-1	9433	OG68	OG
spco-11 fr	9434	OG69	OG
col-16;spco-9	9435	OG70	OG
gran; ipa	9436	OG71	OG
smco-5;col-1	9437	OG72	OG
col-16;col-4	9438	OG73	OG
smco-8;spco-4	9439	OG74	OG
cot-1;col-16	9440	OG75	OG
cot-1;fr	9441	OG76	OG
cot-1;col-17	9442	OG77	OG
smco-8 cot-1	9443	OG78	OG
scr;fr	9444	OG79	OG
smco-7;gna-1	9445	OG80	OG
spco-6;fr	9446	OG81	OG
smco-7;cr-1	9447	OG82	OG
col-16;mcb	9448	OG83	OG
col-16 gna-1	9449	OG84	OG
gna-1 col-15	9450	OG85	OG
smco-7 gran	9451	OG86	OG
spco-4;smco-7	9452	OG87	OG
spco-4;gna-1	9453	OG88	OG
col-4;gna-1	9454	OG89	OG
smco-8 col-4	9455	OG90	OG
smco-7 mcb	9456	OG91	OG
col-15;fr	9457	OG92	OG
mcb;fr	9458	OG93	OG
col-4;gran	9459	OG94	OG
mcb;spco-4	9460	OG95	OG

JJ. Hyphal Morphology Mutants

See Seiler S., and M. Plamann 2003. The genetic basis of cellular morphogenesis in the filamentous fungus *Neurospora crassa.* Mol Biol Cell. 14:4352-64.

FGSC #	Locus	MT	Strain #
9722	*gs-1*	a	8-6
9723	*apl-4*	A	437
9724	*alg-1*	A	33-39
9725	*sst-4*	A	433
9726	*gpi-3*	A	31-5
9727	*cdc-42*	A	14-7
9728	*cdc-25*	a	7-10
9729	*cdc-42*	A	10-36
9730	*cpc-1*	A	29-62
9731	*pod-6*	A	36-5
9732	*ypk-1*	A	28-3
9733	*cdc-25*	a	179A
9734	*mss-4*	A	34-10
9735	*ypk-1*	A	20-20
9736	*mss-4*	A	18-2
9737	*erg-13*	a	24-9
9738	*gs-1*	a	8-6
9739	*apl-4*	a	437
9740	*alg-1*	a	33-39
9741	*sst-4*	A	433
9742	*gpi-3*	a	31-5
9743	*cdc-42*	a	14-7
9744	*cdc-25*	A	7-10
9745	*cdc-42*	A	10-26
9746	*cpc-1*	A	29-62
9747	*pod-6*	A	36-5
9748	*ypk-1*	a	28-3
9749	*cdc-25*	A	179A
9750	*mss-4*	a	34-10
9751	*ypk-1*	a	20-20
9752	*mss-4*	A	18-2
9753	*erg-13*	a	24-9
9754	*gs-1*	A	8-6
9755	*apl-4*	a	437
9756	*alg-1*	A	33-39
9757	*gpi-3*	A	31-5
9758	*cdc-42*	a	14-7
9759	*cdc-25*	A	7-10
9760	*cdc-42*	a	10-36
9761	*cpc-1*	a	29-62
9762	*ypk-1*	a	28-3
9763	*cdc-25*	a	179A
9764	*mss-4*	A	34-10
9765	*ypk-1*	a	20-20
9766	*mss-4*	a	18-2
9767	*erg-13*	A	24-9
9768	*gs-1*	A	8-6
9769	*apl-4*	A	437
9770	*alg-1*	a	33-39
9771	*gpi-3*	a	31-5
9772	*cdc-25*	a	7-10
9773	*cdc-42*	a	10-36
9774	*cpc-1*	a	29-62
9775	*ypk-1*	A	28-3
9776	*mss-4*	a	34-10
9777	*ypk-1*	A	20-20
9778	*mss-4*	a	18-2
9779	*erg-13*	a	24-9

Hyphal Morphology Mutants, continued from previous page

FGSC #	*Locus*	MT	Strain #
9780	*sar-1*	a	14-15
9781	*sec53*	A	4-11
9782	*pod-1*	A	29-43
9783	*act-1*	a	33-29
9784	*erg-9*	a	428
9785	*erg-9*	a	8-2
9786	*drs-2*	A	27-46
9787	*gpi-3*	a	33-15
9788	*gpi-3*	A	34-15
9789	*sec-27*	a	5-1
9790	*sec-27*	A	33-4
9791	*mcb*	A	21-13
9792	*mcb*	a	14-4
9793	*cdc-24*	A	24-21
9794	*cdc-24*	A	8-8
9795	*cdc-24*	a	19-3
9796	*sar-1*	A	14-15
9797	*sec53*	A	4-11
9798	*pod-1*	A	29-43
9799	*act-1*	A	33-29
9800	*erg-9*	a	428
9801	*erg-9*	a	8-2
9802	*drs-2*	a	27-46
9803	*gpi-3*	A	33-15
9804	*gpi-3*	A	34-15
9805	*sec-27*	A	5-1
9806	*sec-27*	A	33-4
9807	*mcb*	A	21-13
9808	*mcb*	a	14-4
9809	*cdc-24*	A	24-21
9810	*cdc-24*	A	8-8
9811	*cdc-24*	A	19-3
9812	*sar-1*	A	14-15
9813	*sec53*	a	4-11
9814	*pod-1*	a	29-43
9815	*act-1*	A	33-29
9816	*erg-9*	A	428
9817	*sar-1*	a	14-15
9818	*sec53*	a	4-11
9819	*pod-1*	A	29-43
9820	*act-1*	a	33-29
9821	*drs-2*	a	27-46
9822	*gpi-3*	a	33-15
9823	*gpi-3*	a	34-15
9824	*sec-27*	A	5-1
9825	*mcb*	a	21-13
9826	*mcb*	A	14-4
9827	*cdc-24*	a	24-21
9828	*cdc-24*	a	8-8
9829	*cdc-24*	a	19-3
9830	*drs-2*	A	27-46
9831	*gpi-3*	A	33-15
9832	*gpi-3*	a	34-15
9833	*sec-27*	a	5-1
9834	*mcb*	a	21-13
9835	*mcb*	A	14-4
9836	*cdc-24*	a	24-21
9837	*cdc-24*	a	8-8
9838	*cdc-24*	A	19-3
9839	*met-12*	A	31-12

Hyphal Morphology Mutants, continued from previous page

FGSC #	*Locus*	MT	Strain #
9840	*met-12*	A	21-9
9841	*pod-5*	a	14-25
9842	*met-12*	A	32-6
9843	*pod-5*	A	14-25
9844	*pod-5*	a	5-5
9845	*hsp-70*	a	16-17
9846	*png-1*	A	22-9
9847	*pod-6*	A	31-21
9848	*pod-6*	A	36-5
9849	*pod-6*	A	29-76
9850	*cot-1*	a	31-11
9851	*cot-1*	A	33-3
9852	*mdm-12*	A	37-22
9853	*lrg-1*	a	35-19
9854	*lrg-1*	a	22-16
9855	*met-12*	a	31-12
9856	*met-12*	A	21-9
9857	*met-12*	A	32-6
9858	*pod-5*	A	5-5
9859	*hsp-70*	A	16-17
9860	*png-1*	a	22-9
9861	*pod-6*	A	29-76
9862	*cot-1*	a	31-11
9863	*cot-1*	A	33-3
9864	*mdm-12*	A	37-22
9865	*lrg-1*	A	35-19
9866	*lrg-1*	A	22-16
9867	*met-12*	A	31-12
9868	*pod-5*	a	14-25
9869	*pod-5*	a	5-5
9870	*hsp-70*	a	16-17
9871	*pod-6*	A	31-21
9872	*pod-6*	a	31-21
9873	*cot-1*	A	31-11
9874	*cot-1*	a	33-3
9875	*lrg-1*	A	35-19
9876	*lrg-1*	A	22-16
9877	*met-12*	a	31-27
9878	*pod-5*	A	14-25
9879	*pod-5*	A	5-5
9880	*hsp-70*	A	16-17
9881	*png-1*	A	22-9
9882	*png-1*	a	22-9
9883	*cot-1*	A	31-11
9884	*cot-1*	a	33-3
9885	*pod-6*	A	36-5
9886	*ire-1*	a	35-32
9887	*ire-1*	A	35-32
9888	*ire-1*	A	35-32
9889	*ire-1*	a	35-32
9890	*cdc-42*	A	14-17
9891	*cdc-42*	a	14-17
9892	*cdc-42*	a	14-17
9893	*cdc-25*	A	4-5
9894	*cdc-25*	A	4-5
9895	*cdc-25*	a	4-5
9896	*cdc-25*	a	4-5
9897	*gcd-11*	A	33-6
9898	*gcd-11*	a	33-6
9899	*gcd-11*	A	33-6

Hyphal Morphology Mutants, continued from previous page

FGSC #	*Locus*	MT	Strain #
9900	*gcd-11*	a	33-6
9901	*sec-21*	A	27-24
9902	*cdc-42*	A	14-17
9903	*sec-21*	A	27-24
9904	*bem-1*	a	24-8
9905	*bem-1*	a	24-8
9906	*bem-1*	A	24-8
9907	*bem-1*	A	24-8
9908	*gfa-1*	a	27-8
9909	*gfa-1*	a	27-8
9910	*gfa-1*	A	27-8
9911	*gfa-1*	A	27-8
9912	*ipp-1*	A	18-7
9913	*ipp-1*	A	18-7

KK. Mutants from the KO project with gene symbols in the FGSC database

		FGSC number mating type	
Locus	Allele	A	a
NCU02133.2 (sod-1)	KO		11215
NCU03725.2 (vib-1)	KO	11309	11308
NCU06205.2 (rco-1)	KO	11371	11372
NCU09068.2 (nit-2)	KO		11392
NCU06245.2 (plc-1)	KO		11411
NCU07024.2 (os-2)	KO	11436	
NCU05210.2 (uvs-2)	KO	11444	11445
NCU09315.2 (nuc-1)	KO		11448
NCU08294.2 (nit-4)	KO	11007	11008
NCU06656.2 (acu-15)	KO	11013	11014
NCU06028.2 (qa-1F)	KO	11035	11034
NCU00902.2 (wc-2)	KO		11124
NCU02815.2 (os-1)	KO	11696	11695
NCU02356.2 (wc-1)	KO	11712	11711
NCU03616.2 (smco-7)	KO		12467
NCU03833.2 (cnb-1)	KO		12469
NCU03727.2 (ham-2)	KO	12091	
NCU02178.2 (sad-1)	KO	11152	11151
NCU07534.2 (qde-1)	KO	11157	11156
NCU00274.2 (mus-21)	KO	11162	11163
NCU08346.2 (un-1)	KO		11164
NCU09644.2 (uvs-3)	KO	11167	11168
NCU08566.2 (ro-11)	KO	11947	11946
NCU09061.2 (het-e)	KO		12098
NCU01376.2 (pho-2)	KO	11192	11193
NCU05458.2 (cya-4)	KO		12351
NCU08850.2 (mus-18)	KO	12356	12357
NCU06493.2 (gna-1)	KO		12370
NCU09731.2 (mus-8)	KO	12414	12413
NCU02741.2 (mei-3)	KO	12434	12433
NCU03533.2 (het-6)	KO	12442	12443
NCU06577.2 (mus-26)	KO	12058	
NCU08484.2 (mus-27)	KO		12518
NCU03493.2 (het-c)	KO	12202	

This is a preliminary list. Additional mutants will be deposited in the FGSC collection during the publication of this catalog. Please check the FGSC web-site for updates.

Part VII: *SORDARIA FIMICOLA*

Sordaria fimicola stocks were received from Dr. Y. Kitani and from Dr. Lindsay Olive through the courtesy of Dr. Kitani. All cultures are homothallic and of A1 isolate. Details of the life cycle, cytology, and formal genetics are referred to in "An Introduction to the genus Sordaria" (Fields, 1970. Neurospora Newsletter 16:14-17). Other Sordaria species are listed in part IV, “Other genera related to Neurospora.” Most strains in this category have not been ordered in many years and are therefore considered "Archival."

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
				LINKAGE I - g CHROMOSOME		
WILD TYPE						
wt	-	g^+	2918			A1
CORONA						
cor	-	g^+	2769	corona formation around inoculum, self sterile	X	2
GREY OF *g* LOCUS						
g_1	1	g_1	2770	grey ascospores	UV	3-1
g_6	6	g_6	2778	as above	X	3-9
g_7	7	g_7	2779	as above	X	3-10
g_8	8	g_8	2780	as above		3-11
g_9	9	g_9	2781	as above	X	3-12
g_{10}	10	g_{10}	2782	as above	X	3-13
HYALINE OF *g* LOCUS						
h_2	2-1	h_2	2771	hyaline ascospore, with mat	X	3-2
h_{2a}	2-2	h_{2a}	2772	as above, modified by gene conversion		3-3
h_{2y}	2-3	h_{2y}	2773	as above		3-4
h_3	3	h_3	2774	as above, with mat	X	3-5
h_4	4-1	h_4	2775	hyaline ascospore	X	3-6
h_{4b}	4-2	h_{4b}	2776	as above, modified by gene conversion		3-7
h_5	5	h_5	2777	light grey ascospores	UV + cytosine	3-8
h_{11}	11	h_{11}	2783	hyaline ascospores	ICR170	3-14
h_{12}	12	h_{12}	2784	as above	ICR170	3-15
MAT						
mat	-	g^+	2785	slow growth, compact hyphae	X	4
PARTIALLY FERTILE						
pf-1(st-9)	-	g^+	2789		UV	8
RESTRICTED GROWTH						
r-1	-	g^+	2787			6
SPOTTY						
sp	-	g^+	2786	slow growth, perithecia produced in spotted pattern	UV	5
STERILITY						
st-9 *(possibly pf-1)*	-	g^+	2789	partially fertile, with protoperithecia and a few perithecia	UV	8
st-22	-	g^+	2768	small, empty perithecia, self sterile	X	1
st-52	-	g^+	2790	partially fertile; few perithecia with asci and ascospores	X	9
st-60		g^+	2788	normal growth, but sterile	X	7
st-64	-	g^+	2791	partially fertile; ascospores of variable color with slow maturation	NA	10

* Allele no. follows symbol: i.e., h_2; whereas dash(-) indicates locus: i.e., a-3.

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
MULTIPLE MUTANT STRAINS						
$g^{+}\ mat/i_{1}$			6303			28
$g^{+}\ mat/i_{1}\ TL\text{-}1$			6324			43
$g_{6}\ mat$			6302			27
$g_{6}\ mat/i_{1}$			6305			30
$h_{5}\ mat$			6301			26
$mat\ g_{6}\ h_{5}$			6315			36a
$mat\ g_{6}\ h_{5}$			6316			36b
$mat\ h_{2}\ h_{5}$			6317			37a
$mat\ h_{2}\ h_{5}$			6318			37b
$sp\ g^{+}\ cor$			6306			31a
$sp\ g^{+}\ cor/i_{1}$			6307			32b
$sp\ g_{1}\ h_{5}$ cor			6319			38a
$sp\ g_{1}\ h_{5}$ cor			6320			38b
$sp\ g_{6}\ _{c}or$			6321			39
$sp\ g_{6}\ h_{5}$ cor			6313			35a
$sp\ g_{6}\ h_{5}$ cor/i_{1}			6314			35b
$sp\ g_{7}\ cor$			6322			40
$sp\ h_{4b}\ cor$			6310			33
$sp\ h_{5}\ cor$			6311			34a
$sp\ h_{5}\ cor/i_{1}$			6312			34b
			LINKAGE II - m CHROMOSOME			
ABORTIVE						
a-3	–	g^{+}	2792		X	7
MUMMY						
m_{1}	–	g^{+}	2794	mummified spores, tawny color	X	23-1
m_{2}	–	g^{+}	2795	as above	X	23-2
m_{3}	–	g^{+}	2796	as above	X	23-3
RESTRICTED GROWTH						
r-9	-	g^{+}	2797		X	24
STERILITY						
st-412	–	g^{+}	2793	self sterile	X	22
			LINKAGE III - t-y CHROMOSOME			
BLACKBERRY						
blb	-	g^{+}	2669	bands of darkly pigmented hyphae radiating from colony edge toward center	S	-
TAN						
t_{1}	1	g^{+}	2799	tan ascospores, gene conversion frequency is low	X	31-1
t_{2}	2	g^{+}	2800	as above	X	31-2
t_{3}	3	g^{+}	2801	as above	X	31-3
t_{4}	4	g^{+}	2802	tan ascospores	S	31-4
t_{5}	5	g^{+}	2803	tan ascospores, slow growth	cytosine	31-5
t_{6}	6	g^{+}	2804	tan ascospores	S	31-6
t_{7}	7	g^{+}	2805	tan ascospores, gene conversion frequency is low	X	31-7
t_{8}	8	g^{+}	2806	tan ascospores	ICR170	31-8
YELLOW						
y_{1}	1	g^{+}	2807	yellow ascospores	ICR170	32-1
y_{2}	2	g^{+}	2808	as above	UV	32-2
y_{3}	3	g^{+}	2809	as above		32-3
y_{4}	4	g^{+}	2810	as above	UV	32-4

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
				LINKAGE IV - i CHROMOSOME (with some blue mutants (which would be i alleles))		
BLUE OF i LOCUS						
blu_3	*3*	g^+	2813	blue ascospores	X	41-2
blu_4	*4(?)*	g^+	2814	blue ascospores	X	42
$blu_4\ Hrec\ i$			6335			95a
$blu_4\ Hrec\ i$			6336			95b
$blu_4\ Hrec\ i$			6337			95c
$blu_4\ Hrec\ i$			6338			95d
$blu_4\ rec^-$			6334			94
blu_6	*6(?)*	g^+	2816	bluish ascospores	UV	44
blu_6	–	g^+	2839	bluish-grey ascospores	ICR170	613
$blu_6\ Rec^+$			6328			92a
$blu_6\ Rec^+$			6329			92b
$blu_6\ Rec^+$			6330			92c
$blu_6\ Rec^+\ i$			6331			92d
$blu_6\ rec^-$			6332			93a
$blu_6\ Rec^- i$			6333			93b
blu_7	*7(?)*	g^+	2817	as above	S	45
blu_9	–	g^+	2836	dark-grey (cyan) ascospores	ICR170	610
$g^+\ Rec^+$			6325			91a
$g^+\ Rec^+$			6326			91b
$g^+\ Rec^+$			6327			91c
INDIGO						
i_1	1	g^+	2811		X	41-1
i_2	2	g^+	2812	dark blue ascospores	X	41-2
i_2	2	g^+	6375			N38
i_5	5(?)	g^+	2815	as above		43
i_8	–	g^+	2840	greenish ascospores	S	614
i_{10}	–	g^+	2841	grey ascospores	UV	615
				LINKAGE V (and some brown mutants)		
BROWN						
br_1	1(?)	g^+	2819	brown ascospores in homozygote	X	51
br_2	2(?)	g^+	2820	brown ascospores	S	52
br_3	3(?)	g^+	2821	as above	X	53
br_5	5(?)	g^+	2823	as above	UV	55
br_6	6(?)	g^+	2824	as above	X	56
br_7	7(?)	g^+	2825	as above	X	57
brown			6345		NG	N38
				GROUP VI - COLOR MUTANTS		
AMBER						
am	–	g^+	2830	amber ascospores	ICR170	64
BLACK						
bl	–	g^+	2837	ascospores slightly lighter than wild type but look black and not as brown as wild type	X	611
CAMBRIDGE						
cam	–	g^+	2832	light tan ascospores	ICR170	66
CITRINE						
ci	–	g^+	2831	greenish yellow-brown ascospores	ICR170	65

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
COLUMBIA						
col	–	g_1	2827	yellowish ascospores, no linkage with other y	UV	61
HAZEL						
ha	–	g^+	2833	hazel ascospores	67	
KYO						
kyo	–	g_1	2829	light grey ascospores	X	63
MOUSE-GREY						
mo	–	g^+	2834	mouse-grey ascospores	ICR170	68
OLIVE						
o	–	g^+	2828	olive-green ascospores	X	62
SMOKY						
sm	–	g^+	2838	smoky brownish-grey ascospores	X	612
SULPHUR						
su	–	g^+	2835	light and bright yellow ascospores	ICR170	69

GROUP VII - SPORE SHAPE (and other characters)
PART I

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
APICULATE						
api-1	–	g^+	2844	apiculate spores in homozygote	X	713
api-2	–	g^+	2845	as above	X	714
BANDED						
band	–	g^+	2848	band-like dark zone formation, mycelial pigment at band, dense perithecia	ICR170	726
NON-DISCHARGE						
dis-1	–	g^+	2846	poor ascospore discharge regardless of good fertility		724
dis-2	–	g^+	2849	poor ascospore discharge, fair fertility, light mycelial pigmentation		727
dis-3	–	g^+	2850	poor ascospore discharge and perithecial formation	ICR170	728
dis-4	–	g^+	2851	no spore discharge, few small perithecia	ICR170	729
dis-5	–	g^+	2852	as above	ICR170	730
DARK MYCELIUM						
dm-1	–	g^+	2853	mycelial color very dark; reduced fertility	ICR170	731
dm-2	–	g^+	2854	dark mycelium, rare fertile perithecia	ICR170	732
dm-3	–	g^+	2855	dark mycelium, self-sterile	S(?)	733
dm-4	–	g^+	2856	dark mycelium	S(?)	734
HALO						
halo	–	g^+	2847	halo formation around inoculum	S(?)	725
LOBED SPORES						
lo	–	g^+	2843	ascospores numerous, various in size, sporadic in germination, and round are produced in homozygous asci; wild type epistatic	UV+ 5 bromo-uracil	712

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
ROUND SPORE						
ro	–	g^+	2842	round spores in homozygote, wild type epistatic	X	711
				PART II		
DENSE COLONIAL EDGE						
ded	–	g^+	2857	dense small perithecia at top of slant	ICR170	735
PETIT PERITHECIA						
pp	–	g^+	2858	small perithecia with a few asci containing normal octads	S(?)	736
PERITHECIA SCATTERED						
ps	–	g^+	2859	perithecia of fair fertility scattered across mycelium	X	737
PERITHECIA VACANT						
pv	–	g^+	2860	normal size but empty perithecia	ICR170	738
HYALOMYCELIUM						
hym-1	–	g^+	2861	mycelial pigmentation very light; self-sterile	ICR170	739
hym-2	–	g^+	2862	slight mycelial pigmentation, dark spores		740
hym-3	–	g^+	2863	slight mycelial pigmentation; fertile, but a subnormal number of perithecia and spores discharged	UV	741
hym-4	–	g^+	2864	light mycelial pigmentation; spore pigmentation nearly normal, fertile	S(?)	742
hym-5	–	g^+	2865	slight mycelial pigmentation; fertile, spore pigmentation normal	S(?)	743
PARTIALLY FERTILE						
pf-2	–	g^+	2866	partial fertile perithecia	S(?)	744
pf-3	–	g^+	2867	almost sterile, but a few large partially fertile perithecia	S(?)	745
pf-4	–	g^+	2868	almost sterile, with small, partially fertile perithecia	ICR170	746
pf-5	–	g_1	2869	relatively poor spore discharge regardless of near normal fertility; smaller than normal	ICR170	747
				GROUP VIII - DWARF and RESTRICTED GROWTH		
DWARF						
dw-1	–	g^+	2870	dark mycelium, fertile		811
dw-2	–	g_1	2871	colony size smaller than dw-1, fertile		812
dw-3	–	g_1	2872	each colony very small, very fertile	S	813
dw-4	–	g^+	2873	very slow growth, self-sterile	X	814
dw-5	–	g^+	2874	fertile, less dwarfed colonies	X	815
dw-6	–	g^+	2875	small, dense colony developing expanded growth, fertile	ICR170	816
dw-7	–	g^+	2876	self-sterile, slow growth	ICR170	817
dw-8	–		6358		NG	N21
dw-9	–		6350		NG	N13
dw-10	–		6359		NG	N22
dw-11	–		6365		NG	N28
dw-12	–		6366		NG	N29

Allele number g locus FGSC stock Number in other

Symbol*	in locus	allele	number	Comments	Mutagen	collection
dw-13	–		6367		NG	N30
dw-14	–		6368		NG	N31
dw-15	–		6369		NG	N32
dw-16	–		6371		NG	N34
dw-17	–		6372		NG	N35
dw-19	–		6378		NG	N41
dw-20	–		6379		NG	N42
dw-21	–		6380		NG	N43
RESTRICTED GROWTH						
r-2	–	g^+	2877	mycelium more dense than normal, fertile	X	822
r-3	–	g^+	2878	dense and thin random growth, areas of densely clumped perithecia		823
r-4	–	g^+	2879	slow and dense growth, dark mycelium		824
r-5	–	g^+	2880	fertile perithecia densely produced, forming ringed zone about 1 cm from inoculum	UV+ 5 bromo uracil	825
r-6	–	g^+	2881	thick, fertile mycelial growth	X	826
r-7		g^+	2882	dark, thick mycelial growth, makes small number of large perithecia	S(?)	827
r-8	–	g_1	2883	fertile perithecia produced on small dense colony; germination of discharged spores from secondary colonies	X	828
r-10	–	g^+	2884	growth slow, fertility low, mycelia sparse	X	830
r-11	–	g_1	2885	slow growth, fertile	UV	831
r-12	–	g_1	2886	slow growth, very fertile	UV	832
r-13	–	g^+	2887	ascospore color in homozygote lighter than normal; slow growth, fertile	ICR170	833
r-14	–	g^+	2888	growth slow, colonies covered with an even density of fertile perithecia	ICR170	834
r-15	–	g^+	2889	fertile, dense, slow growth	S	835
r-17	–	g^+	2891	fertile, slow growth	ICR170	837
r-18	–	g^+	2892	early, irregular growth with dark and light mycelial zones	ICR170	838
r-22	-		6355		NG	N18
r-26	–		6352		NG	N15
r-27	–		6360		NG	N23
r-29	–		6361		NG	N24
r-30	–		6362		NG	N26
r-31	–		6363		NG	N26
r-32	–		6353		NG	N16
r-34	–		6364		NG	N27
r-35	–		6370		NG	N33
r-36	–		6356		NG	N19
r-38	–		6373		NG	N36
r-39	–		6374		NG	N37
r-41	–		6376		NG	N39
r-43	–		6347		NG	N8
r-44	–		6348		NG	N9
r-45	–		6349		NG	N10

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
GROUP IX - ABORTIVE SPORE PRODUCTION						
ABORTIVE						
a-4	-	g^+	2893		S	92
a-5	-	g^+	2894	perithecia very small in homokaryon; large abortive perithecia produced in hybrid heterokaryon	ICR170	93
a-6	-	g_1	2895	relatively large perithecia, mostly empty asci		94
a-7	-	g^+	2896	growth and perithecial size normal; almost perfectly abortive	UV	95
a-8	-	g^+	2897	dwarf-like growth; zonation of perithecia	UV	96
a-9	-	g^+	2898	few relatively large perithecia	UV	97
a-10	-	g^+	2899	tan ascospores in homozygote, wild type color epistatic, various spore sizes in heterozygote	ICR170	98
a-11	-	g^+	2900	growth and perithecial size nearly normal; relatively large no. of spores, some viable	UV	99
a-12	-	g^+	2901	growth thin; few relatively large perithecia	ICR170	910
a-13	-	g^+	2902	growth and perithecial size normal, few in number	ICR170	911
a-14	-	g^+	2903	growth normal, rather small , abundant perithecia yielding relatively large number of spores	ICR170	912
a-15	-	g^+	2904	mycelial color very light; less than normal number of perithecia	ICR170	913
a-16	-	g^+	2905	mycelial color darker than normal; perithecial size varies	ICR170	914
GROUP X - TRANSLOCATION						
TRANSLOCATION						
L-1	-	g^+	2906		X	101
L-2	-	g_1	2907		S	102
L-3	-	g^+	2908		X	103
L-4	-	g^+	2909		S	104
L-5	-	g^+	2910		S	105
L-6	-	g_1	2911	with i_1	S	106
L-7	-	g_1	2912		UV(?)	107
L-8	-	g^+	2913		S(?)	108
L-9	-	g^+	2914		S(?)	109
L-10	-	g^+	2915		S(?)	110
L-11	-	g_1	2916		S	111
L-12	-	g^+	2917		S(?)	112

REFERENCES

1. El-Ani, Olive and Kitani 1961 Am J. Bot. 48:716-723; Kitani, Olive and El-Ani 1962 Am. J. Bot. 49:697-706; Kitani and Olive 1967 Genetics 57:767-782, Genetics 62:23-66, PNAS 66:1290-1297; Kitani and Whitehouse 1974. Molec. gen. Genet. 131:47-56.
2. Perkins, D.D., A.S. El-ani, L.S. Olive and Y. Kitani 1963 Am. Naturalist 97:249-252
3. Pollock, R. and G.A. Johnson 1972 Can. J. Genet. Cytol. 14:943-948
4. Olive, L.S. 1956 Am. J. Bot. 43:97-107
5. Kitani, Y. 1978 Genetics 89:467-497
6. Kitani, Y. 1978 Japan J. Genetics 53:301-308
7. Kitani, Y. 1988 Fungal Genetics Newsletter 35:16-20

Part VIII. Key to Symbols
Allele Designation:

The number usually refers to an isolation number. Numbers without prefixes indicate the original Beadle and Tatum mutants. The few exceptions are indicated by underlining the allele numbers.

Prefixes used are as follows:

A	M. Ahmad
AB	Used by Thomas E. Johnson
ALS	Alice L. Schroeder
ANTAS	Used by John H. Chalmers, Jr.
AR	Alan Radford
B	Brookhaven National Laboratory--used by Val Woodward;also by M.E. Case et al. to refer to pan-2 alleles
BAT	Used by J.L. Reissig
BC	Used by R.L. Metzenberg
BE	Bruce Eberhart
BS	B.R. Smith
BVS	B.V. Smith
C	California Institute of Technology
C-	Cornell University
CA	Canberra--used by D. Smyth
car	Used by A.M. Kapular
CD	Used by R.H. Davis
CJS	Carol J. Smarr--used by D.D. Perkins
CL	Used by A.S. Sussman
CM	Used by A.M. Eberhart
CN	Used by N.F. Robertson
CR	Used by W.M. Thwaites to denote citrulline resistant
CR-	Used by H. Bertrand
CU	Columbia University
D	Duke University--used by S.R. Gross
D	Used by G.A. Marzluf
DBL	D.B. Lee
DFC	D.F. Caroline
DH	Dorothy Halsall
DJ	David Jacobson
DK	Used by S.R. Gross
DL	A.M. DeLange--used by N.B. Raju
DS	David Stadler
DW	Dow Woodward
E	Emerson--used by Sterling Emerson; also used by T. Ishikawa to refer to *ad-8* mutants
ER	Used by V.E.A. Russo
F	Used by D. Woodward, et al. to refer to *ad-4* mutants
FB	Frank Buxton
FK	Fraser and Käfer
FLR	Used by S.R. Gross
FS	Florida State--used by DeBusk/Selitrennikoff
G	B. Gowdridge--used by M.J. Mayo
GH	George Hoffmann
GN	Used by G.W. Charlang
GNB	George N. Bistis
H	Hungate--used by Frank Hungate
HC	Ho Coy Choke
HK	Homare Kuwana
HS	Hugh Sweeney
HY	Used by Julian Hartley
I	Used by G.A. Marzluf
j	Used by I.B. Barthelmess
JBM	Joyce B. Maxwell
JC	J.B. Courtright
JFL	J.F. Lehman--used by R.L. Metzenberg
JH	Johns Hopkins Univ.--used by W.D. McElroy
JI	John Innes (Inst.)--used by J.R. Fincham
JL	John Leslie
JP	Used by M.L. Sargent
K	Used by D.G. Catcheside; also by K.C. Atwood for K22 (*amyc*)
KG	Kwansei Gakuin--used by H. Kuwana
KGP	K.G. Perrine - Used by G. Marzluf
KH	K.S. Hsu
KO	Used by A. Radford
KS	Kansas State--used by V. Woodward
L	C.C. Lindegren
L	L. Livingston
LD	Lori Dunn
LLM	Laura Livingston Mays
LO	Lori Olson
LP	Lakshmi Pendyala
LW	Lloyd Wolfinbarger
M	B.D. Maling
MB	Monica Bjorkman
MD	Michael C. Deeley
MEP	Used by R.H. Davis
MK	Used by V.E.A. Russo
MKG	Used by R.L. Metzenberg
MN	Mutant Neurospora--used by D.E.A. Catcheside
MW	Used by A.S. Sussman
N	Dorothy Newmeyer
NAN	Used by Morris Grindle
NM	Noreen Murray
NMR	Used by G.A. Marzluf
NS	W.N. Strickland
OP	Used by G.J.Sorger
ORS	Used by O. Mylyk
OY	O.C. Yoder
P	Perkins--used by D.D. Perkins; also by N.E. Murray nee Parker
PB	Used by Thomas E. Johnson
PD	Peter Dodd
PJR	Peter J. Russell
PR	Designates partial reversion
R	Rockefeller--used by E.L. Tatum
RC	Reed College
RES	R.E. Subden
RLM	R.L. Metzenberg
RLP	R. LePage
RP	R.L. Phillips
RS	R.W. Siegel--used by D.D. Perkins

RU	Rice University
RW	Ruth Williams--used by L.G. Williams
RWT	R.W. Tuveson
S	Stanford--used by E.L. Tatum
SAT	Sharon A. Thomas
SC	South Carolina--used by Mishra & DeLange
SDS	San Diego State
SF	Used by H.G. Gratzner
SG	Sam Gross--used by D.D. Perkins
STL	St. Lawrence
SUE	Used by R.E. Subden
SV	S.J. Vollmer
T	Texas--used by R.P. Wagner
T	Tokyo--used by T. Ishikawa
TB	Thomas Baker
TJS	T.J. Schmidhauser
TL	T. Legerton
TM	Used by D.G. Catcheside and T. Angel nee Maxia
TP	Thomas Paulus
U	Used by G.A. Marzluf
UA	Univ. of Alberta--used by K.K. Jha
UCLA	Univ. of California, Los Angeles
UFC	United Fruit Co.--used by R.D. Goos
UG	Univ. of Georgia--used by Branch Howe
UK	Univ. of Kansas--used by J.A. Kinsey
UM	Univ. of Michigan--used by R.H. Davis
UT	Univ. of Texas
UV	Used by M. Grindle
UVC	Used by M. Grindle
UW	Univ. of Wisconsin--used by R.L. Metzenberg
UWO	Univ. of Western Ontario--used by W.L. Greer
V	N.V. Vigfusson
V	Virginia--used by R.H. Garrett
WRN	Used by T.W. Seale to designate reversion by nitrous acid.
WRR	Used by G.A. Marzluf
WRU	Used by T.W. Seale to designate reversion by ultraviolet
Y	Yale--used by E.L. Tatum(1945-49);
X	Used by B.M. Eberhart, also N.H. Giles (to 1973)
Z	H. Zalkin

Suffixes used are as follows:

Ab	aberration	(r)	resistant
(d)	dependent	(s)	sensitive
(p)	pH-sensitive	(t)	temperature-sensitive
pr	partial reversion	T	translocation (reciprocal or insertional)

In addition, in cases where more than one gene mutation has been recovered from a stock, a suffix is added to the isolation number to differentiate the two; i.e., Y30539y is an allele of *ylo-1*; y30539r an allele of *rib-2*.

Genetic Background:

The symbols are designed to provide the general nature of the background of each stock. No attempt is made to provide detailed information. Several nonidentical lines of Emerson, Lindegren and St. Lawrence wild types are in use. As stocks improved, a given laboratory often changed to different but related wild types. Where detailed information is essential, the investigator should contact the Stock Center. For origin of some of the wild type strains, see Barratt, R.W., "Origin of Important Wild Type Stocks of *N. crassa*", Neurospora Newsletter 2:24-25 and Neurospora Newsletter 3:19; Case, M.E. et al. "Further Information on the Origin of the Yale and Oak Ridge Wild Type Strains of *N. crassa*", Neurospora Newsletter 8:25-26, Catcheside, D.G. 1975 "Occurrence in Wild Strains of *Neurospora crassa* of Genes Controlling Genetic Recombination", Aust. J. Biol. Sci. 28:213-225 and Newmeyer, D. et al. 1987 "An annotated pedigree of *Neurospora crassa* laboratory wild types, showing the probable origin of the nucleolus satellite and showing that certain stocks are not authentic", Fungal Genetics Newsletter 34:46-51.

For many of the original mutant strains of Beadle and Tatum, only incomplete records are available as to whether existing strains are original or derived. Where any doubt occurs, the symbol O? is employed to indicate uncertainty.

Symbols used are as follows:

A	Abbott	M	Mixed	AxM	Abbott crossed with mixed
C	Chilton	RL	Rockefeller-Lindegren	AxC	Abbott crossed with Chilton
E	Emerson	SL	St. Lawrence	LxE	Lindegren crossed with Emerson
L	Lindegren	AxL	Abbott crossed with Lindegren		

Numbers after symbols (as SL4) refer to the number of backcrosses to the indicated background. SL4 should be read "back-crossed into St. Lawrence background four times."

Locus symbols used for *Neurospora tetrasperma*

A/a	mating type alleles
d	lethal producing deliquescent asci; wild type allele D (formerly called 1,L)
E	lethal preventing ascospore maturation on certain media, producing 8-spored asci on other media (dominant); wild type allele e
I	lethal producing indurated asci (dominant); wild type allele i
v	dwarf or yellow dwarf; wild type allele v

Mutagen :

Symbols used to indicate the mutagen employed are as follows:

A	acridine ICR-170	UV+M	ultraviolet + mustard simultaneously
AFT-B	Alfatoxin B1	MDAB	methyl-dimethylaminobenzene
2-AP	2-Aminopurine	MMS	methyl methane sulfonate
BUDR	5-bromodeoxyuridine	N	neutrons
Co-60	cobalt 60	NA	nitrous acid
D	Disruption	NG	N-methyl-N'-nitrosoguanidine
DEB	diepoxybutane	4-NQO	4-nitroquinoline 1-oxide
DEO	diepoxyoctane	O	no mutagen, allele present in parent strain
DS	diethyl or dimethyl sulfate	P	beta propiolactone
EMS	ethyl methane sulfonate	RIP	Repeat Induced Point mutation
FUDR	5-fluorodeoxyuridine	TR	transformation
G	gamma radiation	S	spontaneous
HA	hydroxylamine	S35	sulfur 35
ICR-170	acridine ICR-170	UV	ultraviolet light
M	mustard (nitrogen or sulfur)	X	x-rays
MC	methylcholanthrene	KO	Knock Out/gene disruption

Locus symbols used for Neurospora interspecific hybrids

A	mating type alleles	S	sitophila	C	crassa
T	tetrasperma	E	England	V	Virginia, USA

Obtained from:

AA	A. Almasan
AD	Anne Desjarsin
AGD	A. Gib DeBusk
AJG	A.J. Griffiths
AL	Alan Lambowitz
ALS	Alice L. Schroeder
AMK	Alan M. Kapular
AML	Ann Matthews Lacy
AMS	Adrian M. Srb
AMW	Angela M. Wellman
AR	Alan Radford
AS	Alfred Sussman
ATCC	American Type Culture Collection
BB	Barry Bowman
BBG	Bronx Botanical Garden
BCT	Barbara C. Turner
BDM	Barbara D. Maling
BME	Bruce M. Eberhart
BRS	B.R. Smith
BSR	B. Seidel-Rogol
BSS	B.S. Strauss
BV	Barbara Valent
BVS	Bonita V. Smith
BW	Brian White
CBS	Centraalbureauvoor Schimmelcultures
CFC	C.F. Curtis
CIT	Calif. Inst. of Tech.
CMI	Commonwealth Mycological Institute
CPS	C.P. Selitrennikoff
CS	Chuck Staben
CTY	Carl T. Yamashiro
CWH	C.W. Hesseltine
CWM	Clint W. Magill
CWS	Carolyn W. Slayman
CY	Charles Yanofsky
DAS	David A. Smith
DDP	David D. Perkins
DE	Dan Ebbole
DEC	D.E.A. Catcheside
DGC	D.G. Catcheside
DJJ	David J. Jacobson
DJL	David J. Luck
DJW	David J. West
DLE	David L. Edwards
DMB	David M. Bonner
DMH	Dorothy M. Halsall
DNP	D. Newmeyer Perkins
DPM	D.P. Mahoney
DRG	Donna R. Galeazzi
DRS	David R. Stadler
DS	D.R. Smyth
EGB	Edward G. Barry
EGS	Emory G. Simmons
EJM	Edward J. Mullaney
EK	Etta Käfer
ELT	Edward L. Tatum
ER	Edward Reich
ESJ	Eric S. Jacobsen
EWR	Edith Wong Rao
FD	Frank Doe
FGSC	Fungal Genetics Stock Center
FHG	Frank H. Gaertner
FJD	F.J. de Serres
FRL	Frank R. Lauter
FJL	Franz J. Leinweber
FPB	Frank P. Buxton
GAM	George A. Marzluf
GAS	G.A. Scarborough

GM	Gregory May
GRH	George R. Hoffman
GS	George Sorger
GWC	Gisela W. Charlang
GWG	G.W. Grigg
HA	Harold Aurich
HB	Helmut Bertrand
HBH	H. Branch Howe
HCC	Ho Coy Choke
HDB	H.D. Braymer
HDV	Hans de Vries
HFT	Hector F. Terenzi
HGG	Howard G. Gratzner
HGK	H.G. Kølmark
HI	Hirokazu Inoue
HK	Homare Kuwana
HWS	H. Wayne Shew
HVE	Hans VanEtten
IBB	I.B. Barthelmess
JAD	John A. DeMoss
JAK	John A. Kinsey
JBC	J.B. Courtright
JBM	Joyce B. Maxwell
JCK	John C. Krug
JCM	J.C. Murray
JFF	Jerry F. Feldman
JFL	John F. Leslie
JFW	J.F. Wilson
JH	J. Hartley
JHC	J.H. Chalmers, Jr.
JJL	Jennifer J. Loros
JLR	Jose L. Reissig
JM	Jaime Mora
JRF	J.R. Fincham
JW	Jan Weijer
JWT	John W. Taylor
KAZ	Kurt Zeller
KEA	Kenneth E. Allen
KDM	Kenneth D. Munkres
KF	Kouhei Furuya
KH	Kojhi Hasunuma
KJM	K.J. McDougall
KKJ	Krishna K. Jha
KN	Kazuo Nakamura
KOD	Kerry O'Donnell
KSH	K.S. Hsu
LB	Leon Belcour
LG	Laura Garnjobst
LGW	Larry G. Williams
LLM	Laura L. Mays
LRL	Laura R. Livingston
LTC	Lung-Ting Chang
LW	Lloyd Wolfinbarger
MA	Majeed Ahmad
MB	Monika Björkman
MBM	Mary B. Mitchell
MEC	Mary E. Case
MF	Mark Farman
MHF	Michael Freitag
MG	Morris Grindle
MGS	Michael G. Schechtman
MJM	M. Jean Mayo
ML	Melanie Loo
MLP	Martin L. Pall
MLS	Malcom L. Sargent
MS	Marie Shields
MU	Martin Urban
NBR	N.B. Raju
NCM	N.C. Mishra
NEM	Noreen E. Murray
NFR	N.F. Robertson
NGB	Neil G. Brink
NK	Nancy Keller
NHH	N.H. Horowitz
NJW	N.J. Weston
NRRL	Northern Regional Research Laboratory
OCY	Olen C. Yoder
OG	Olivera Gavric
OMM	Orest M. Mylyk
PCH	P.C. Huang
PJR	Peter J. Russell
PMM	P.M. Mohan
PSL	P. St. Lawrence
PT	Phillips Thayer
RBC	R.B. Cain
RBF	Richard B. Flavel
RDG	Roger D. Goos
REB	R.E. Beever
REN	Robert E. Nelson
RES	Ronald E. Subden
RF	Robert Fuerst
RH	Ruth Halaban
RHD	Rowland H. Davis
RHG	R.H. Garrett
RKL	R.K. Littlewood
RLM	R.L. Metzenberg
RLP	R.L. Phillips
RM	Ramesh Maheshwari
RMD	Ruth M. DeBusk
RPW	Robert P. Wagner
RRB	R.R. Burk
RTP	Robert T. Pollock
RWB	Raymond W. Barratt
RWH	Roy W. Harding
RWT	Robert W. Tuveson
SB	Stuart Brody
SD	Steve Dennison
SE	Sterling Emerson
SEG	S.E. Gochenaur
SRG	Samson R. Gross
SRS	S.R. Suskind
SW	Susan Wellman
TEJ	Thomas E. Johnson
THP	T.H. Pittenger
TI	Tatsuo Ishikawa
TM	Tadako Muryama
TMO	Tong-Man Ong
TWS	Thomas W. Seale
VEAR	V.E.A. Russo
VWW	Val W. Woodward
WK	W. Klingmuller
WKB	William K. Bates
WLG	W.L. Greer
WMT	William M. Thwaites
WNS	W.N. Strickland
WSM	Walter S. McNutt
YK	Yoshiaki Kitani

CLONED GENES

A limited selection of individual genes is available from the FGSC. Individual clones from cosmid libraries can also be supplied. Identified clones are listed following descriptions of the libraries on following pages. In all cases, shipments will be made in the form of *E. coli* cells containing the relevant plasmid. Fees are described on the FGSC web-site. Fosmid clones from the Broad Institute Aspergillus genome are available as individual clones. **Cloning vectors and tagging vectors are listed in Section A. For the most recent list of clones and cloning vectors, consult the FGSC web-site.**

Cloned gene	Plasmid name	Reference
AMA1	pRG-AMA1-NotI	Genetics 155:647-656
AMA1	pRG-AMA1-niiA	
AMA1	pRG-AMA1-niaD	
actin	pSF5	Fidel et al. 1988. Gene 70:283-293
acuE (malate synthase)	pRAS12	Sandeman & Hynes 1989. MGG 218:87-92
acvA (aminoadipyl-cys-val synthetase)	pSTA207	MacCabe et al. 1990. EMBO J. 9:279-287
acvA (penicillin acyltransferase)	pSTA200	MacCabe et al. 1990. EMBO J. 9:279-287
ade3	pLH107	Hamer, FGN 45: 13-14
alcA	pAST30	1994 Mol Cell Biol 14:5333-5348
alcR (regulatory)	palcR (SalI- SalI)	Felenbok et al, Gene 73:385-396
amdR (acetamidase regulation)	pALX-1	Andrianopoulos & Hynes 1988. Mol Cell Biol 8:3532
amdS (acetamidase)	p3SR2	Hynes et al. 1983. Mol. Cell. Biol. 3:1430-1439
Aras	pAST33	1994 Mol Cell Biol 14:5333-5348
Aras (cDNAunder control of PalcA)	pAST40	1994 Mol Cell Biol 14:5333-5348
areA	pAR4-322-1	Davis and Hynes, unpublished
argB (ornithine transcarbamylase)	pILJ16	Johnstone et al. 1985. EMBO J. 4:1307
argB	pDC1	Aramayo et al. 1989. Genetics 122:65-71
argB	pMS12	M. Stringer (unpubl)
benA (β-tubulin)	pβ-5	May et al. 1987. Gene 55:231-243
benA	pbenA3, pbenA7, pbenA10 pbenA13, pbenA715, pbenA16	Oakley Cell Motil Cytoskel 22:170-174
bimC	pAEBamI	Enos & Morris 1990. Cell 60:1019-1027
bimG (protein phosphatase)	pBG4	Doonan & Morris 1989. Cell 57:987-996
calmodulin-dependent protein kinase	p4b-11	Kornstein et al. 1992 Gene 113:75-82
crnA (nitrate transport)	pSTA4	Johnstone et al. 1990. Gene 90:181-192
facA (acetyl-CoA synthetase)	pRAS7	Sandeman & Hynes 1989. MGG 218:87-92
fadA^{d+}	pSM8P2	Embo J. 15:5184-5190
flbA (genomic)	pBN29	Mol Microbiol 14:323-334
flbA (cDNA)	pBN30	ibid.
gdhA (glutamate dehydrogenase)	pSJG1	Gurr et al. 1986. Curr. Genet. 10:761-766
hxA (xanthine dehydrogenase)	pBAN884	Glatigny and Scazzocchio, J Biol Chem 270:3534-3550
ipnA (isopenicillin N synthetase	pSTA204	MacCabe et al. 1990. EMBO J. 9:279-287
lamA (lactamase)	pLAM7	Katz & Hynes 1989. Genetics 122:331-339
leu-2	pLH105	Hamer, FGN 45:13-14
mipA (γ-tubulin)	pLO6[genomic]	Oakley & Oakley 1989. Nature 338:662
mipA (γ-tubulin)	pTH2[cDNA]	ibid.
niaD (nitrate reductase)	pSTA8	Johnstone et al. 1990. Gene 90:181-192
niiA (nitrite reductase)	pNIIA	Johnstone et al. 1990. Gene 90:181-192
nimA (protein kinase)	pSAO1	Osmani et al. 1987. J. Cell Biol. 104:1495-1504
nudC	pnudC/6.4	Osmani et al. 1990. J. Cell Biol. 111:543-551
pyrG (orotidine 5'-monophosphate decarboxylase)	ppyrG	Oakley et al. 1987. Gene 61:385-399
	pJR15	ibid.
riboB	pLO1, pPL1	Oakley et al. 1987. Gene 53:293-298
rodA (condial rodlet layer)	pTA51	Stringer et al. 1991. Genes & Devel 5:1161-1171
spl1	pLH112	Hamer, FGN 45: 13-14
trpC (trifunctional)	pHY201	Mullaney et al. 1985. MGG 199:37-45
tubA (α tubulin)	pDP485	Doshi et al. 1991. MGG 225:129-141
tubB (α tubulin)	pDP6031	Doshi et al. 1991. MGG 225:129-141
tubC (β-tubulin)	pβ-14-2	May et al. 1987. Gene 55:231-243
uaZ (urate oxidase)	bAN640	Oestreicher et al, Gene 132:185-192
wA (polyketide synthase?)	pNK3	Mayorga & Timberlake 1990. Genetics 126:73-79

Aspergillus Genomic libraries

pWE15 and pLORIST2 cosmid libraries

FGSC distributes these cosmid libraries, each of which consists of 30 microtiter plates, together. Together, the two libraries give good coverage of the *A. nidulans* genome and form the basis of the chromosome specific and minimal compressed libraries. They are made from the strain A4.
These libraries were used in the construction of the *Aspergillus nidulans* physical map at the University of Georgia.
A list of identified clones in the pWE15 and pLORIST2 libraries is available online

Chromosome specific libraries

All clones from the pWE15 and pLORIST2 libraries showing hybridization to chromosome-specific probes were reisolated to microtiter plates according their chromosome linkage (Brody et al. 1991. Nucleic Acids Res.19:3105-3109). A total of 38 chromosome specific plates resulted. These can be sent as a complete set or as individual chromosome subsets.

Aspergillus Minimal Compressed library

This subset of the pWE15/pLORIST2 libraries was picked to 16 microtitre plates based upon the data of Prade et al. (1997) Proc Natl Acad Sci USA 94:14565-14569. Each clone is adjacent in the plates to adjacent or overlapping DNA from the genome.

Unordered Genomic DNA libraries

AMA-NotI Genomic library
AMA-niiA Genomic library
AMA-niiD Genomic library

Autonomously replicating plasmid library containing inserts of approximately 9 kb.
See: Osherov and May. Genetics, 155:647-656 and Osherov, *et al*. Fungal Genet. Biol. 31:181-188

Aspergillus cDNA libraries

24 h developmental cDNA library constructed by R.Aramayo

The developmental poly(A)+ mRNA used to construct this library was prepared as follows: conidia from the strain FGSC A26 (biA1) were germinated in a liquid medium and allowed to grow 18 h. Mycelia was harvested on top of filter paper and placed onto appropriately supplemented minimal medium. Induced mycelia were then allowed to develop for 24 h prior to harvest and mRNA extraction. Poly(A)+ mRNA was prepared using standard procedures. The cDNA library was constructed using the lambda ZAP-cDNA TM+ kit lot # UC105. The primary library contained approximately 100,000 clones. After plating this primary library, the phage were harvested and stored at -70 C. This library has not been amplified.

Lambda GT10 cDNA library
Prepared from hyphae of a strain called R153 (wA3 pyroA4) grown on yeast extract glucose medium.
See: Cell. 1988 Apr 22;53(2):237-44. From Greg May

UniZAP cDNA library
Prepared from hyphae of FGSC #A4 grown on minimal medium.
See: (1992) J. Biol. Chem. 267, 15737-15743. From Greg May

For both the Lambda GT10 and UniZAP cDNA libraries, RNA was prepared using hot phenol plus SDS and the polyA+ RNA was made using oligo dT cellulose. These are both sent as a sample of packaged phage.

+ Lambda ZAP are proprietary vectors owned by Stratagene Cloning Systems. Stratagene has kindly allowed FGSC to distribute these libraries for research purposes only to non-profit institutions. These libraries may not be used for commercial purposes nor may they be used to reconstitute the lambda zap vectors. Request for and acceptance of these libraries constitutes acceptance of the following terms: The Lambda ZAP vectors shall not be used for the reproduction, amplification or modification of the vector. Neither the Lambda ZAP vectors nor derivatives of them shall be offered for resale. Neither the Lambda ZAP vectors nor derivatives of them shall be distributed or transferred to third parties.

Aspergillus nidulans strains

I. Alphabetical Listing of Genetic Loci and Alleles

Translocation refers to parent strain. The term "none" signifies tested in diploids; the term "none?" signifies tested in crosses, or not tested but derived from translocation free stocks. Consult numerical list for translocations in FGSC strains.

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
ALANTOIC ACID UTILIZATION						
aaX1	VI	A279	*yA2;pyroA4*	A220		none
ABACUS						
abaA14	VIIIR	A589, A590	*biA1*	A26	NA	none
ACONIDIAL						
acoA49	VII	A1068, A1071				
acoB202	II	A075				
acoC193	VII	A1073, 1076				
aco3		A1067				
aco14		A1069				
aco55		A1072				
aco70		A1074				
aco445		A1082				
ACRIFLAVINE RESISTANT						
AcrA1	IIL	A36, A204 & others	*pabaA1 yA2;coA1*	--	S	(*VI;VII*)
AcrA3	IIL	A346	*biA1;adC1;sC12;pyroA4*	A259	S	none
acrB2	IIR	A338				
ACTIDIONE RESISTANCE						
ActA1	IIIL	A231, A412, A607	*riboA1 yA1;nicB8*	A122	UV	none
actB2	VII	A529	*biA1;wA2;carA1*	--	S	
ACETATE NON-UTILIZATION						
acuD254	VR	A649	*pabaA1 yA2*	A234	UV	none
acuE201	IR	A650	*pabaA1 yA2*	A234	UV	none
acuF205	VII	A651	*pabaA1 yA2*	A234	UV	none
acuG223	VR	A652	*pabaA1 yA2*	A234	UV	none
acuH253	V	A653	*pabaA1 yA2*	A234	UV	none
acuJ211	IL	A654	*pabaA1 yA2*	A234	UV	none
acuK248	I	A655	*pabaA1 yA2*	A234	UV	none
acuL217	I	A656	*pabaA1 yA2*	A234	UV	none
*acuM30*1	--	A953	*wA3;pyroA4*			
ADENINE REQUIRING						
adA55	IL	A216, A218	prototroph	--	UV	none?
adB57	VIIIR	A217	prototroph	--	UV	none?
adC1	IIR	A259, A346 & others	*yA2 (veA*$^{+}$*)*	--	X	*T1(III→VIII;IV)*
adD3	IIR	A268, A565 & others				
adE8	IR	A42	*biA1*	A26	UV	none
adE20	IR	A226, A428 & others	*biA1*	A26	UV	none
adF15	IR	A46	*biA1*	A26	UV	none
adF17	IR	A273, A306				
adG14	IL	A37, A611 & others	*biA1*	A26	UV	none
adH23	IIL	A239, A382 A285 et al.	*biA1*	A26	UV	none
*adI50**	IIIL	A285 and others	*biA1*	A26	UV	none
AFLATOXIN REGULATION						
aflR	IV	A1052			D	

* *adI50* strains cannot use acetate as a carbon source

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Translocation
ASPARTATE HYDROXAMATE RESISTANT						
ahrA3	VIIIR	A680	*biA1*	A26	NG	none
ALCOHOL DEHYDROGENASE						
alcR125	VII	A752, A952	*biA1*			
alcΔ500	--	A950	*pabaA1;riboB2*			
ACETAMIDE UTILIZATION						
amdA7	VIIR	A749, A752				
amdI18	IIIR	A749, A750				
amdI66	IIIR	A751, A752				
amdR-44	IIR	A746				
amdS1005	IIIR	A752				
ANEURIN REQUIRING						
anA1	IL	A31, A201 & others	*biA1*	A26	UV	none
anB2	II	A261, A382	*biA1;AcrA1 wA3*	A123	UV	none
AROMATIC METABOLITE REQUIRING						
aromA1248	VIII	A1066				
ASPARAGINE NON-UTILIZATION						
apnA1	IIL	A659	*pabaA1;fwA1*	--	NG	
RAS						
A-ras		A986, A987, A988, A1059				
ARGININE REQUIRING						
argA1	VIR	A230				
argB2	IIIL	A89	*biA1*	A26	UV	none
argC3	VIIIR	A256	*biA1*	A26	UV	
argD11	V	A646	*biA1*	A26	UV	none
BENOMYL RESISTANCE						
benA10	VIIIR	A524	*biA1;AcrA1*	--	UV	
benA19	VIIIR	A523	*biA1;AcrA1*	--	UV	
benA33	VIIIR	A820	*pabaA1 yA2*	--	UV	
benB29	IIR	A565, A566	*suA1adE20 yA2 adE20;AcrA1; phenA2;pyroA4;lysB5;nicB8*	--	UV	
benC28	VIIR	A529	*biA1;AcrA1*	--	UV	
BIOTIN REQUIRING*						
biA1;veA1	IR	A26, many others	wild type (*veA*$^+$)	A4	X	none
* *veA1* occurs simultaneously with *biA1*						
BLOCKED IN MITOSIS						
bimA1	I	A780		A154	UV	
bimB3	III	A1065				
bimC4	VI	A777		A154	UV	
bimD6	IV	A1061 - A1064				
bimE7	VI	A776		A154	UV	
bimG11	VIII	A778	*riboA1 yA2;nicB8*	A122	UV	
BLUE ASCOSPORES						
blA1	IIR	A268	*yA2;wA3;sC12*	--	NA	
BRISTLE MORPHOLOGY						
brlA42	VIIIR	A583, A729	*biA1*	A26	NA	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
alc(p)::brlA		A107, A1078				
rbrlA		A1079, A1080				
BROWN CONIDIA						
bwA1	VIR	A77, A112-115, A366 & others	[2n]proA1 yA2;wA3// *adG14 pabaA1 biA1*	--	S	*T1(III→VIII)* *T1(VI;VII)*?
CARBOXIN RESISTANCE						
carA1	VIIR	A529	*biA1;wA2;ornB7*	--	UV	
carB2	VIIIR	A525	*biA1;benA10 fwA1*	--	UV	
carC9	IIIR	A528	*biA1;benA10 fwA1*	--	UV	
CATALASE						
catA	III	A1053, A1055			D	
catB	VIII	A1054, A1055			D	
▵-catC::argB-▵C		A1101	*pabaA, yA2, ▵-argB::trpC-▵-B, veA1*			
▵-catC::argB▵C, ▵-catA::argB▵-A		A1102	*pabaA, biA1, metG1, ▵-catB::argB▵B, veA1*			
▵-catC::argB▵-C, ▵-CatA::argB▵-A, ▵-catB::argB			A1103 pabaA1, yA2, biA1,▵-B, veA1			
CHARTREUSE CONIDIA						
chaA1	VIIIR	A23, A204 & others	*biA1;choA*1	A1	S	*T1(I;VII)*
chaA2	VIIIR	A372, A413	*biA1;sA2*	A316	S	*T1(V;VIII)*
CHLORONEB RESISTANCE						
chlA10	IIIL	A536	*biA1;AcrA1*	--	UV	none?
CHOLINE REQUIRING						
choA1	VIIR	A1, A607 & others	*biA1*	A26	UV	none
choC3	VIIIR	A669	*pabaA biA1*		NG	
COLORLESS ASCOSPORES						
clA6	IL	A280				
clB1	IL	A674	*yA2;wA2;sC12*		UV	
NITRATE AND HYPOXANTHINE UTILIZATION						
cnxA5	VIIIR	A555	*biA1*	A26	DES	none
cnxB2[*]	VIIIR	A381, A449 & others	*AcrA1;wA3;nicB8*	--		none
cnxB11	VIIIR	A557	*biA1*	A26	DES	none
cnxB50[†]	VIIIR	A266	*biA1*	A26	UV	none
cnxC[§]	VIIIR	A558	*biA1*	A26	DES	none
cnxE16[‡]	IIR	A63, A337, A462 & many others	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
cnxF8	VIIR	A560	*biA1*	A26	DES	none
cnxG	VI	A559	*biA1*	A26	DES	none
cnxH3	IIIL	A553, A662 & others	*biA1*	A26	DES	none
COMPACT MORPHOLOGY						
coA1	VIIIR	A29, A120, A449	*pabaA1 biA1*	--	S	*T1(VI;VII)*
COLONIAL - TEMPERATURE SENSITIVE						
cotA1	V	A827				
CARBON REPRESSION						
creA204	IL	A748	*areA217*	--	NG	
creB15	IIR	A747	*areA217*	--	NG	
creC27	IIR	A671	*areA217*	--	NG	

[*] also called *ni21/11*

[†] also called *ni50*

[§] cnxAB & C are one gene thas shows intragenic complentation between groups of certain mutants

[‡] also called *ni3*

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
CHOLINE-O-SULFATE NONUTILIZATION						
csuA6	V	A539	*suA1adE20 adE20 biA1 sB3;choA1;chaA1*	A168	NG	
CYSTEINE UTILIZATION						
cysA1	VL	A756	*mecA biA1 anA1*	--	UV	
cysB102	IIL	A753	*yA1;pyroA4;metB3*	--	S	
cysC103	VL	A754	*yA1;pyroA4;metB*3	--	S	
DILUTE CONIDIAL COLOR						
dilA1	IIIL	A489, A644 & more	*yA2;pyroA4*	A220?	UV	
DARK CONIDIA						
drkA1	VII	A588	*biA1*	A26	NA	none
drkB5	II	A685			UV	
FLUOROACETATE RESISTANCE (ACETATE NON-UTILIZATION)						
facA303	VR	A502, A613 & others	*wA3;pyroA4*	--	S	*T1(VI;VII)*
facB101	VIIIR	A409, A420 & others	*wA3;pyroA4*	--	S	*T1(VI;VII)*
facC102	VIIIR	A427	*wA3;pyroA4*	--	S	*T1(VI;VII)*
fanA3	V	A675	*biA1;facA303*	--	S	none?
fanB52	VII	A676	*biA1;facA303*	--	S	none?
fanD151	VIII	A673	*biA1;facA303*	--	S	none?
fanE7	VI	A677	*biA1*	A26	S	none?
FLUFFY AUTOLYTIC DOMINANT						
fadA		A1035, A1036, A1037, A1056		D		
FATTY ACID SYNTHASE						
fasA	VIII	A1038			D	
fasB	VIII	A1038			D	
FLUFFY LOW brlA						
flbA		A1034				
FLUFFY MORPHOLOGY						
fluG1	III	A744	*pabaA1 yA2*	A234	NG	none
fluG701		A1081, A1084 -A1087				
FLUOROPHENYLALANINE RESISTANCE						
fpaA1	IL	A275	*biA1*	A26	S	none
fpaA91	IL	A387, A439 & others	*proA11 yA2;pyroA4*	--	NG	
fpaB37	IL	A422, A507 & others	*riboA1 biA1*	A158	S	none
fpaC43	VII	A286	*riboA1 biA1*	A158	S	none
fpaD11	III	A273	*adF17 pabaA yA2*	--	S	?
fpaD43	III	A582				
fpaI64	IL	A717				
FRUCTOSE NON-UTILIZATION						
frA1	IVR	A59, A276	*yA2;pyroA4*	A220	UV	none
FAWN CONIDIA						
fwA1	VIIIR	A378, A524 & others	*biA1*	A26	S	none
fwA2	VIIIR	A371, A440 & others	*AcrA2;lysB5*	A205	S	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans- location
GALACTOSE NON-UTILIZATION						
galA1	IIIL	A211 & many others	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galB3 (=*araA*)	II	A215	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galC4	VIII	A291	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galD5	IL	A212, A213, A608	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galE9	IIIL	A214	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galF2	VIII	A718	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
galG2	VIIIR	A714				
GALACTOSE NON-UTILIZATION/MOLYBDATE RESISTANCE						
gamA55	I	A696	*biA1*	A26	S	none
gamB65	VIIIR	A697	*biA1*	A26	S	none
gamC66	?	A698	*biA1*	A26	S	none
GABA TRANSAMINASE						
gatA	VIIR	A848				
GLUTAMATE DEHYDROGENASE						
gdhA1	IIIL	A699	*biA1*	A26	NG	none
gdhB2	VI	A689	*biA1*	A26	NG	none
HISTIDINE REQUIRING						
hisA10	IV	A277	*yA2 biA1;AcrA1;riboB2*	--	UV	none?
hisB179	I	A727	*proA yA2;chaA1*	--	UV	
hisC38	VIIIR	A257	*biA1;AcrA1 wA3;nicB8*	--	UV	none
hisG113	II	A715	*proA yA2;chaA1*	--	UV	
hisH13	VIII	A278	*yA2 biA1;AcrA1;riboB2*	--	UV	none
hisJ122	VIIR	A299	*biA1;sB3*	A41	NA	none?
HYPOXANTHINE NON-UTILIZATION						
hxA1	VR	A258, A554	*biA1*	A26	DES	none
hxB13	VII	A552	*biA1*	A26	DES	none
ABNORMAL HYPHAL MORPHOLOGY						
hypA	I	A1129	*wA2, pyroA4*			
hypB	VII	A1130	*chaA, pyroA4*			
hypC	III	A1131	*pyroA4*			
hypD		A1132	*biA1, paba*			
hypE	VIII	A1133	*pyroA4*			
ISOLEUCINE REQUIRING						
ileA1	IIR	A295	*biA1;sB3*	A41	NA	none
ileA3	IIR	A254, A505	*biA1*	A26	UV	none
IMAZALIL RESISTANCE						
imaA4	VIIR	A529	*biA1;AcrA1*	--	UV	none?
imaB9	V	A532	*biA1;AcrA1*	--	S	none?
imaC10	IIR	A533	*biA1;AcrA1*	--	S	none?
imaD13	VIIIR	A534	*biA1;AcrA1*	--	S	none?
imaG18	IIIL	A535	*biA1;AcrA1*	--	NG	none?
imaH19	III	A537	*biA1;AcrA1*	--	NG	none?

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
INOSITOL REQUIRING						
inoA1	IIR	A678	*biA1*	A26	UV	none
inoB2	IVR	A679	*biA1*	A26	NG	none
INTEGRATION OF GABA METABOLISM (=*amdR*)						
intA^{C}*2*	II	A660	*biA1*	A26	NG	none
IODOACETATE RESISTANCE						
IodA1	IIL	A462, A492	*biA1;wA3;nicB8*	--	S	*T1(III→VIII)*
IVORY CONIDIOPHORES						
ivoA1	IIIL	A687			S	
ivoB63	VIIIR	A729			S	
LACTOSE NON-UTILIZATION						
lacA1	VIR	A58, A349 & others	*yA2;pyroA4*	A220	UV	none
lacB3	IIR	A292	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
LEUCINE REQUIRING						
luA1	IL	A55, A406	*biA1*	A26	UV	none
LYSINE REQUIRING						
lysA1	VIR	A38, A350*	*wA1(veA*$^{+}$)		X	Ab VI?
lysB5	VL	A66, A205 & others	*biA1*	A26	UV	none
lysD7	VIIR	A300	*biA1;sB3*	A41	NA	none?
lysD18	VIIR	A294, A606	*biA1;sB3*	A41	NA	none?
lysD20	VIIR	A418, A645	*biA1;sB3*	A41	UV	*T1(III;VIII)*
lysE13	VR	A296	*biA1;sB3*	A41	UV	none?
lysE14	VR	A298	*biA1;sB3*	A41	UV	none?
lysE231	VR	A301	*biA1;sB3*	A41	UV	none?
lysF51	IR	A297	*biA1;sB3*	A41	UV	none?
lysF88	IR	A293, A376	*biA1;sB3*	A41	UV	none?
* Contains Ab VI (Inversion?)						
MALTOSE NON-UTILIZATION						
malA1	VIIR	A57, A461 & others	*yA2;pyroA4*	A220	UV	none
MANNOSE NON-UTILIZATION						
manA1	VIIIR	A670				
MONOAMINE UTILIZATION						
mauA2	IVR	A681	*yA2;pyroA4 meaA8*		NG	
mauB4	IIR	A682	*yA2;pyroA4 meaA8*		NG	
METHYLAMMONIUM RESISTANCE						
meaA8	IVR	A672	*biA1*	A26	DES	none
meaB6	IIIL	A451, A496 & others	*biA1*	A26	DES	none
METHIONINE INHIBITION						
mecB10	IL	A758, A759	*biA1 anA1*	A31?	UV	
mecC13	?	A703	*biA1 anA1*	A31?	UV	none
MEDUSA						
medA15	IL	A586	*biA1*	A26	NA	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
MELANIN PRODUCTION						
melA1	VII	A657				
melB^{0}*2*	VIIR	A667				
METHIONINE REQUIRING						
methA17	IIL	A757	*adF9 yA1*	--	UV	
methB3	VIR	A272	*yA2;pyroA4*	A220	UV	none
methD10	IIIL	A755	*adF9 biA1*	--	UV	
methE6	VIIR	A719	*biA1*	A26	UV	none
methG1	IVL	A219 & many others	*biA1*	A26	UV	none
methH2	IIIL	A34, A644	*biA1*	A26	UV	none
MORPHOLOGICALLY ABNORMAL						
moC96	III	A232			P	
MOLYBDATE RESISTANT						
molA67	VIR	A707	*biA1*	A26	S	none
molB35	II	A716	*biA1*	A26	S	none
MUTAGEN SENSITIVE						
musK228	VIIIR	A840, A1031	*biA1;acrA1;nicA2*	A605	γ	*T2(IL;IIIL)*
musL222	IR	A841	*biA1;acrA1;nicA2*	A605	γ	*T2(IL;IIIL)*
musM225	VIR	A828	*biA1;acrA1;nicA2*	A605	γ	*T2(IL;IIIL)*
musN227	VIIR	A842, A1030	*biA1;acrA1;nicA2*	A605	γ	*T2(IL;IIIL)*
musO226	III or VIIR	A843	*biA1;acrA1;nicA2*	A605	γ	*T2(IL;IIIL)*
musP234	II or VII	A844	*pabaA1 yA2*	A610	UV	none
musQ230	IIR	A845	*biA1;acrA1;nicA2*	A605	γ	T2(IL;IIIL)
musR223	IIIL	A846	*biA1;acrA1;nicA2*	A605	γ	T2(IL;IIIL)
musS224	III or VIIR	A847	*biA1;acrA1;nicA2*	A605	γ	T2(IL;IIIL)
NITRATE NON-UTILIZATION						
niaD15	VIIIR	A691	*biA1*	A26	NA	none
NICOTINAMIDE REQUIRING						
nicA2	VL	A495, A605 & others	*wild type (veA*$^{+}$*)*	A4	X	
nicB8	VIIR	A122, A317 & others	*biA1*	A26	UV	none
nicC10	VI	A11	*biA1;AcrA1; wA3*	--	UV	none
NITRITE NON-UTILIZATION						
niiA4	VIIIR	A713				
NEVER IN MITOSIS						
nimA5	III	A781		A154	UV	
nimE6		A1127	*metG1,riboA1, yA2*			
nimG10		A1122	*chaA, lac, nic*			
nimQ20		A1123	*methB3, choA1 wA2*			
nimP22		A1124	*pyroA4, chaA1*			
nimO18		A1125	*pabaA4, yA2*			
nimT23		A1128	*pabaA4*			
NITRATE PATHWAY REGULATOR						
nirA14	VIIIR	A260, A472 & others	*biA1;phenA3*	--	S	*T1(I;IV)*
NUCLEAR DISTRIBUTION						
nudA1	--	A944-A948				
nudA (snfC1524)		A1011	*nudF6 pyrG89*		UV	
nudA (snfC1232)		A1019, A1020	*nudF6 pyrG89*		UV	
nudA GFP		A1106				
nudC3	--	A779	*wt* x *pabaA1 pyrG89;fwA1 uaY9*	A4 x A154	UV	

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
NUCLEAR DISTRIBUTION, continued						
nudF6		A1011 & others				
nudF GFP		A1104				
OLIGOMYCIN RESISTANT						
[oliA6]	cyto.	A666	*pabaA1 yA2*	A234	S	none
oliC2	VIIR	A450, A453 & others	*pabaA1 yA2*	A234	S	none
ORNITHINE REQUIRING						
ornA4	IVR	A43, A358	*biA1*	A26	UV	none
ornB7	VIIIR	A379				
ornB9	VIIIR	A353				
ornB20	VIIIR	A263	*biA1*	A26	UV	none
ornC31	IIIR	A668				
PALE CONIDIA						
pA2	VR	A35, A460, A495	*adG14 biA1*	A37	S	none
P-AMINOBENZOIC ACID REQUIRING						
pabaA1	IR	A610	*biA1*	A26	X	none
pabaA6	IR	A28, A595 & others	*biA1*	A26	UV	none
pabaA18	IR	A305, A308, A309	*biA1*	A26		none
pabaA108	IR	A333, A334	*biA1*	A26?	UV	none?
pabaA125	IR	A335, A336, A571	*biA1*	A26?	UV	none?
pabaB22	IVR	A426, A493 & others	*biA1*	A26	UV	none
ACID PHOSPHATASE DEFICIENT						
pacA1	IV	A241	*rA1 biA1*	--	UV	none
pacC5	VI	A242	*biA1*	A26	UV	none
ALKALINE PHOPHATASE DEFICIENT						
palA1	IIIL	A243, A287	*rA1 biA1*	--	UV	none
palB7	VIIIR	A244, A381 & others	*rA1 biA1*	--	UV	none
palC4	IVR	A250, A497 & others	*rA1 biA1*	--	UV	none
palD8	VIIR	A245, A581 & others	*rA1 biA1*	--	UV	none
palF15	VIIR	A247, A400 & others	*rA1 biA1*	--	UV	none
ACID & ALKALINE PHOSPHATASE DEFICIENT						
palcA1	IIL	A248	*rA1 biA1*	--	UV	none
palcC4	VIIIR	A712				
PANTOTHENIC ACID REQUIRING						
pantoA1	VIIIR	A340	*yA2;thiA1* (veA^+)	--	X	*T(III→VII;IV)*
pantoA10	VIIIR	A665				
pantoB100	VIIR	A397, A453 & others			UV?	
pantoC3	IIIL	A662				
PYRUVATE DEHYDROGENASE						
pdhA4	IR	A637	*yA2 pabaA1*	A234	UV	none
pdhB2(ts)	V	A628	*yA2 pabaA1*	A234	UV	none
pdhB4	V	A634	*yA2 pabaA1*	A234	UV	none
pdhC1	VIIIL	A627, A635(ts)	*yA2 pabaA1*	A234	UV	none
PHENYLALANINE REQUIRING						
phenA2	IIIR	A498, many more	*biA1*	A26	UV	none
phenA3	IIIR	A260, A402	*biA1*	A26	S	none
phenB6	VIIR	A394, many more	*biA1*	A26	UV	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
PIMARICIN RESISTANCE						
pimA1	IVR	A530	*biA1;AcrA1*	--	UV	none?
pimB10	IL	A531	*biA1;AcrA1*	--	S	none?
PYRUVATE KINASE						
pkiA2(ts)	V	A630	*yA2 pabaA1*	A234	UV	none
PENTOSE PHOSPHATE PATHWAY						
pppA1	II	A690	*biA1*	A26		none
pppB1	III	A688	*biA1*	A26	NG	none
PRECOCIOUS						
pre1		A1089				
PROLINE REQUIRING						
proA1	I	A32, many more	*biA1*	A26	UV	none
proA2	IL	A792, A793				
proA5	I	A45	*biA1*	A26	UV	none
proA11	I	A387	*yA2;pyroA4*	A220	UV	none
proB3	I	A692	*biA1*	A26	UV	none
proB4	I	A658	*biA1*;*wA3*	A51	UV	*T1(III→VIII)*; *T1(VI;VII)*
proB94	IL	A386, A453	wild type (veA^{+})	A4	UV	none
PROPIONYL-CoA SYNTHASE						
▵-pscA::pyrG		1134	*biA1; facA303; ▵-mcsA::argB; pyrG89; veA1*			
▵-pscA::pyrG		1135	*biA1; ▵-mcsA::argB; pyrG89; veA1*			
▵-pscA::pyrG		1136	*biA1; pyrG89; veA1*			
PUTRESCINE REQUIRING						
puA1	IIR	A338, A341	*biA1*;wA3	A51	UV	*T1(III→VIII)* *T1(VI;VII)*
puA2	IIR	A682, A701	*biA1*	A26	NG	none
PUTRESCINE NON-UTILIZATION						
punA11	IIR	A700	*biA1*	A26	UV	none
PYRUVATE CARBOXYLASE						
pycA2	V	A632	*yA2 pabaA1*	A234	UV	none
pycA12(ts)	V	A625	*yA2 pabaA1*	A234	UV	none
pycB4	V	A624	*yA2 pabaA1*	A234	UV	none
PYRIMIDINE REQUIRING						
pyrD23	VIIIR	A723, A724	*biA1*	A26	NG	none
pyrF11	IL	A721			NG	
pyrG89	IL	A722, A767 & others	*pabaA1;fwA1 uaY9*	--	NG	
pyrN25	VIII	A813, A814			NG	
PYRIDOXINE REQUIRING						
pyroA4	IVR	A33, A220 & others	*biA1*	A26	UV	none
pyroB12	IL	A693	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
RECOMBINATION DEFICIENT						
rec-402		A543(dp), A597(hap)	duplication YP 511	A542	NG	
rec-408		A546(dp), A598(hap)	duplication YP 511	A542	NG	
rec-412		A549(dp)	duplication YP 511	A542	NG	
rec-444		A548(dp), A599(hap)	duplication YP 511	A542	NG	
rec-469		A544(dp), A600(hap)	duplication YP 511	A542	NG	
rec-471		A547(dp), A562(hap)	duplication YP 511	A542	NG	
RIBOFLAVIN REQUIRING						
riboA1	IL	A158, many more	*biA1*	A26	UV	none
riboB2	VIIIR	A353, A612 & others	*biA1;AcrA1 wA3*	A123	UV	none
riboC3	V	A311	*yA2;pyroA4*	A220	UV	
riboD5	VR	A258, A504 & others	*biA1*	A26	UV	none
riboE6	IIR	A64	*biA1;wA3*	A51	UV	*T1(VI;VII)* *T1(III→VIII)*
riboF8	I	A726	*biA1*	A26	NA	none
RODLETLESS						
rodA	IIIR	A849	*pabaA1 yA2; ΔargB::trpCΔB; veA1 trpC801*	A851	D	
SULPHATE NON UTILIZATION						
sA1	IIIL	A40, A417 & others	*biA1*	A26	UV	none
sA2	IIIL	A316, A368 & others	*biA1*	A26	UV	none
sA4	IIIL	A2, A339 & others	*biA1*	A26	UV	none
sA49	IIIL	A404	*biA1*	A26	NG	none
sA91	IIIL	A405	*biA1*	A26	NG	none
sA130	IIIL	A602	*biA1*	A26	NG	none
sB3	VIR	A41, many more	*biA1*	A26	UV	none
sB25	VIR	A383	*riboA1;AcrA1;chaA1*	--	NG	none
sC12	IIIL	A24, many more	*wild type (veA$^+$)*	A4	NM	none
sC22	IIIL	A384	*riboA1 yA2*	A361	NG	none
sC63	IIIL	A603	*biA1*	A26	NG	none
sC84	IIIL	A604	*biA1*	A26	NG	none
sD50	VIIIR	A249, A398, A431, A434	*biA1*	A26	UV	none
sD85	VIIIR	A419, A421 & others	*biA1*	A26	NG	none
sD157	VIIIR	A420	*biA1*	A26	NG	none
sE15	VIIIR	A385, A399 & others	*biA1*	A26	NG	none
sF211	VIIR	A388, A403 & others	*biA1;pyroA4*	A33	NG	none
SORBITOL NON-UTILIZATION						
sbA3	VIR	A500, A510 & others	*biA1;wA3*	A51	UV	T1(III→VIII) T1(VI;VII)
SALT SENSITIVITY						
sltA1	VIR	A702	*biA1*	A26	NG	none
SMALL COLONIAL SIZE						
smA1	IIIL	A66, A436, A501	*biA1*	A26	UV	none
SUPPRESSOR OF MMS SENSITIVITY						
smsA61	VR	A395	*biA1;sB3*		UV	none
SUPPRESSOR OF NUCLEAR DISTRIBUTION						
snaA26		A945	*pyrG89;chaA1;nudA1*		UV	
snaB76		A946	*pyrG89;chaA1;nudA1*		UV	
snaC108		A947	*pyrG89;chaA1;nudA1*		UV	
snaD385		A944	*pyrG89;chaA1;nudA1*		UV	
snaE285		A948	*pyrG89;chaA1;nudA1*		UV	

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
SUPPESSOR OF *nudF*						
snfC1524 (nudA)		A1011, A1012	*nudF6 pyrG89*		UV	
snfC1232 (nudA)		A1019, A1020	*nudF6 pyrG89*		UV	
snfE798		A1013	*nudF6 pyrG89*		UV	
snfA890 (tubA22)		A1014, A1015, A 1016	*nudF6 pyrG89*		UV	
snfB1267		A1017	*nudF6 pyrG89*		UV	
snfD860		A1018	*nudF6 pyrG89*		UV	
snfD1468		A1021	*nudF6 pyrG89*		UV	
snfD1292		A1022, A1023	*nudF6 pyrG89*		UV	
snfD1555		A1024, A1025	*nudF6 pyrG89*		UV	
snf1364		A1026, A1028	*nudF6 pyrG89*		UV	
snf1062		A1027	*nudF6 pyrG89*		UV	
snf1422		A1029	*nudF6 pyrG89*		UV	
SORBOSE RESISTANCE						
sorA2	I	A705	*biA1;adH23 AcrA1 wA3;nicB8*	--	S	
sorB11	IIIL	A728	*biA1;adH23 AcrA1 wA3;nicB8*	--	S	
SPERMIDINE SENSITIVITY						
spsA1	IIIL	A701	*biA1;puA2*	--	NA	
SUPPRESSOR OF sbA3						
ssbA1	IV	A1	*biA1*	A26	UV	
STERIGMATOCYSTIN CLUSTER						
stcB	IV	A1048			D	
stcE	IV	A1041			D	
stcF	IV	A1049			D	
stcI	IV	A1051			D	
stcJ	IV	A1040			D	
stcK	IV	A1039			D	
stcL	IV	A1046, A1047			D	
stcN	IV	A1042			D	
stcP	IV	A1043, A1044			D	
stcQ	IV	A1045			D	
stcU	IV	A1047			D	
stcW	IV	A1050			D	
STUNTED CONIDIOPHORES						
stuA1	IL	A584, A585	*biA1*	A26	NA	
SUPPRESSORS						
suA1adE20	IL	A47, many more	*adE20;pyroA4*	A227	S	
suC11adE20	IVL	A443, A486 A517, A639	*pabaA1 yA2 adE20 AcrA1; coA1 cnxB2*	--	S	none
suA1palB7	VIIIR	A281	*biA1;palB7*	A244	S	none?
suB2palB7	VI	A284	*biA1;palB7*	A244	S	none?
suC6palF15	V	A282	*biA1;palF15*	A247		none?
suD2palA1	I	A287	*biA1;palA1*	A243		
suB4pro	IIIR	A423, A441, A454 and others	*proA biA1*	A45	S	
SUCCINATE NON-UTILIZATION						
sucA1	?	A694	*biA1;wA3*	A51	UV	*T1(III→VIII)* *T1(VI;VII)*

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans-location
SWOLLEN CELLS						
swoA		A1108, A1109				
swoA		A1107	*wA3*			
swoB		A1110				
swoC		A1112	wA3			
swoC		A1111				
swoD		A1113				
swoE		A1114				
swoF		A1115, A1116				
swoG		A1117				
swoH		A1118	*chaA-1*			
swoH		A1119				
SULPHANILAMIDE RESISTANT						
SulA1	IL	A507, A511 & others	*yA2;pyroA4*	A220	UV	none
AMMONIUM REGULATION						
tamA200	VIR	A822, A823	*biA1*	A26 UV		none
MOUND SHAPED COLONY						
telA1	VIIR	A695	*biA1*	A26	S	none
THIAZOLE REQUIRING						
thiA1	IIR	A14	*yA2 (veA*$^{+}$*)*	A647?	X	*T(III→VIII;IV)*
thiA4	IIR	A52, A337	*biA1*	A26	UV	none
TRYPTOPHAN REQUIRING						
trypA69	II(R?)	A235	*pabaA1 yA2*	A234	UV	none
trypB403	I(L?)	A236	*pabaA1 yA2*	A234	UV	none
trypC801	VIII	A237	*pabaA1 yA2*	A234	UV	none
trypD432	II(R?)	A238	*pabaA1 yA2*	A234	UV	none
TEMPERATURE SENSITIVE						
tsB5	VIR	A708	*biA1*	A26	UV	none
tsC17	IIR	A720	*biA1*	A26	UV	none
tsD15	VIII	A269	*biA1*	A26	UV	none
tsE6	V	A725	*adF15 biA1*	A46	EMS	
TUBULIN						
tubA4	VIIIR	A821			UV	
tubA22 (*snfA890*)		A1014, A1015, A 1016	*nudF6 pyrG89*		UV	
tubA GFP		A1105				
UREA NON-UTILIZATION						
uY5	VII	A262	*biA1*	A26	DES	none
URIC ACID NON-UTILIZATION						
uaX10	VI	A264	*biA1*	A26	DES	none
uaY9	VIIIR	A551, A729, A722	*biA1*	A26	DES	none
UREASE DEFICIENT						
ureA1(uruA)	VIIIR	A683				
ureB3 (uX)	VIIIR	A684				
ureD4 (uZ)	VIIIR	A648				

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	Strain of origin FGSC#	Mutagen	Trans- location
ULTRAVIOLET SENSITIVE						
See Kafer and Mayor 1986 Mutation Res. 161:119-134 for original designations of *uvs* mutants.						
uvs-5	--	A327	*adE20 biA1;wA3;methG pyroA4*	A139	UV	none
uvsA101	IR	A579, A831	*pabaA108 biA1*	--	UV	
uvsB110	IVC	A333, A577, A832	*pabaA108 biA1*	--	UV	
uvsB312	IVC	A573	*yA2;AcrA1;pyroA4*		UV	none
uvsB413	IVC	A561, A609	*pabaA6 yA2 adE8* biA^{+} *Dp(I→II)*yA^{+} *adE20 biA1*	A542	NG	
uvsB504	IVC	A827	*suA1adE20 adE20 biA1;ssbA3;sB3;choA1;chaA1*	A168	UV	
uvsB505	IVC	A826	*suA1adE20 adE20 biA1;ssbA3;sB3;choA1;chaA1*	A168	4-NQO	
uvsC114	VIIIR	A334, A570, A833	*pabaA108 biA1*	--	UV	
uvsD153	V(L?)	A335, A571, A834	*proA1 pabaA125 biA1;pyroA4*	--	UV	
uvsD308	V(L?)	A574	*biA1;niiB1*	--	UV	
uvsE182	VR	A572, A835	*proA1 pabaA125 biA1;pyroA4*	--	UV	
uvsF201	IL	A389, A567, A836	*riboA1 yA2*	A361	UV	none
uvsH77	IVL	A330, A568, A837	*adE20 biA1;wA3;methG*	A139	UV	none
uvsH304	IVL	A329, A576	*yA2;AcrA1;pyroA4*	--	UV	none
uvsH311	IVL	A575	*yA2;AcrA1;pyroA4*	--	UV	none
uvsI501	IIIL	A838				
uvsJ1	VL	A569, A578, A839	*adE20? biA1;methG?*	--	UV	none
VELVET-LOOKING CONIDIA						
veA1	VIIIR	in most strains, exceptions indicated by veA^{+}	X of A4→A26 (*biA1;veA1*)		X	none
WHITE CONIDIA						
wA1	IIL	A38	wild type of Yuill(1936)	--	S	none
wA2	IIL	A75, A344 & others	*yA2(*veA^{+}*)*	A647?	X	T1(III→VIII;IV)
wA3	IIL	A191 & many others	*pabaA1 biA1*	--	S	T1(VI;VII)
wA4	IIL	A69, A436, A439	*biA1;smA1;lysB5*	A66	S	none
wB1	VII	A824	*proA1 pabaA6 adE20 biA1; Dp(IR→IIR)yA2*	--	INAH	
WET-WHITE CONIDIA						
wetA6	VIIR	A580, A581	*biA1*	A26	UV	none
EXTRACELLULAR PROTEASE						
xprD1(areA1)	IIIR	A661	*pabaA1 biA1;trypC801 hisC38*		UV	
YELLOW CONIDIA						
yA2	IR	A71, A83, many more	wild type (*veA*$^{+}$)	A4	X	none
$y^{o}A91$	IR	A425, A445 & others	*biA1;phenA2*	A498	S	none?
YELLOW-GREEN CONIDIA						
ygA1	IIR	A270, A706	*biA1*	A26	S	none

II. *A. nidulans* Aberration Strains

1. Translocation strains

T2(I;III) : A605, A828
T1(I;IV) : A260
T1(I;VII) : A1, A129, A354, A430, A438
T2(I;VII) : A355
T1(I;VIII) : A125, A304, A352
T2(I;VIII) : A398, A431, A434
T1(II;III) : A111, A414
T1(II;IV) : A345
T1(II;VII) : A50, A429
T1(III;VII) : A395, A418, A447

T2(III;VII) : A843
T3(III;VII) : A847
T1(III→VIII) : A309, A212
T1(III→VIII;IV) : A647
T1(IV;VIII) : A250, A276, A435, A470
T1(V;VI) : A40, A370, A373, A518, A521
T2(V;VI) : A333
T1(V;VIII) : A316, A372, A413
T1(VI;VII) :A27, A29, A36, A482, A519, A520
T2(VII→II) : A844

2. Other aberration strains

a. aberration induced simultaneously with *adE20* and *T1(II;VII)*? : A50, A428, A429

b: *T1(VI;VII) T1(III→VIII)* strains : A3, A64, A215, A291, A292, A693, A694, A718
c. intrachromosomal aberrations : A261, A382
d. *T1(I;V;VII;VIII)* - possibly related to *T2(I;VII)* : A347* A348
e. *Ab(VI)* : A38, A350, A638, A795

* A347 derived via vegetative transfer from A348 which is translocation-free, but may have a minor duplication, originating in crosses with *T1(III→VIII).*

3. Duplication strains and derivatives

Dp(I→II) - segment of IR, distal to *pabaA* translocated to IIL : A228,A229,A542-A549,A563
Haploid sectors of Dp(loss of duplicated segment) : A595-A600

III. Wild Type Aspergillus Strains (*A. nidulans* unless otherwise indicated)

FGSC no.	Description	FGSC no.	Description
A4	Glasgow wild type	A96	Grindle wild isolate #44
A90	Grindle wild isolate #2	A251	*A. heterothallicus* A #WB5096
A92	Grindle wild isolate #26	A252	*A. heterothallicus* a #WB5097
A94	Grindle wild isolate #36	A732	*A. niger* N400 (=ATCC 9029)
A815	*A. oryzae*	A991	Soil, Birmingham 1962 (A65)
A992	Soil, Birmingham, 1954 (B1)	A993	Polyporus sporophore, 1962 (C31)
A994	Collybia sporophore, 1962 (D34)	A995	Soil, Durham, 1962 (E43)
A996	Soil, Kent, 1962 (F108)	A997	Soil, Cornwall, 1963 (G143)
A998	Soil, Kent 1962, (H109)	A999	Soil, Edgebaston, 1962 (I66)
A1000	Compost, Birmingham, 1962 (J67)	A1001	Compost, Birmingham,1962(K68)
A1002	Soil, Pembroke, 1962 (L80)	A1003	Soil, Pembroke, 1962 (M85)
A1004	Soil, Cambridgeshire, 1962 (N89)	A1005	Soil, Warwickshire, 1962 (Q106)
A1006	Soil, Portsmouth, 1962 (R99)	A1007	Soil, Pembrokeshire, 1962 (U114)
A1008	Soil, Devon, 1962 (V154)	A1099	*A. niger* Lemore
A1100	*A. fumigatus* (AF293)	A1120	*A. flavus* NRRL 3357
A1121	*A. niger* (NRRL 3)	A1141	*A. fumigatus* WVU1943
A1142	*A. fumigatus* WVU 2026	A1143	*A. niger* NRRL 3 (from DOE)
A1144	*A. niger* NRRL 328 (from DOE)		
A1163	*A. fumigatus* CEA10		

IV. *A. nidulans* Mitotic and Meiotic Mapping Strains

Mitotic mapping strains (see main stock list for genotypes- 43 strains)

A44, A68, A70, A79, A104, A105, A146, A154, A155, A159, A163, A283, A288, A374, A375, A407, A477, A478, A480, A526, A591, A614, A615, A616, A617, A618, A641, A643, A743, A745, A760, A761, A763, A782, A783, A784, A785, A786, A787, A788, A818, A866, A867

Meiotic mapping strains (usually 4 or more markers- 69 strains)

Linkage Group I	A71, A87, A121, A193, A208, A275, A362, A363, A376, A432, A439, A463 A466, A475, A479, A483, A494, A507, A515
Linkage Group II	A239, A254, A268, A338, A505, A864
Linkage Group III	A423, A456, A457, A458, A471, A490, A496, A516, A789, A790, A791, A792
Linkage Group IV	no T:A512, A517, A639; with *T1(IV;VIII)*: A250, A276, A435
Linkage Group V	A258, A491, A495, A504, A508, A613, A865
Linkage Group VI	A459, A464, A794, with *Ab(VI)*:A795
Linkage Group VII	A424, A444, A467, A481, A506, A796
Linkage Group VIII	A269, A380, A401, A442, A484, A516
Main Meiotic Standards	A610, A611, A612

V. Other Special Purpose *A. nidulans* Strains

1. Combinations of color mutants: *yA2, wA3, chaA1, bwA1*
prototrophic, no T : A78, A84, A112-A118, A366 (set of 10 strains)

2. Pairs of strains for diploids with all homologues marked:
A159/A154; A68/A154; A283/A154; A465/A480; A477/A480; A513/A480; A591/A592; A593/A594; A743/A592

3. Strains for teaching, mitotic recombination or "mutagenesis" diploids:
A550/A515; A475/A477; A591/A592; A593/A594; A743/592; A818/819; A283/817

4. Set of strains for control, T/+ and T/T strains
a) *T1(I;VII)* : A424 (no T); A430 (T); A438 (T); A439 (no T)
b) *T2(I;VIII)* : A432 (no T); A431 (T); A434 (T); A433 (no T)

5. Strains for triploid: A475//A473/A480

6. Strains for diploids to map centromeres:

Linkage Group I	:A475/A474 or A550 A476/A474 or A550 A479/A476 or A474 or A550 A363/A477 or A154
Linkage Group II	:A338/A480
Linkage Group III	:A457/A458
Linkage Group IV	:A517/A476
Linkage Group V, *T1(V;VI)/T*	:A518/A370 or A521
Linkage Group VI	:A464/A377
Linkage Group VII, *T1(VI;VII)/T*	:A519/A520

7. Strains for teaching meiotic recombination: *w, cha* and green strains ± *AcrA1*:
A188, A205, A222, A356, A359, A360, A452

8. Strains for mutant selection by biotin starvation with *biA1*:
A26, A194, A357, A378, A391, A392

9. Back cross strains: Standard in Montreal

a. (*veA*$^+$)	BC VIII	A17, A18, A80, A81 A82, A83, A126	a. = back crosses of *adG14 proA1 pabaA1 yA2;wA3*
	BC IX	A343	
b. (*veA1*)	BC V	A360, A365	b. = back crosses of *yA2;AcrA1;lysB5;chaA1*
	BC IV	A204, A205	
c. (*wA3;chaA1*)	BC V	A222, A223	c. = crosses between strains of a. and b.
(*wA3;cha*$^+$)		A221	

10. Unmapped *rec*$^-$ mutants induced in A542 (Dp strain YP 511 of Y. Parag):

rec$^-$ mutants	Original Duplication strains		Derived spontaneous haploids	
rec-402 YP 2(3)	YP528	A543	M2826	A597
rec-408 YP 8(3)	YP529	A546	M2827	A598
rec-412 YP B2	YP533	A549	--	--
rec-444 YP44(3)	YP530	A548	M2828	A599
rec-469 YP69(3)	YP531	A544	M2829	A600
rec-471 YP71(3)	YP532	A547	YP532y	A562
Hyper-*rec* mutant				
uvsB413 YP popB13	YP511A (lost)	--	YP511Ay	A561

11. Temperature sensitive mutant set:

The FGSC has received a set of 1150 *A. nidulans* Temperature Sensitive mutants from Drs. S. Harris and J. Hamer. These are described in Harris et al. Genetics 136:517-532 (1994). Please contact the FGSC for more information.

VI. NUMERICAL LISTING OF ASPERGILLUS STOCKS

Other lists of stocks include those given by Barratt, et al. 1965 (Genetics 52:233-246 [1] and [2] refer to Figures therein), Barratt (Aspergillus News Letter 11:23-24) and Dorn, 1967 (Genetics 56:619-631). Numbers in parentheses refer to Figures in Käfer, 1965 (Genetics 52:217-232). Numbers with an "A" prefix (e.g. A26) in origin column refer to FGSC stock number. All strains are *A. nidulans* unless noted otherwise.

FGSC#	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A1	*biA1;ssbA1;choA1 T1(I;VII)*		M7	UV of A26
A2	*biA1;sA4*	none	M27	UV of A26
A3	*biA1;wA3;sA6 T1(III→VIII);T1(VI;VII)?*		M29	UV of A51
A4	Glasgow wild type (*veA*$^+$)	none	M139	Yuill, 1950
A11	*biA1;AcrA1 wA3;nicC10*		G0119	UV of A123
A14	*yA2;thiA1 T(III→VIII;IV) (veA*$^+$*)*		M420	X of *yA2,veA*$^+$*T(III→VIII;IV)*
A17	*adG14;(veA*$^+$*)*		M635	BC VIII[1]
A18	*adG14 yA2(veA*$^+$*)*		M640	BC VIII[1]
A23	*pabaA1 yA2;chaA1*	none	M755	Cross 507
A24	*sC12;(veA*$^+$*)*		M801	NM of A4
A26	*biA1;veA1*	none	M804	X of A4
A27	*pabaA1 biA1;wA3 T1(VI;VII)*		M805	X of A26 and S
A28	*pabaA6 biA1*	none	M807	UV of 26
A29	*pabaA1 biA1;coA1 T1(VI;VII)*		M809	X of A26 and S
A31	*anA1 biA1**	none	M812	UV of A26
A32	*proA1 biA1*	none	M813	UV of A26
A33	*biA1;pyroA4*	none	M815	UV of A26
A34	*biA1;methH2**	none	M818	UV of A26
A35	*adG14 biA1;pA2*	none	M820	S in A37
A36	*pabaA1 yA2;AcrA1;coA1 T1(VI;VII)*		M822	S in *pabaA1* *yA2;coA1;T1(VI;VII)*
A37	*adG14 biA1*	none	M823	UV of A26
A38	*wA1;lysA1 AbVI? (veA*$^+$*)*		M829	X of *wA1*
A40	*biA1;sA1 T1(V;VI)*		M837	UV of A26
A41	*biA1;sB3*	none	M834	UV of A26
A42	*adE8 biA1**	none	M851	UV of A26
A43	*biA1;ornA4*	none	M232	UV of A26
A44	*suA1adE20 adE20 biA1;AcrA1;phenA2; pyroA4;lysB5;sB3;choA1;coA1 chaA1*	none	M857	Cross 474[2]
A45	*proA5 biA1*	none	M861	UV of A26
A46	*adF15 biA1*	none	M862	UV of A26
A47	*suA1adE20 adE20;pyroA4*	none	M864	S in A227
A50	*adE20 biA1 T(II;VII) Ab?*		M871	UV of A26
A51	*biA1;wA3 T(III;VIII); T(VI;VII)*		M879b	yA2;adC1x pabaA1biA1;wA3
A52	*biA1;thiA4*	none	M882	UV of A26
A55	*luA1 biA1*	none	M892	UV of A26
A56	*biA1;ornB9*	none	M893	
A57	*yA2;pyroA4;malA1*	none	M895	UV of A220
A59	*yA2;frA1 pyroA4 T1(IV;VIII)*		M897	UV of A220
A64	*biA1;wA3 riboE6 T1(III→VIII);T1(VI;VII)*		M903b	UV of A51
A66	*biA1;smA1;lysB5*	none	M905	UV of A26
A68	*suA1adE20 yA2 adE20;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;riboB2*	none	M911	Cross of Forbes:MSD
A69	*biA1;wA4;smA1;lysB5*	none	M912	S in A66
A70	*suA1adE20 adE20 biA1;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;chaA1*	none	M915	C 434 [2]
A71	su*A1adE20 riboA1 pabaA1 yA2 adE20;AcrA1 wA2*	none	M59	C KK[3]
A72	*adG14 proA1 pabaA1 yA2;wA3*	none	M140	BC I [1]
A74	*adG14 proA1 pabaA1 yA2;wA3;(veA*$^+$*)*	none	M387	BC II of A72
A75	*suA1adE20 adE20 biA1;wA2;ssbA1;choA1;chaA1*	none	M391	C 362 [2]
A77	*suA1adE20 yA2;methG1;bwA1;chaA1*		M544	C 314 [2]

* Contain UV induced morphological mutation

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A78	*wA3* (may carry *suA1adE20, yA2* and/or *chaA1)*	none	M552	C 419 [1]
A79	*suA1adE20 pabaA1 yA2 adE20;cnxE16;sC12; pyroA4;nicA2;sB3;choA1;chaA1*	none	M626	C 400 (4)
A80	*adG14 proA1 pabaA1;(veA*$^+$*)*	none	M632	BC VIII[1]
A81	*adG14 pabaA1 yA2;(veA*$^+$*)*	none	M639	BC VIII[1]
A82	*pabaA1 yA2;(veA*$^+$*)*	none	M641	BC VIII[1]
A83	*yA2;(veA*$^+$*)*	none	M643	BC VIII[1]
A84[†]	*yA2;chaA1*	none	M701	C 419 [1]
A87	*riboA1 adG14 proA1 pabaA1 yA2*	none	M841	C X [2]
A89	*biA1;argB2*	none	G034	UV of A26
A90	Grindle wild isolate 2		2 (MG)	
A91	Grindle white spores		2w (MG)	UV of A90
A92	Grindle wild type 26		26 (MG)	
A93	Grindle yellow spores		26y (MG)	UV of A92
A94	Grindle wild type 36		36 (MG)	
A95	Grindle white spores		36w (MG)	UV of A94
A96	Grindle wild type 44		44 (MG)	
A97	Grindle yellow spores		44y (MG)	UV of A96
A104	*yA2 adE20;AcrA1;phenA2;pyroA4;lysB5; sB3;nicB8;coA1*	none	M301	C 282 (4)
A105	*biA1;AcrA1 wA3;phenA2;pyroA4; lysB5;sB3;nicB8;coA1*	none	M276	C 280 (4)
A108	*adE20 biA1;wA2 cnxE16;sC12;methG1; nicA2;choA1;chaA1*	none	M455	C 349
A111	*proA2 biA1 T1(II;III)*		M233	UV of A26
A112†	*yA2;bwA1*	none	M545	set of protrotroph (not *veA*$^+$) color mutants from C 419 (includes A78 A84 and A36)
A113†	*bwA1*	none	M546	
A114†	*bwA1;chaA1*	none	M547	
A115†	*wA3;bwA1*	none	M548	
A116†	*yA2*	none	M549	
A117†	prototroph, wild type color (no *veA*$^+$)	none	M550	
A118†	*chaA1*	none	M551	
[†] May contain *suA1adE20*				
A120	*pabaA1 yA2 adE20;AcrA1;coA1*	none	M286	C 281 (4)
A121	*suA1adE20 riboA1 proA1 pabaA1 adE20;chaA1*	none	M310	C 300
A122	*riboA1 yA2;nicB8*	none	M15a	C 4
A123	biA1;Acr1;wA3		M74	C69
A125	*riboA1 biA1;AcrA1;pyroA4;sB3;nicB8 T1(I;VIII)*		M78	C 62 [6]
A126	*pabaA1 yA2;wA3;(veA*$^+$*)*	none	M740	BC VIII [1]
A129	*pabaA1 yA2 adE20;choA1 T1(I;VII)*		M260=M96	C 103
A139	*adE20 biA1;wA3;methG1 pyroA4*	none	M180	C 235
A146	*pabaA1;AcrA1;phenA2;pyroA4;lysB5; sB3;nicB8;riboB2 chaA1*	none	M927	C 434 [2]
A147	*AcrA1;lysB5;sB3;chaA1*	none	M940	C 434 [2]
A148	*suA1adE20 pabaA1 yA2 adE20;lysB5*	none	M951	C 461 [2]
A154	*adE20 biA1;wA2 cnxE16;sC12;methG1; nicA2;lacA1;choA1;chaA1*	none	M1043	C 500
A155	*suA1adE20 pabaA1 yA2 adE20;AcrA1;phenA2;*	none	M1056	C 474 [2]
A158	*riboA1 biA1 (*abnormal for penicillin synthesis*)*	none	M827	UV of A26
A159	*suA1adE20 pabaA1 yA2 adE20;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;riboB2*	none	M1295	C 283 (4)
A163	*suA1adE20 yA2 adE20;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;coA1*	none	M300	C 282 (4)
A168	*suA1adE20 adE20 biA1;ssbA3;sB3;choA1;chaA1*	none	M878	C 75
A173	*suA1adE20 pabaA1 yA2 adE20;phenA2;nicB8*	none	M947	C 461 [2]
A183	*riboA1 pabaA1 yA2;wA3*	none	M1072	C 630 [1]
A186	*riboA1 pabaA1 biA1*	none	M1078	C 630 [1]

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A187	*pabaA1 yA2*	none	M1079	C 630 [1]
A188	*riboA1;wA3*	none	M1085	C 640 [1]
A191	*wA3*	none	M1088	C 640 [1]
A192	*adG14*	none	M1090	C 639 [1]
A193	*riboA1 adG14 pabaA1 yA2;wA3*	none	M1202	C 637 [1]
A194	*yA2 biA1*	none	M1205	C 638 [1]
A201	*anA1*	none	M1243	C 758 [1]
A202	*riboA1 anA1*	none	M1244	C 758 [1]
A204	*AcrA1;chaA1*	none	M1240	C 751 [1]
A205	*AcrA1;lysB5*	none	M1241	C 751 [1]
A206	*riboA1 adG14 yA2*	none	M1250	C 758 [1]
A208	*suA1adE20 riboA1 proA1 pabaA1 adE20; choA1;chaA1*	none	M279	C 300
A211	*biA1;wA3;galA1*	none	RR-10	Cross by Roberts
A212	*galD5 biA1;wA3; (T1 III→VIII)*		RR-6	Cross by Roberts
A213	*galD5 biA1;wA3; (T1(VI;VII)*		RR-7	Cross by Roberts
A214	*biA1;wA3;galE9*	none	RR-31	Cross by Roberts
A215	*biA1;wA3;galB3; T1(III→VIII);T1(VI;VII)*		RR-13	UV of A51
A216	*adA55*		AM-55 (RG)	UV of green prototroph from cross A82^{++} X A34
A217	*adB57*		AM-57 (JMF)	
A218	*adA55 yA2 biA1;AcrA1;riboB2*		A-201	Cross of A216 of JMF
A219	*biA1;methG1*	none	M800	UV of A26
A220	*yA2;pyroA4*	none	M1105	*yA2;sC12* X A33
A222	*AcrA1 wA3;lysB5;chaA1*	none	M1251	Cross 762
A223	*wA3;lysB5;chaA1*	none	M1252	Cross 762
A227	*adE20;pyroA4*		P78 (RHP)	Cross AAA
A228	*yA2 adE$^+$biA$^+$ Dp1(I→II) adE20 biA1*		P575 (RHP)	Duplication from *adE20* cross
A229	*yA2 adE$^+$ biA$^+$Dp1(I→II)yA$^+$ adE20 biA1 pyroA4*		P529 (RHP)	
A230	*yA2;wA2;argA1;(veA$^+$)*		B66 (BWB)	Cross of A344 X *biA1;argA1* (T?)
A231	*riboA1 yA2;ActA1;nicB8*	none likely	B115 (BWB)	UV of A122
A232	*yA2;adD3;sA1 moC96*		B172 (BWB)	
A234	*pabaA1 yA2*	none	A148 (CFR)	from cross by JMF
A235	*pabaA1 yA2;trypA69*		A148 (CFR)	UV of A234
A236	*trypB403 pabaA1 yA2*		A148 (CFR)	UV of A234
A237	*pabaA1 yA2;trypC801*		A148 (CFR)	UV of A234
A238	*pabaA1 yA2;trypD432*		A148 (CFR)	UV of A234
A239	*biA1;adH23 AcrA1 wA3;nicB8*	none	M6	Cross 59
A241	*biA1;pacA1*		(GD)	Recomb. as A243
A242	*biA1;pacC5*	none	(GD)	UV of A26
A243	*biA1;palA1*		(GD)	Recombinants, UV induced in *rA1 biA1* & separated from *rA1* in crosses
A244	*biA1;palB7*		(GD)	
A245	*biA1;palD8*		(GD)	
A247	*biA1;palF15*		(GD)	
A248	*biA1;palcA1*		(GD)	
A249	*biA1;sD50 T2(I;VIII)*		(GD)	
A250	*yA2;frA1 palC4 pabaB22 pyroA4 T1(IV;VIII)*		(GD)	Cross by GD
A251	*A. heterothallicus*		WB5096	Wild types of Raper
A252	*A. heterothallicus*		WB5097	
A254	*biA1;AcrA1 wA3 ileA3 cnxE16 adD3*	none likely	(GD)	Cross of E. Forbes
A256	*pabaA1;wA3;argC3 facB101 riboB2*		(GD)	Cross of E. Forbes
A257	*biA1;AcrA1 wA3;nicB8;hisC38*		(GD)	UV of T-free strain of J. Foley
A258	*nicA2 hxA1 riboD5*		(GD)	Cross of Darlington
A259	*biA1;adC1;sC12;pyroA4*	none	(GD)	Cross R (2)
A260	*biA1;phenA3;nirA14 T1(I;IV)*		(GD)	S in *biA1;phenA3;T1(I;IV)*

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A261	*biA1;AcrA1 wA3 anB2 (Ab likely)*		(GD)	UV of A123
A262	*biA1;uY5*		(GD)	DES of A26
A263	*biA1;ornB20*	none	(GD)	UV of A26
A264	*biA1;uaX10*		(GD)	DES of A26
A266	*biA1;cnxB50*	none	(GD)	UV of A26
A268	*yA2;wA2 thiA4 cnxE16 adD3 blA1*		(GD)	Cross of Apirion
A269	*pabaA1;tsD15 fwA2 facB101 riboB2*		(GD)	Cross of Forbes
A270	*biA1;ygA1*	none	(GD)	S in A26
A272	*yA2;pyroA4;methB3*		(GD)	UV of A220(CFR)
A273	*adF17 pabaA1 yA2;fpaD11*		(GD)	mutant of Sinha
A275	*fpaA1 adG14 pabaA1 yA2*		(GD)	Cross of McCully
A276	*yA2;frA1 pabaB22 pyroA4 T1(IV;VIII)*		(GD)	Cross of Siddiqi
A277	*yA2 biA1;AcrA1;hisA10;riboB2*		(GD)	UV induced in T-free strain of JMF
A278	*yA2 biA1;AcrA1;riboB2 hisH13*		(GD)	
A279	*yA2;pyroA4;aaX1*		(GD)	induced in A220(?)
A280	*clA6 proA1 pabaA1 yA2;palB7*		(GD)	Cross of Apirion
A281	*biA1;suA1palB7 palB7*		(GD)	S in A244
A282	*biA1;suC6palF15;palF15*	none?	(GD)	S in A247
A283	*suA1adE20 yA2 adE20;AcrA1;galA1; pyroA4;facA303;sB3;nicB8;riboB2*	none	(GD)	MSF of McCully
A284	*biA1;suB2palB7;palB7*	none?	(GD)	S in A244
A285	*biA1;adI50*	none	(GD)	UV of A26
A286	*riboA1 biA1;fpaC43*	none likely	(GD)	S in A158
A287	*biA1 suD2palA1;palA1*	none?	(GD)	S in A243
A288	*suA1adE20 yA2 adE20;wA3;galA1;pyroA4; facA303;sB3;nicB8;riboB2*	none	(GD)	MSE of McCully
A291	*biA1;wA3;galC4 T1(III→VIII);T1(VI;VII)*		(CFR)	UV of A51
A292	*biA1;wA3 lacB3 T1(III→VIII);T1(VI;VII)*		(CFR)	NA of A51
A293	*lysF88 biA1;sB3*	none likely	(GD)	NA of A41, Pees
A294	*biA1;sB3;lysD18*	none likely	1B (GD)	NA of A41, Pees
A295	*biA1;ileA1;sB3*	none likely	IVC10 (EP)	NA of A41
A296	*biA1;lysE13;sB3*	none likely	ID1 (EP)	NA of A41
A297	*lysF51 biA1;sB3*	none likely	IE1 (EP)	NA of A41
A298	*biA1;lysE14;sB3*	none likely	ID2 (EP)	NA of A41
A299	*biA1;sB3;hisJ122*	none likely	IIC2 (EP)	NA of A41
A300	*biA1;sB3;lysD7*	none likely	IB2 (EP)	NA of A41
A301	*biA1;lysE231;sB3*	none likely	(EP)	NA of A41
A303	*proA1 yA2;AcrA1 T1(VI;VII)*		P129 (RHP)	Cross of RHP
A304	*proA1 pabaA1 yA2;phenA2 T1(I;VIII)*		P97 (RHP)	Cross 2(6)
A305	*proA2 pabaA18 biA1;phenA2;lysB5*		P138 (RHP)	Cross of RHP
A306	*adF17 pabaA1 yA2*		P112 (RHP)	Cross of RHP?
A307	*proA1 pabaA1;nicB8*		P87 (RHP)	Cross of RHP?
A308	*pabaA18 biA1*	none?	P115 (RHP)	UV of A26?
A309	*proA2 pabaA18 yA2 T1(III→VIII)*		P117 (RHP)	Cross of?
A310	*proA1 biA1;AcrA1;pyroA4*	none	P254 (RHP)	Cross 38 (3)
A311	*adE20 biA1;wA2;nicA2 riboD3*		P12 (RHP)	Cross of RHP
A312	*suA1adE20 yA2 adE20;AcrA1;phenA2;lysB5*		P20 (RHP)	Cross of RHP?
A314	*proA1 pabaA1 yA2;wA3 adC1;(veA*$^{+}$*)*	none	M821	C M811 x M813
A315	*adG14 pabaA1 yA2*	none	M825	Cross V (2) of Pontecorvo
A316	*biA1;sA2 T1(V;VIII)*		M845	UV of A26
A317	*biA1;nicB8 (*Contains UV induced morphological mutation*)*	none	M873	UV of A26
A319	*anA1 yA2;wA3 adC1;sC12*	none	M1128	Cross n, EK
A320	*suA1adE20 riboA1 proA1 adE20 biA1;pyroA4*		(GD)	Cross g, EK
A326	*biA1;methG1;flA1*		(JLA)	mutant in A219?
A327	*adE20 biA1;wA3;methG1 pyroA4;uvs-5*	none?	(RWT)	UV of A139
A329	*adE20 biA1;wA3;uvsH4 methG1 pyroA4*	none?	(RWT)	UV of A139
A330	*adE20 biA1;wA3;uvsH77 methG1 pyroA4*	none?	(RWT)	UV of A139

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A333	*pabaA108 biA1;uvsB110 T2(V;VI)*		UT501 (GJOJ)	UV of *pabaA108 biA1*
A334	*pabaA108 biA1;uvsC114*		UT503 (GJOJ)	UV of *pabaA108 biA1*
A335	*proA1 pabaA125 biA1;pyroA4;uvsD153*		UT517 (GJOJ)	UV of *proA1 pabaA125 biA1;pyroA4*
A337	*riboA1 biA1;wA3 thiA4 cnxE16*	none	M23	C 50
A338	*yA2;wA3 puA1 cnxE16 adC1 acrB2*		M94	C 85
A339	*suA1adE20 pabaA1 yA2 adE20;sA4*	none	M146	C 136
A340	*proA1 biA1;phenA2;pantoA1 T1(III→VIII;VII)*		M347	C 243
A341	*suA1adE20 proA1 pabaA1 yA2 adE20;*	none	M426	C 347
A342	*suA1adE20 adE20 biA1;AcrA1;choA1 chaA1*	none	M771	C 365
A343	*adG14 proA1 pabaA1 yA2;wA3;(veA*$^{+}$*)*	none	M799	BC IX of A72
A344	*yA2;wA2 adC1;sC12;(veA*$^{+}$*)*	none	M814	C J (2)
A345	*biA1;sC12;pyroA4 T1(II;IV)*		M854	Cross (2)
A346	*biA1;AcrA3 adC1;sC12;pyroA4*	none	M875	S in A259
A347	*anA1 adE20 biA1;wA2;lysB5 T(I;V;VII;VIII)*		M900	S in A348
A348	*anA1 adE20 biA1;wA2;lysB5*	none	M921	C 512
A349	*adE20 biA1;lacA1;choA1;chaA1*	none	M917	C 496
A350	*biA1;phenA2;lysA1 (Ab VI) sB3*		M918	C 346
A352	*riboA1 adG14 yA2;phenA2 T1(I;VIII)*		M962	C 2 (6)
A353	*biA1;ornB9 riboB2*		M966	C 494
A354	*AcrA1;lysB5;T1(I;VII)*		M1014	C 515
A355	*anA1 adE20 biA1;wA2;lysB5;T2(I;VII)*		M1054	C 542b
A356	*riboA1 biA1*	none	M1076	C 630 [1]
A357	*biA1;wA3*	none	M1089	C 640 [1]
A358	*riboA1 adG14 proA1 yA2;ornA4*		M1101	C 3
A359	*pabaA1;wA3*	none	M1231	C 639 [1]
A360	*AcrA1;lysB5;chaA1*	none	M1239	C 752 (BC V)
A361	*riboA1 yA2*	none	M1265	C 630 [1]
A362	*riboA1 anA1 adG14 proA1 pabaA1 yA2*	none	M1267	C 773
A363	*suA1adE20 riboA1 anA1 luA1 pabaA1 yA2 adE20 biA1;AcrA1*	none	M1274	C 792
A364	*suA1adE20 proA2 yA2 adE20;AcrA1 wA2*	none	M1277	Dipl. 629
A365	*yA2;AcrA1;lysB5;chaA1*	none	M1279	C 752 (BC V)
A366	*yA2;bwA1;chaA1*	none likely	M1282	C 789
A367	*suA1adE20 proA1 yA2 adE20;AcrA1 wA2*	none likely	M1285	Dipl. 628
A368	*riboA1 yA2;sA2*	none	M1301	C 785
A369	*pabaA1 biA1;sB3*	none	M1303	C 788
A370	*adG14;sA1;pyroA4;chaA1;T1(V;VI)*		M1309	C 838
A371	*AcrA1;lysB5;fwA2*	none	M1318	S in A205
A372	*biA1;sA2;chaA2 T1(V;VIII)*		M1319	S in A316
A373	*anA1;sA1;lysB5;chaA1;T1(V;VI)*		M1324	C 838
A374	*suA1adE20 yA2 adE20;AcrA1;sA4;pyroA4; pA2;lacA1;nicB8;riboB2*	none	M1335	C 569
A375	*suA1adE20 adE20 biA1;AcrA1;sA4;pyroA4; pA2;lacA1;nicB8;riboB2*	none	M1343	C 569
A376	*suA1adE20 lysF88 pabaA1 yA2 adE20*	none	M1346	C 841
A377	*riboA1 yA2 adE20*	none	M1368	C 847
A378	*biA1;fwA1*	none	M1370	S in A26
A379	*ornB7 fwA1(veA*$^{+}$*)*		M1371	Cross of AJC
A380	*lysB5;fwA2 cnxB2 facB101 palB7 chaA1*	none	M1373	C 804
A381	*cnxB2 palB7*	none	M1376	C 804
A382	*yA2;adH23 AcrA1 wA3 anB2*	none	M1383	Cross of AJC
A383	*riboA1;AcrA1;sB25;chaA1*		M1398	NG of M1421
A384	*riboA1 yA2;sC22*	none?	M1400	NG of riboA1;yA2
A385	*biA1;sE15*	none?	M1402	NG of A26
A386	*proB94;(veA*$^{+}$*)*	none?	M1414	UV of A4

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A387	*fpaA91 proA11 yA2;pyroA4*		M1415	NG of orig *proA11*
A388	*biA1;pyroA4;sF211*	none?	M1433	NG of A33
A389	*uvsF201 pabaA1*	none	M1444	C 915
A390	*fpaA91 pabaA1 biA1;pyroA4*	none	M1447	C 883
A391	*biA1;chaA1*	none	M1466	C 843
A392	*yA2 biA1;chaA1*	none	M1469	C 843
A393	*suA1adE20 proB94 yA2 adE20;AcrA1 wA2*	none	M1474	Dipl 860
A394	*biA1;phenB6*	none?	M1490	UV of A26
A395	*biA1;smsA61;sB3;lysD20 T1(III;VII)*		M1493	UV of A41
A397	*pantoB100*		M1498	UV?(BMR)
A398	*biA1;lysB5;sD50 T2(I;VIII)*		M1500	C 980
A399	*facB101 riboB2 sE15*	none	M1503	C 898
A400	*yA2 adE20;AcrA1;sF211 palF15 choA1*	none?	M2281	C 2116
A401	*facB101 riboB2 palB7 chaA1 sE15*	none likely	M1581b	C 1932
A402	*phenA3;palB7 chaA1 nirA14*	none likely	M1626	C 1045
A403	*pabaA1;wA3;pyroA4;sF211*	none likely	M1631	C 966
A404	*biA1;AcrA1 wA3;sA49;lysB5*	none likely	M1641	C 1164
A405	*pabaA1 yA2;sA91*	none likely	M1643	C 1166
A406	*luA1 yA2*	none	M1824	C 1605
A407	*adE20 biA1;AcrA1;phenA2;pyroA4;lysB5;lacA1;choA1;riboB2 chaA1*	none	M1832	C 1608
A408	*pabaA1 yA2;wA3*	none	M1849	C 1621
A409	*pabaA1;facB101 chaA1*	none?	M1854	C 1701
A410	*pabaA1 biA1;riboB2 chaA1*	none	M1869	C 434
A411	*proA1 pabaA1 yA2*	none	M1885	C 1709
A412	*pabaA1 yA2;ActA1*	none	M1897	C 1649
A413	*pabaA1;sA2;chaA2 T1(V;VIII)*		M1907	C 1708
A414	*riboA1 proA2 yA2;ActA1 T1(II;III)*		M1937	C 1760
A415	*riboA1 proA2 biA1;ActA1*	none	M1940	C 1760
A416	*riboA1;chaA1*	none	M1941	C 1754
A417	*pabaA1;sA1;chaA1*	none	M1942	C 1754
A418	*pabaA1 yA2;lysD20 T1(III;VII)*		M1944	C 1732
A419	*biA1;sD85*	none	M1951	NG of A26
A420	*pabaA1;sD157 facB101*	none	M1986	C 1801
A421	*riboA1;sD85*	none	M1987	C 1794
A422	*fpaB37 riboA1 biA1*	none	M1990	S in A158
A423	*riboA1 proA1 yA2;sC12 phenA2 suB4pro*	none	M1998	C 1846
A424	*suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;AcrA1;pyroA4;phenB6 sF211 malA1 nicB8;chaA1*	none	M2006	C 1530
A425	y^{o}*A91 biA1;phenA2*	none	M2012	S in A498
A426	*yA2;pabaB22 pyroA4*	none	M2023	C 1783
A427	*pabaA1;AcrA1;sD85 facC102*	none	M2027	C 1802
A428	*pabaA1 adE20 biA1*	none, other Ab?	M2032	C 1716
A429	*pabaA1 adE20 biA1 T(II;VII) Ab?*		M2033	C 1716
A430	*suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;pyroA4;phenB6 sF211 malA1;chaA1 T1(I;VII)*		M2039	C 1530
A431	*galD5 suA1adE20 riboA1 adE20 biA1;sD50 T2(I;VIII) fwA2 facC102*		M2054	C 1808
A432	*galD5 suA1adE20 riboA1 adE20 biA1;AcrA1;fwA2 facB101*	none	M2055	C 1809
A433	*fpaB37 SulA1 anA1 pabaA1 yA2 adE20;pyroA4;cnxB2 chaA1 T1(VI;VII)?*		M2056	C 1822
A434	*fpaB37 anA1 pabaA1 yA2 adE20;sD50 T2(I;VIII) cnxB2 chaA1 (galC7?)*		M2057	C 1822
A435	*frA1 T1(IV;VIII) palC4 pabaB22 pyroA4;chaA1*		M2070	C 1911
A436	*adE20 biA1;wA4;smA1;lysB5*	none	M2071	C 1914
A437	*proA1;wA3;nicA2;malA1*	none	M2072	C 1923

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A438	*fpaA91 anA1 adE20 biA1;wA2;lysB5;chaA1 T1(I;VII)*		M2074	C 1519
A439	*fpaA91 anA1 adE20 biA1;AcrA1 wA4;ActA1;choA1*	none	M2076	C 1518
A440	*riboA1 yA2;AcrA1;fwA2*	none	M2102	C 1844
A441	*riboA1 proA1 biA1;wA3; sC12 galA1 ActA1 phenA2 suB4pro*	none	M2108	C 1838
A442	*facB101 riboB2 chaA1 sE15 nirA14*	none	M2113	C 1932
A443	*pabaA1 yA2 adE20;AcrA1;suC11adE20;coA1 cnxB2*	none	M2131	S in rec. from 1799
A444	*suA1adE20 yA2 adE20;AcrA1; phenB6 sF211 malA1 choA1 nicB8*	none?	M2132	C 1942
A445	*riboA1 y^{o}A91*	none	M2136	C 1903
A447	*anA1 yA2;wA3;adI50 galA1 ActA1; sF211 lysD20 T1(III;VII) choA1 nicB8*		M2150	C 1736
A448	*proA1;AcrA1;galE9 sA1 adI50 ActA1;chaA1*	none	M2151	C 1868
A449	*AcrA1;lysB5;coA1 cnxB2*	none	M2152	C 1799
A450	*pabaA1 yA2;oliC2*	none?	M2153	S in A187
A451	*pabaA1;meaB6 cnxH3 sC12*	none	M2158	C 332
A452	*SulA1 anA1 pabaA1;wA3;ssbA1 chaA1*	none	M2162	C 1950
A453	*oliC2 pantoB100*	none	M2165	C 1945
A454	*riboA1 proA1 yA2;ActA1 suB4pro*	none	M2167	C 1846
A456	*proA1 yA2;galE9 adI50 methH2 dilA1*	none	M2176	C 1969
A457	*proA1 biA1;galE9 sC12 dilA1 phenA2;choA1*	none	M2186	C 1973
A458	*riboA1 proA1 yA2;AcrA1; adI50 methH2 galA1 ActA1 suB4pro*	none	M2187	C 1972
A459	*suA1adE20 pabaA1 yA2 adE20;AcrA1; lacA1 bwA1 sbA3;sF211*	none	M2198	C 1952
A460	*AcrA1;lysB5 pA2*	none	M2200	C 2128
A461	*proA1 biA1;phenA2;malA1;riboB2*	none	M2204	C 1975
A462	*pabaA1 y^{o}A91;IodA1 cnxE16*	none	M2205	C 1976
A463	*suA1adE20 proB94 lysF88 pabaA1 yA2 adE20;wA2*	none	M2207	C 1985
A464	*suA1adE20 pabaA1 yA2 adE20;AcrA1; lacA1 bwA1 sB3 sbA3*	none	M2209	C 1952
A466	*galD5 suA1adE20 riboA1 anA1 proB94 lysF88 pabaA1 yA2 adE20*	none	M2213	C 2113
A467	*yA2 adE20;lacA1;phenB6 oliC2 sF211 palF15 malA1 choA1 nicB8*	none likely	M2214	C 2116
A468	*SulA1;AcrA1 wA3;galA1;pyroA4;facA303; lacA1 sB3;choA1;riboB2 chaA1*	none	M2216	C 1987
A469	*AcrA1;lysB5;sD85 fwA2*	none likely	M2218	C 1983
A470	*proA1 biA1;methG1 frA1 T1(IV;VIII);chaA1*		M2219	C 1929
A471	*proA1 yA2;meaB6 sC12 methH2 dilA1*	none likely	M2220	C 2108
A472	*riboB2 nir14*	none	M2221	C 1932
A474	*SulA1 adE20;AcrA1;ActA1;choA1;chaA1*	none	M2234	C 2112
A475	*fpaB37 galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1;sD85 fwA2*	none	M2235	Dipl. 2195
A476	*SulA1 adE20;AcrA1 wA3;ActA1; lysB5;choA1;chaA1*	none likely	M2239	C 2112
A477	*SulA1 adE20;AcrA1 wA3;ActA1;pyroA4; lysB5;sB3;choA1;chaA1*	none	M2240	C 2125
A478	*SulA1 adE20;AcrA1 wA3;ActA1;pyroA4 ssbA1;lysB5;sB3;choA1;riboB2 chaA1*	none	M2242	C 2125
A479	*galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1*	none	M2243	C 1523
A480	*proA1 y^{o}A91;IodA1;phenA2;methG1; nicA2;sbA3;malA1;riboB2*	none likely	M2246	C 1974
A481	*yA2 adE20; phenB6 oliC2 sF211 malA1 choA1 nicB8*	none likely	M2247	C 2120

FGSC #	Genotype	Translocation	Depositor's Stock # or initials	Origin of strain or lesion
A482	*bwA1 sbA3;phenB6 oliC2;riboB2 T1(VI;VII)*		M2248	C 2121
A483	*fpaB37 galD5 suA1adE20 SulA1 riboA1 anA1 pabaA1 yA2 adE20 biA1*	none likely	M2255	C 1523
A484	*AcrA1;lysB5;sD85 fwA2 facC102*	none likely	M2256	C 1983
A485	*riboA1 adE20;fwA2*	none	M2259	C 2105
A486	*riboA1 yA2 adE20;methG1 suC11adE20*	none	M2303	C 2134
A488	*pabaA1 yA2;sC12*	none	M2270	C 1762
A489	*riboA1 biA1;dilA1;choA1*		M2271	C 1967
A490	*proA1;meaB6 cnxH3 adI50 dilA1*	none likely	M2272	C 2108
A491	*AcrA1;lysB5 pA2 facA303 hxA1 riboD5*	none	M2310	C 2133
A492	*pabaA1* y^{o}*A91;IodA1*	none	M2274	C 1978
A493	*pabaB22*	none likely	M2276	C 1907
A494	*galD5 suA1adE20 riboA1 yA2 adE20;AcrA1*	none	M2277	C 1951
A495	*lysB5 nicA2 pA2*	none	M2278	C 2127
A496	*pabaA1 yA2;meaB6 adI50*	none likely	M2279	C 2108
A497	*AcrA1;palC4 pabaB22;chaA1*	none	M2280	C 1911
A498	*biA1;phenA2*	none likely	M2013	C 1632
A499	*suA1adE20 pabaA1 yA2 adE20;phenB6 sF211*	none	M2282	C 1951
A500	*biA1;methG1;nicA2;sbA3;malA1*	none	M2283	C 1977
A501	*adE20 biA1;smA1 ActA1*	none	M2284	C 1935
A502	*SulA1;AcrA1;lysB5 facA303;sB3;chaA1*	none	M2285	C 2125
A503	*proA1 yA2;methH2 dilA1*	none	M2286	C 1969
A504	*AcrA1;lysB5 pA2 riboD5*	none	M2287	C 2127
A505	*pabaA1 yA2;AcrA1 wA3 ileA3*	none likely	M2288	C 1642
A506	*AcrA1;phenB6 oliC2 sF211 malA1 choA1 nicB8*	none	M2289	C 2120
A507	*fpaB37 SulA1 anA1 pabaA1*	none	M2295	C 1950
A508	*AcrA1;nicA2 facA303 hxA1 riboD5;sB3;chaA1*	none	M2309	C 2133
A509	*riboA1 adE20*	none	M2203	C 2110
A510	*pabaA1 yA2 adE20;AcrA1;nicA2;sbA3*	none	M2298	C 1955
A511	*SulA1;ActA1;choA1;chaA1*	none	M2325	C 2107
A512	*AcrA1;palC4 pabaB22 pyroA4;chaA1*	none likely	M2307	C 1911
A514	*anA1 adE20 biA1;AcrA1;ActA1;sB3;fwA2*	none	M2356	C 2216
A515	*fpaB37 galD5 suA1adE20 riboA1 yA2 adE20;pyroA4;facA303;chaA1*	none likely	M2313	C 2217
A516	*galE9 meaB6 adI50 ActA1;chaA1 sE15 nirA14*	none?	M2328	C 2124
A517	*riboA1 yA2 adE20;methG1 suC11adE20 palC4 pabaB22 pyroA4*	none	M2316	C 2135
A518	*AcrA1;lysB5 facA303 hxA1;lacA1 sB3 sbA3 T1(VR;VIR)*		M2318	C 2131
A519	*suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;wA2;oliC2 malA1 choA1 nicB8 T1(VIR;VIIR)*		M2319	Dipl. 1955
A520	*pabaA1;AcrA1;sB3 sbA3;phenB6;riboB2 T1(VIR;VIIR*)		M2320	Dipl. 1998
A521	*suA1adE20;AcrA1;galA1;pyroA4;pA2 facA303 riboD5;sbA3 T1(VR;VIR)*		M2321	C 2131
A522	*pabaA1 yA2 adE20;AcrA1;facA303;lacA1 sB3 T1(VR;VIR)*		M2322	C 2131
A523	*biA1;AcrA1;benA17*		33 (JMvT)	UV of *biA1;AcrA1*
A524	*biA1;benA10 fwA1*		5 (JMvT)	Cross *biA1;AcrA1;benA10* X *fwA1 ornB7*
A525	*suA1adE20 yA2 adE20;phenA2;pyroA4;lysB5;nicB8;benA10 fwA1 carB2*		10 (JMvT)	from diploid of JmvT
A526	*suA1adE20 yA2 adE20;wA3;galA1;pyroA4;facA303;sB3;nicB8;benA10 fwA1 carB2*		321 (JMvT)	from diploid of JmvT
A528	*biA1;phenA2 carC9*		125 (JMvT)	JMvT cross
A529	*biA1;AcrA1;ActB2 oliC13 imaA4 benC28 choA1 carA1*		218 (JMvT)	

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A530	*biA1;AcrA1;pimA1*		181 (JMvT)	UV of *biA1;AcrA1*
A531	*pimB10 proA1 pabaA1 yA2*		313 (JMvT)	JMvT cross
A532	*biA1;AcrA1;imaB9*		146 (JMvT)	S in *biA1;AcrA1*
A533	*biA1;AcrA1 imaC10*		147 (JMvT)	S in *biA1;AcrA1*
A534	*biA1;AcrA1;imaD13*		250 (JMvT)	S in *biA1;AcrA1*
A535	*biA1;AcrA1;imaG18*		248 (JMvT)	NG of *biA1;AcrA1*
A536	*biA1;AcrA1;chlA10 imaG18*		305 (JMvT)	UV of *biA1;AcrA1*
A537	*biA1;AcrA1;imaH19*		247 (JMvT)	NG of *biA1;AcrA1*
A538	*yA2;csuA6;sB3;choA1*	none likely		H. Arst cross 255
A539	*biA1 adE20;csuA6;sB3;chaA1*	none likely		H. Arst cross 213
A542	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1*		YP 511 (YP)	Cross of YP 156 X Dp
A543	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-402*		YP 528 (YP)	NG in YP 511
A544	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-469*		YP 531 (YP)	NG in YP 511
A546	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-408*		YP 529 (YP)	NG in YP 511
A547	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-471*		YP 532 (YP)	NG in YP 511
A548	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-444*		YP 530 (YP)	NG in YP 5113/20/1998
A549	*pabaA6 yA2 adE8 biA*$^+$ *Dp(I→II)yA*$^+$*adE20 biA1;rec-412*		YP 533 (YP)	NG in YP 511
A550	*anA1 adE20 biA1;AcrA1;ActA1;sB3;choA1;fwA2*	none	M2358	C 2216
A551	*uaY9*		Black 3 (BRS)	
A552	*hxB13*		Black 4 (BRS)	
A553	*biA1;cnxH3*		Black 5 (BRS)	DES of A26
A554	*hxA1*		Black 7 (BRS)	
A555	*biA1;cnxA5*		Black 29(BRS)	DES of A26
A556	*biA1;cnxE14*		Black 30(BRS)	DES of A26
A557	*biA1;cnxB11*		Black 31(BRS)	DES of A26
A558	*biA1;cnxC*		Black 32(BRS)	DES of A26
A559	*biA1;cnxG*		Black 33(BRS)	DES of A26
A560	*cnxF8*		Black 34(BRS)	
A561	*pabaA6 yA2 adE8;uvsB413*		YP 511 Ay	Loss of duplicated segment from A545
A562	*pabaA6 yA2 adE8;rec-471*	none likely	YP 532y	Loss of duplicated segment from A547
A563	*proA1 pabaA6 yA*$^+$*adE20 biA1 (Del IR); Dp(I→II) yA2 adE*$^+$*biA*$^+$*uvsB110;nicA2 riboD5*		YP 300/2	UV of *Dp(I→II) YP300*
A564	*suA1adE20 yA2 adE20;wA3;galA1; uvsB413;facA303;sB3*	none likely	YP 524	
A565	*yA2;adD3 benB29*		C1465 (HNA)	Strain 309 of JMvT
A566	*pabaA1;benB29*		C1605 (HNA)	Cross *yA2;adD3 benB29* *pabaA1;AcrB14 creB304*
A567	*uvsF201 riboA1 yA2*	none	M1392	UV of A361
A568	*yA2;uvsH77*	none likely	M2346	C 2407
A569	*riboA1;AcrA1;uvsJ1;chaA1*	none likely	M2382	C 2431
A570	*pabaA108 biA1;uvsC114*	none likely	M2393	C 2408
A571	*pabaA125 biA1;uvsD153;fwA2*	none likely	M2398	C 2409
A572	*anA1 biA1;pyroA4;uvsE182*	none likely	M2403	C 2410
A573	*AcrA1;uvsB312 pyroA4;riboB2*		M2435	C 2442
A574	*riboA1 biA1;uvsD308;chaA1*	none likely	M3628	C 2219
A575	*anA1 yA2;AcrA1;uvsH311;fwA2*	none likely	M2457	C 2445
A576	*AcrA1;uvsH304;chaA1*	none likely	M2503	C 2444
A577	*yA2;AcrA1;uvsB110;riboB2 chaA1*	none likely	M2506	diploid 2449

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A578	*pabaA1 yA2;uvsJ1*	none likely	M2522	C 2496
A579	*uvsA101;adD3*		M2527	UV of *adD3*
A580	*biA1;wetA6*	none likely	G0241	UV of *biA1*
A581	*yA2;wetA6 malA1 palD8 nicB8*		G712	Cross Glasgow 0241 X 71
A582	*yA2;niaD15 brlA42 fpaD43*		G816	Cross Glasgow 0248 X *yA2;niaD15 fpaD43*
A583	*biA1;brlA42*	none	G0248	NA of A26
A584	*luA1 stuA1 proA1 yA2*		G134	
A585	*stuA1 biA1*	none	G0256	NA of A26
A586	*medA15 biA1*	none	G0255	NA of A26
A587	*medA15 galD5 riboA1;nicB8*			
A588	*biA1;drkA1*	none	G070	NA of A26
A589	*adH23;abaA14 chaA1*		G830	Cross Glasgow 01 X 82
A590	*biA1;abaA14*	none	G01	NA of A26
A591	*fpaB37 suA1adE20 riboA1 pabaA1 yA2 adE20; AcrA1;galA1 ActA1;pyroA4;facA303;sB3; oliC2 malA1;fwA2*	none	M2626	diploid 2340a
A592	*SulA1 anA1 biA1;wA2 cnxE16;methG1;* nicA2;sbA3;choA1;chaA1	none	M2461	diploid 2477
A593	*fpaB37 suA1adE20 riboA1 pabaA1 yA2 adE20; AcrA1;galA1 ActA1;pyroA4;facA303;sB3; oliC2 malA1;fwA2*	none	M2627	diploid 2340b
A594	*adE20 biA1;wA2 cnxE16;methG1;nicA2; sbA3;choA1;chaA1*	none	M2492	diploid 2478
A595	*pabaA6 yA2 adE8*		M2824	haploid from A542
A596	*pabaA6;yA*$^+$ *adE20 biA1(on II?)*		M2831	haploid from A542
A597	*pabaA6 yA2 adE8;rec-402*		M2826	haploid from A543
A598	*pabaA6 yA2 adE8;rec-408*		M2827	haploid from A546
A599	*pabaA6 yA2 adE8;rec-444*		M2828	haploid from A548
A600	*pabaA6 yA2 adE8;rec-469*		M2829	haploid from A544
A601	*biA1;sA31*	none?	M1456	NG of A26
A602	*biA1;sA130*	none?	M1853	NG of A26
A603	*biA1;sC63*	none?	M2880	NG of A26
A604	*biA1;sC84*	none?	M2881	NG of A26
A605	*biA1;AcrA1;nicA2 T2(I;III)*		M2499	C 2439
A606	*AcrA1;lysD18;riboB2*	none likely	M2750	C 2580
A607	*yA2;ActA1;choA1*	none	M2878	diploid 2600b
A608	*galD5 suA1adE20 anA1 biA1;chaA1*	none	M1996	C 1791
A609	*uvsB413;riboB2 chaA1*	none?	M2838	C 2658
A610	*pabaA1 yA2*	none	M2600	C 1621
A611	*adG14 biA1*	none likely	M2601	C 1621
A612	*AcrA1;riboB2 chaA1*	none likely	M2386	C 2464
A613	*AcrA1;nicA2 pA2 facA303 hxA1 riboD5*	none	M2697	C 2468b
A614	*SulA1 adE20;AcrA1 wA3;ActA1;methG1; nicA2;sbA3;choA1;riboB2 chaA1*	none	M2843	diploid 2365
A615	*SulA1 adE20;AcrA1 wA3;ActA1;methG1; nicA2;lacA1 sB3;choA1;riboB2 chaA1*	none	M2844	diploid 2365
A616	*SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;nicA2;sbA3;choA1;riboB2 chaA1*	none	M2485	diploid 2478
A617	*anA1 adE20 biA1;AcrA1;ActA1;pabaB22 pyroA4;nicA2;sbA3;choA1;fwA2*	none	M2848	diploid 2358
A618	*SulA1 adE20;AcrA1;ActA1 galA1;pyroA4; nicA2;sB3;oliC2 malA1;fwA2*	none	M2851	diploid 2349
A624	*yA2 pabaA1;pycB4*	none?	WG135 (CJB)	UV of A234
A625	*yA2 pabaA1;pycA12*	none?	WG257 (CJB)	UV of A234
A626	*wA3;pyroA4;pdhC2*	none?	WG195 (CJB)	CJB cross
A627	*yA2 pabaA1;pdhC1*	none?	WG107 (CJB)	UV of A234

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A628	*yA2 pabaA1;pdhB2*	none?	WG206 (CJB)	UV of A234
A629	*yA2 pabaA1 pycB5*	none?	WG218 (CJB)	UV of A234
A630	*biA1;pkiA2(ts) nicA2 riboD5*	none?	WG256 (CJB)	CJB cross
A631	*biA1;wA3;pycB4*	none?	WG136 (CJB)	CJB cross
A632	*yA2 pabaA1;pycA2*	none?	WG102 (CJB)	UV of A234
A633	*yA2 pabaA1;pkiA9*	none?	WG193 (CJB)	UV of A234
A634	*yA2 pabaA1;pdhB4*	none?	WG228 (CJB)	UV of A234
A635	*yA2 pabaA1;pdhC2(ts)*	none?	WG194 (CJB)	UV of A234
A636	*pdhA4(ts);wA3;pyroA4*	none?	WG143 (CJB)	UV of A234
A637	*yA2 pabaA1 pdhA1*	none?	WG097 (CJB)	CJB cross
A638	*yA2;lysA1 (AbVI)*	Ab VI	M2558	A350 X A187
A639	*yA2 adE20 biA1;AcrA1;methG1 suC11adE20 pyroA4;chaA1*	none?	M2477	C 2467
A640	*phenB6 pantoB100 sF211 malA1 nicB8*	none?	M2251	C 2120
A641	*suA1adE20 yA2 adE20;AcrA1;galA1;pyroA4; nicA2;sB3;choA1;riboB2*	none	M2574	diploid 2350
A642	*biA1;AcrA1;ActA1;nicA2;sbA3;choA1;chaA1*	none?	M2902	diploid 2344
A643	*proA2 yA2;AcrA1;ActA1;pabaB22 pyroA4; nicA2;sbA3;choA1;riboB2 chaA1*	none	M2974	C 2703
A644	*riboA1 yA2;methH2 dilA1*	none?	M2652	C 2561
A645	*biA1;AcrA1;lysD20 T(III;VII);chaA1*		M2724	C 2586
A646	*biA1 argD11*	none?	G036	UV of A26
A647	*yA2;ve*$^{+}$ *T1(III→VIII;IV)*		G0257	
A648	*biA1;ureD4*		G0286	
A649	*pabaA1 yA2;acuD254*	none?	G0300	UV of A234
A650	*pabaA1 yA2;acuE201*	none?	G0301	UV of A234
A651	*pabaA1 yA2;acuF205*	none?	G0302	UV of A234
A652	*pabaA1 yA2;acuG223*	none?	G0303	UV of A234
A653	*pabaA1 yA2;acuH253*	none?	G0304	UV of A234
A654	*acuJ211 pabaA1 yA2*	none?	G0305	UV of A234
A655	*pabaA1 yA2;acuK248*	none?	G0306	UV of A234
A656	*pabaA1 yA2;acuL217*	none?	G0307	UV of A234
A657	*pabaA1 biA1;melA1*		G0315	
A658	*proB4 pabaA1 biA1*		G137	
A659	*yA2;AcrA1 apnA1 wA3;choA1*		G247	cross 1297 of Arst
A660	*pabaA1;intA*^{C}*2*		G248	cross 445 of Arst
A661	*pabaA1 yA2;xprD1*		G332	
A662	*pantoC3 cnxH3 sC12*		G338	cross 1126 of Arst
A663	*yA2 xprD1 sC250 cnxH3;pantoB100*		G344	
A665	*pantoA10*	none	G853	cross 961 of Arst
A666	*[oliA6] pabaA1 yA2*		G0274	S in R 21
A667	*pabaA1 biA1;melB*^{0}*2*		G0316	UV of *pabaA1 biA1*
A668	*ornC31*		G345	cross 1432 of Arst
A669	*pyroA4;choC3 fwA1*		G852	cross after NG of *pabaA1biA1*
A670	*pabaA1 biA1;AcrA1;facA303;manA1*		G851	NG of *mnrA455*
A671	*biA1;wA7 creC27*		G245	
A672	*yA2;meaA8 pyroA4*		G420	cross after DES of A26
A673	*biA1;facB302 fanD151*	none?	G085	S in *biA1 facB302*
A674	*clB1 yA2;wA2;sC12*		G064	UV of *yA2;wA2;sC12*
A675	*biA1;facA303 fanA3*	none?	G083	S in *biA1 facA303*
A676	*biA1;facA303 fanB52*	none?	G084	S in *biA1 facA303*
A677	*biA1;fanE7*	none	G083	S in A26
A678	*biA1;inoA1*		G0101	UV of A26
A679	*biA1;wA5;inoB2*		G0102	NG of A26
A680	*biA1 ahrA3*		G0275	NG of A26
A681	*luA1 biA1;mauA2*		G0278	NG of *yA2;pyroA4 meaA8*

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A682	*wA3 puA2 mauB4*		G0279	NG of *yA2;pyroA4 meaA8*
A683	*biA1;ureA1*		G0283	
A684	*biA1;ureB3*		G0284	
A685	*biA1;drkB5*	none?	G234	UV of A26
A686	*yA2;methH2 gdhA1 galA1*		G323	A699 X G33
A687	*yA2;wA3;sC12 ivoA1 methH2 argB2 galA1*		G324	
A688	*biA1;pppB1*		G325	NG of A26
A689	*pabaA1 yA2;gdhB1 pyroA4*		G416	NG of A26→X G158
A690	*yA2;pyroA4;lacA1;pppA1*		G840	
A691	*biA1;niaD15*		G0125	NG of A26
A692	*proB3 biA1*		G0165	UV of A26
A693	*pyroB12 biA1;wA3 T1(III→VIII);T1(VI;VII)*		G0187	UV of A51
A694	*biA1;wA3;sucA1 T1(III→VIII) T1(VI;VII)*		G0212	UV of A51
A695	*biA1;telA1*		G0223	S in A26
A696	*biA1;gamA55*		G0265	S in A26
A697	*biA1;gamB65*		G0266	S in A26
A698	*biA1;gamC66*		G0267	S in A26
A699	*biA1 gdhA1*		G0268	NG of A26
A700	*biA1;punA11*		G0277	UV of A26
A701	*biA1;puA2;spsA1*		G0280	NA of *biA1;puA2*
A702	*pabaA1 yA2;sltA1*		G0281	NA of A26→X G158
A703	*anA1 biA1;mecC13*		G0282	UV of *anA1 biA1*
A705	*biA1 sorA2*		G186	
A706	*AcrA1 punA11 ygA6*		G242	G0277 X G233
A707	*biA1;molA67*		G616	S in A26
A708	*wA3;tsB5 sB3 sbA3*		G62	
A710	*yA2; telA1 malA1 palD8 nicB8*		G71	G158 X G617
A711	*yA2;phenB6 pantoB100 malA1 wetA6 methE6 palD8 nicB8*		G716	
A712	*pabaA1 yA2;galH7;palcC4 facB101 riboB2*		G820	
A713	*yA2;pyroA4;niiA4*		G833	
A714	*biA1;fwA1 galG2 facC307*		G836	G835 X G813
A715	*proA1 yA2;hisG113;chaA1*		G0296	UV of *proA1 yA2;chaA1*
A716	*biA1;molB35*		G0271	S in A26
A717	*riboA1 fpaI64 biA1*		G0297	
A718	*biA1;wA3;galF2 T1(III→VIII);T1(VI;VII)*		G097	UV of A51
A719	*biA1;methE6*		G0114	UV of A26
A720	*biA1;tsC17*		G0224	UV of A26
A721	*anA1 pyrF11 luA1 yA2;cnxH4*		G190	
A722	*pyrG89 pabaA1;fwA1 uaY9*		G191	NG of *pabaA1;fwA1 uaY9*
A723	*biA1;pyrD23*		G846	NG of A26
A724	*yA2;wA3;pyroD9 araA1*		G848	
A725	*wA3;pyroA4;tsE6*		G0272	
A726	*biA1;riboF8*		G0196	NA of A26
A727	*proA1 hisB179 yA2;chaA1*	none?	G0294	UV of *proA1 yA2;chaA1*
A728	*yA2;sorB11 cnxH14;pyroA4*		G328	G321 X G319
A729	*pabaA1;brlA42 uaY9 ivoB63*		G841	NG of *biA1 abaA6→X G839*
A732-A742	Section IX, *A. niger* mutants			
A743	*riboA1 pabaA1 yA2;AcrA1;galA1 ActA1; pyroA4;lysB5;sB3;oliC2 malA1;fwA2*		M3207	diploid 2720
A744	*pabaA1 yA2;fluG1*	none?	WM355 (WM)	NG of A234
A745	*SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;nicA2;sbA3;malA1;riboB2 chaA1*	none?	M2486	diploid 26
A746	*biA1;pyroA4;niiA4;amdR*$^{-}$*4*		MH345 (MJH)	
A747	*biA1;creB15*		MH532 (MJH)	
A748	*biA1;niiA4;creA204*		MH664 (MJH)	

FGSC #	Genotype	Translocation	Depositor's Stock # or initials	Origin of strain or lesion
A749	*biA1;niiA4;amdA7;amdI18*		MH767 (MJH)	
A750	*biA1;niiA4;amdI93*		MH1176 (MJH)	
A752	*pabaA1;sB43;alcR125 amdA7; amdI66 amdS1005*		MH2238 (MJH)	
A753	*mecB10 anA1 yA2;cysB102*		AP	S in *yA2;pyroA4;methB3*
A754	*mecB10 anA1 yA2;cysC103*		AP	S in *yA2;pyroA4;methB3*
A755	*yA2;methD10;pyroA4*		AP	UV of *adF9 yA2*
A756	*mecB10 anA1 yA2;cysA1*		AP	UV of *mecA biA1 anA1*
A757	*yA2;methA17;pyroA4*		AP	UV of *adF9 yA2*
A758	*mecB10 proA2 pabaA2 yA2*		AP	UV of *biA1 anA1*
A759	*mecB10 anA1 biA1;AcrA1;phenA2*		AP	UV of *biA1 anA1*
A760	*pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;chaA1*	none	M3171	diploid 2793
A761	*pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;riboB2 chaA1*	none	M3172	diploid 2793
A762	*pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3;choA1;fwA2*	none	M3271	diploid 2800
A763	*pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;fwA2*	none	M3272	diploid 2800
A764	*pyrG89;AcrA1;ActA1;nicA2;sB3;malA1;chaA1*	none	M3174	diploid 2793
A765	*pyrG89 biA1;AcrA1;ActA1;pyroA4;sbA3; choA1;riboB2 chaA1*	none	M3223	diploid 2775
A766	*pyrG89 biA1;AcrA1;ActA1;pyroA4;nicA2;sbA3; riboB2 chaA1*	none	M3224	diploid 2775
A767	*pyrG89;nicA2*	none	M3376	C 2870
A768	*pyrG89 yA2;riboB2 chaA1*	none	M3091	C 2794
A769	*pyrG89;AcrA1;pabaB22;chaA1*	none	M3097	C 2794
A770	*pyrG89;pabaB22;riboB2*	none	M3098	C 2794
A771	*pyrG89 riboA1;wA3;pyroA4*	none	M3104	C 2781
A772	*galD5 pyrG89;AcrA1;chaA1*	none	M3268	C 2795
A773	*pyrG89;wA3;pyroA4*	none	M3338	GR5 of R. Morris
A774	*fpaB37 galD5 pyrG89 yA2 adE20;AcrA1;pyroA4;facA303;chaA1*	none	M3317	C 2819
A775	*fpaB37 galD5 pyrG89 riboA1 anA1;nicA2;sD85*	none	M3361	C 2874
A776	*pabaA1;AcrA1;bimE7;riboB2 chaA1*		DBE1 (NRM)	UV of A154
A777	*adE20 biA1;wA2 cnxE16;sC12;methG1;nicA2; bimC4 lacA1;choA1;chaA1*		244 (NRM)	UV of A154
A778	*pyrG89 riboA1;pyroA4;nicB8;bimG11*		JD04 (NRM)	UV of A122
A779	*nudC3 pyrG89 pabaA1;wA2;nicA2*			UV A4→x A722
A780	*bimA1;wA2*		50-10 (NRM)	UV of A154
A781	*nimA5;wA2*		507 (NRM)	A154 x A722 x A4
A782	*yA2;AcrA1;ActA1;pabaB22;nicA2;sbA3;choA1; riboB2 chaA1*	none	M3080	diploid 2707
A783	*SulA1;AcrA1;ActA1;pabaB22;nicA2;sbA3;choA1; riboB2 chaA1*	none	M3081	diploid 2707
A784	*yA2;wA3;ActA1;pabaB22;nicA2;sbA3;choA1; riboB2 chaA1*	none	M3082	diploid 2707
A785	*riboA1 pabaA1 yA2;AcrA1;galA1 ActA1;pyroA4 nicA2;sB3;choA1;chaA1*	none	M3252	dipl. 28 (A743/A592)
A786	*SulA1 anA1 biA1;AcrA1;galA1 ActA1;methG1;nicA2; sbA3;choA1;fwA2*	none	M3258	diploid 28
A787	*SulA1 anA1 biA1;wA2 cnxE16;galA1 ActA1;pyroA4; nicA2;sbA3;choA1;fwA2*	none	M3262	diploid 28
A788	*SulA1 anA1 biA1;wA2 cnxE16;galA1 ActA1;methG1; lysB5;sbA3;OliC2 malA1;chaA1*	none	M3264	diploid 28
A789	*riboA1 proA2 pabaA1;sC12 galA1 phenA2 SuB4pro*	none	M3462	C 2202
A790	*proA2 yA2 adE20;wA3;sC12 galA1 phenA2 SuB4pro*	none	M3464	C 2202
A791	*riboA1 proA2;galE9 sC12 dilA1 SuB4pro*	none	M3482	C 2202

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A792	*proA2 pabaA1;galE9 sC12 dilA1 phenA2 SuB4pro*	none	M3483	C 2201
A793	*proA2*	none	M3390	C 2718
A794	*riboA1 biA1;AcrA1;lacA1 BwA1 sB3 sbA3*	none	M3305	C 2715
A795	*yA2;lacA1 BwA1 lysA1(AbVI) sB3 sbA3*	AbVI	M3347	C 2719
A796	*phenB6 pantoB100 sF211 malA1 nicB8;riboB2*	none	M3393	C 2712
A797-A807	Section IX, *A. niger* mutants			
A808-A812	Section VII, *A. awamori* mutants			
A813	*pyrN25*		1744 (HNA)	
A814	*yA2;pyrN25*		1744 (HNA)	
A817	*pabaA1 biA1;wA3 thiA4 cnxE16;actA1*	none	M3433	diploid 27
A818	*suA1adE20 yA2 adE20;acrA1;galA1 actA1;pyroA4 facA303;sB3;choA1 fwA2*	none	M3613	diploid 31
A819	*sulA1 anA1 biA1;wA2 cnxE16;methG1;nicA2;sbA3; malA1;riboB2 chaA1*	none	M3608	diploid 31
A820	*yA2;benA33*		BRO2 (BRO)	UV of *pabaA1 yA2*
A821	*proA1 pabaA1 adE20 yA2;wA3;pyroA4;tubA4*		LO196 (BRO)	
A822	*pabaA1;pyroA4;tamA200*			UV of *biA1*
A823	*biA1 pabaA1;pyroA4;tamA200*			
A824	*proA1 pabaA6 adE20 biA1;acrA1;wB1;riboB2*		728	
A825	*suA1adE20 adE20 biA1;uvsI501; ssbA1;sB3;choA1;chaA1*		B1 (HSK)	NG of A168
A826	*suA1adE20 adE20 biA1;uvsB505 ssbA1;sB3;choA1;chaA1*		B5 (HSK)	4-NQO of A168
A827	*suA1adE20 adE20 biA1;uvsB504 ssbA1;cotA1;sB3;choA1;chaA1*		B4 (HSK)	UV of A168
A828	*biA1;T2(I;III);AcrA1;nicA2;musM225*		EK2755	
A829	*pabaA1;AcrA1;chaA1*	none	EK2389	
A830	*pabaA1;AcrA1;ActA1;choA1;riboB2 chaA1*	none	EK2892	
A831	*uvsA101;pyroA4;choA1;chaA1*	none	EK3935	
A832	*pabaA1;uvsB110;nicA2;chaA1*	none	EK3930	
A833	*pabaA1;choA1;uvsC114 chaA1*	none	EK3571	
A834	*pabaA1;pyroA4;uvsD153;choA1;chaA1*	none	EK3811	
A835	*pabaA1;ActA1;uvsE182;choA1;chaA1*	none	EK3733	
A836	*uvsF201 pabaA1;ActA1;nicA2;sbA3;riboB2 chaA1*	none	EK3813	
A837	*pabaA1;uvsH77 pyroA4;choA1;chaA1*	none	EK3961	
A838	*pabaA1;AcrA1;uvsI501;choA1;riboB2 chaA1*	none	EK3547	
A839	*pabaA1;pyroA4;uvsJ1;choA1;chaA1*	none	EK3938	
A840	*pabaA6;AcrA1;musK228*	none	EK3764	
A841	*riboA1 adE20 biA1 musL222*	none	EK3776	
A842	*riboA1;AcrA1;dilA1;musN227*	none	EK3005	
A843	*pabaA6;sbA3;musO226 T2(III;VII) choA1*		EK3753	
A844	*musP234 T2(VII→II) oliC2 pantoB100 nicB8*		EK3844	
A845	*riboA1 yA2;musQ230;choA1*	none	EK3707	
A846	*SulA1 pabaA1 yA2;musR223*	none	EK3647	
A847	*musS224 T3(III;VII) pantoB100*	none	EK3758	
A848	*biA1;wA3;niiA4 gatA312*		MH1055 (MJH)	
A849	*pabaA1 yA2;ΔargB::trpCΔB ΔrodA::argB;veA1 trpC801*		TMS015(MAS)	D of A851
A850	*biA1;ΔargB::trpCΔB;methG1;veA1 trpC801*		RMS010 (MAS)	
A851	*pabaA1 yA2;ΔargB::trpCΔB;veA1 trpC801*		RMS011 (MAS)	
A852	*diploid:biA1;ΔargB::trpCΔB;methG1;veA1 trpC801* *pabaA1 yA2;ΔargB::trpCΔB;veA1 trpC801*		RMS010 (MAS) RMS011	
A853	*yA2 pabaA1;suA1veA1;veA1*		TU31	
A854	*pabaA1;suA1veA1;veA1*		TU32	
A855	*pabaA1;suD1veA1;veA1*		TU44	
A856	*yA2 pabaA1;suD1veA1;veA1*		TU47	
A857	*pabaA1;suC3veA1;veA1*		TU48	

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A858	*yA2 pabaA1;suC3veA1;veA1*		TU49	
A859	*pabaA1;suB1veA1;veA1*		TU50	
A860	*pabaA1;suC1veA1;veA1*		TU52	
A861	*yA2 pabaA1;suC1veA1;veA1*		TU53	
A862	*pabaA1;suC2veA1;veA1*		TU54	
A863	*yA2 pabaA1;suC2veA1;veA1*		TU55	
A864	*riboA1;AcrA1 wA3 thiA4 cnxE16;choA1*	none	3620	
A865	*biA1;AcrA1;phenA2;nicA2 pA2 facA303 hxA1 riboD5*	none	2926	
A866	*SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;facA303; sbA3;choA1;fwA2*	none	3615	
A867	*suA1adE20 yA2 adE20;wA2 cnxE16; galA1 ActA1;pyroA4; nicA2;sbA3;choA1;riboB2 chaA1*	none	3616	
A868	*riboA1 yA2;puA1*	none	3941	
A869	*yA2;acrB2;choA1*	none	3882	
A870	*yA2;wA3 cnxE16*	none	3883	
A871	*yA2;adC1;choA1*	none	3884	
A872	*biA1*;$apl^{C}7$		CS51	UV of A26
A873	*biA1;alX4*		CS764	UV of A26
A874	*biA1;uaZ11*		CS1131	UV of A26
A876-A943	Section IX, *A. niger* mutants			
A944	*pyrG89;chaA1;nudA1;snaD385*			UV
A945	*pyrG89;chaA1;nudA1;snaA26*			UV
A946	*pyrG89;chaA1;nudA1;snaB76*			
A947	*pyrG89;chaA1;nudA1;snaC108*			
A948	*pyrG89;chaA1;nudA1;snaE285*			
A949	*sulA1 adE20;AcrA1;ActA1;ssbA1 pyroA4;facA303;lacA1 sB3;choA1;chaA1*		S513	
A950	*pabaA1;alc delta 500;riboB2*			
A951	*yA2;pabaA1;acuk248*			
A952	*biAi alcR125*			
A953	*acuM301;wA3;pyroA4*			
A954 - A985	Section IX, *A. niger* mutants			
A986	*biA1*, $argB^{+}$::P_{alcA}: $Aras^{G17V}$, *veA1*		AST27	
A987	*biA1*, $argB^{+}$::P_{alcA}: $Aras^{S22N}$, *veA1*		AST29	
A988	*biA1*, $argB^{+}$::P_{alcA}: *Aras*, *veA1*		AST30	
A989	*yA2, pabaA1; sbrA1; pyroA4; trpC801, veA1*		rM13	
A991	Edgebaston, Birmingham Wild Type		A65	
A992	Birmingham, 1954 Wild Type		B1	
A993	from Polyporus sporophore, 1962 Wild Type	diploid	C31	
A994	from Collybia sporophore, 1962 Wild Type	T(IV,II)	D34	
A995	Soil, Durham, 1962 Wild Type		E43	
A996	Soil, Kent, 1962 Wild Type		F108	
A997	Soil, Cornwall, 1963 Wild Type		G143	
A998	Soil, Kent 1962, Wild Type		H109	
A999	Nicotiana bed soil, Edgebaston, 1962 Wild Type	I66		
A1000	Compost, Birmingham, 1962 Wild Type	diploid	J67	
A1001	Compost, Birmingham, 1962 Wild Type		K68	
A1002	Soil, Pembroke, 1962 Wild Type		L80	
A1003	Soil, Pembroke, 1962 Wild Type	"B" chromosome	M85	
A1004	Soil, Cambridgeshire, 1962 Wild Type	T(VI,VIII)	N89	
A1005	Soil, Warwickshire, 1962 Wild Type		Q106	
A1006	Soil, Portsmouth, 1962 Wild Type		R99	
A1007	Soil, Pembrokeshire, 1962 Wild Type		U114	
A1008	Soil, Devon, 1962 Wild Type		V154	

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A1011	*nudF6 pyrG89 snfC1524*		snf1524	UV of XX20(nudF6 pyrG89)
A1012	*nudF6; wA3; pyroA4; snf1524*		DW38	
A1013	*nudF6 pyrG89 snfE798*		snf798	
A1014	*nudF6 pyrG89; snfA890*		DW15	UV of XX20
A1015	*wA3; pyroA4; snfA890*		DW17	
A1016	*nudF6; wA3; pyroA4; snfA890*		DW16	
A1017	*nudF6 pyrG89 snf1267*		snf1267	
A1018	*nudF6 pyrG89 snfD860*		snf860	UV of XX20
A1019	*nudF6 pyrG89; snfC1232*		snf1232	UV of XX20
A1020	*nudF6; wA3; pyroA4;snfC1232*		DW35	
A1021	*nudF6 pyrG89 snfD1468*		snf1468	UV of XX20
A1022	*nudF6 pyrG89 snfD1292*		snf1292	UV of XX20
A1023	*yA2 riboA1; nicB8 snfD1292*		DW40	
A1024	*nudF6 pyrG89 snfD1555*		snf1555	UV of XX20
A1025	*wA3; pyroA4 snfD1555*		DW45	
A1026	*nudF6 pyrG89 snf1364*		snf1364	UV of XX20
A1027	*nudF6 pyrG89 snf1062*		snf1062	UV of XX20
A1028	*pyrG89; pyroA4 snf1364*		DW61	
A1029	*nudF6 pyrG89 snf1422*		snf1422	UV of XX20
A1030	*pabaA1; AcrA1; ActA1; choA1 musN227; riboB2 chaA1*		EK4048	
A1031	*pabaA1; AcrA1; ActA1; nicA2; choA1; riboB2 chaA1 musK228*		EK4069	
A1032	*pyrG89 yA2; wA2 cnxE16; ActA1; pyroA4; nicA2;sbA3; choA1; riboB2 chaA1*		EK4169	
A1033	*pyrG89 yA2; AcrA1; ActA1; pabaB22; nicA2; sbA3; malA1; fwA2*		EK4172	
A1034	*biA1; flbA*		MBN13	
A1035	*yA2;* $fadA^{G203R}$		RJY115.4	
A1036	*biA1; mthG1; Δ-fadA::argB*		RJY918.5	
A1037	*biA1;* $fadA^{G42R}$		BDNM4	
A1038	*biA1; Δ-fasA::arg/ biA1; Δ fasB*		DDB57/51A	
A1039	*pabaA1, yA2; Δ-stcK::trpC*		TDB4	
A1040	*methG1, Δ-stcJ::argB; biA1*		TDB2	
A1041	*biA1; Δ-stcE::argB2, methG1 wA1*		TJH3.40	
A1042	*pabaA1, yA2; Δ-stcN::trpC*		TAHK45.44	
A1043	*Δ-stcP::argB2; methG1, biA1*		TAHK54.11	
A1044	*biA1; Δ-stcP::argB2*		TAHK64.42	
A1045	*Δ-stcQ::argB2, methG1; biA1*		TAHK67.11	
A1046	*Δ-stcL::argB2 methG1; biA1*		TAHK70.29	
A1047	*Δ-stcL::argB2, Δ-stcU::hph; methG1 biA1*		TAHK78.36	
A1048	*Δ-stcB::argB2, methG1, biA1*		TAHK87.29	
A1049	*Δ-stcF::argB2, methG1, biA1*		TAHK68.44	
A1050	*Δ-stcW::argB2, methG1, biA1*		TAHK79.4	
A1051	*Δ-stcI::argB2, methG1, biA1*		TAHK72.25	
A1052	*Δ-aflR::argB2, methG1, biA1*		TMF4.12	
A1053	*pabaA1, yA2; ΔargB::trpCΔB, catA::argB; trpC801*		TRN1	
A1054	*pabaA1, yA2; ΔargB::trpCΔB, catB::argB; trpC801*		TLK12	
A1055	*biA1; ΔcatA::argBΔA; metG1; ΔcatB::argB*		CLK20	
A1056	*yA2; ΔfadA::argB*		RJY918.10	
A1057	*yA2 pabaA1; pantoC3*		C1	
A1058	*biA1; argB2*		C3	
A1059	*biA1; argB+::Aras:lacZ*		AST32	
A1060	*biA1*		AST33	
A1061	*pyrG89 pabaA; wA3; bimD6 pyroA4; chaA1*		EK4078	
A1062	*pyrG89; bimD6; riboB2 chaA1*		EK4247	
A1063	*riboA1; sC12; bimD6 pyroA4*		M3659 (GMay 6.9)	
A1064	*pabaA1; biA1; bimD6 pyroA4*		M3692	
A1065	*pabaA1 yA2; bimB3*		3132	
A1066	*aromA1248 riboA1 adG14 yA2*		G1100	

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A1067	*aco-3; veA+*		WIM001	
A1068	*paba; acoA49; veA+*		WIM113	
A1069	*aco-14; veA+*		WIM002	
A1070	*yA2; pabaA1; veA+*		WIM126	
A1071	*acoA49; veA+*		WIM003	
A1072	*aco-55; veA+*		WIM004	
A1073	*yA2; pabaA1; acoC193; veA+*		WIM145	
A1074	*aco-70; veA+*		WIM006	
A1075	*yA2; pabaA1; acoB202; veA+*		WIM146	
A1076	*yA2; pabaA1; acoC193; veA1*		WIM202	
A1077	*yA2; pabaA1; biA1; methG1; alc(p)::brlA; veA+*		TU83	
A1078	*yA2; pabaA1; biA1; methG1; alc(p)::brlA1; veA1*		TU84	
A1079	*biA1; pabaA1; pyroA4;Δ-brlA; veA+*		TU85	
A1080	*yA2 pabaA1; biA1; pyroA4; Δ-brlA; veA+*		TU86	
A1081	*yA2; pabaA1; fluG701;* blu-sensitive; *veA+*		TU91	
A1082	*aco-445; veA+*		WIM014	
A1083	*nicB8;* blu-sens; *veA+*		TU95	
A1084	*pabaA1; fluG701; veA1*		TU108	
A1085	*pabaA1; fluG701; veA+*		TU110	
A1086	*yA2 pabaA1; fluG701; veA1*		TU114	
A1087	*wA3; pyroA4; fluG701; veA1*		TU120	
A1088	*yA2; pabaA1; wA3; argB2; pyroA4; veA+*		TU135	
A1089	*pre-1; veA+*		WIM027	
A1090	*met,bi, green, fluG701* suppressor?		TU138	
A1091	*pyro; pabaA1*		WIM142	
A1092	*met, bi,* green,fluG701 suppressor?		TU139	
A1093	*yA2 pabaA1; veA1*		WIM064	
A1094	*wA3; pyroA4; veA1*		WIM065	
A1095	*yA2; pabaA1; △-argB::trpC+; pyroA4; trpC801(?); veA+*		TU130	
A1096	*pabaA1*		WIM243	
A1097	wild type		12S	
A1098	*niaD1*		RAWMI	
A1099	Lemore (*A. niger*)		DL	
A1100	*A. fumigatus*		AF293	
A1101	*pabaA, yA2, △-catC::argB-△ C △-argB::trpC-△ B*		TLK61	
A1102	*pabaA, biA1, △ catC::argB △ C, △ catA::argB △ A, metG1, △ catB::argB △ B, veA1*		CLK36	
A1103	*pabaA1, yA2, biA1, △ catC::argB △ C, △ CatA::argBdeltaA, △ catB::argB △ B, veA1*		CLK35	
A1104	GFP *nudF*		XX	
A1105	GFP *tubA*		XX	
A1106	GFP *nudA*		XX	
A1107	*swoA; wA3*		APW18	
A1108	*swoA*		AXL1	
A1109	*swoA*		AXL4	
A1110	*swoB*		AJB15	
A1111	*swoC*		AGA24	
A1112	*swoC; wA3*		AXL8	
A1113	*swoD*		AGA20	
A1114	*swoE*		AJB5	
A1115	*swoF*		AXL19	
A1116	*swoF*		AJB11	
A1117	*swoG*		APW19	
A1118	*swoH; chaA-1*		APW14	
A1119	*swoH*		AXL20	
A1120	*A. flavus*		NRRL 3357	

FGSC #	Genotype	Trans-location	Depositor's Stock # or initials	Origin of strain or lesion
A1121	*A. niger*		NRRL 3	
A1122	*nimG10, chaA, lac, nic*		SWJ 003	
A1123	*nimQ20, methB3, choA1 wA2*		SWJ 187	
A1124	*nimP22, pyroA4, chaA1*		SWJ 280	
A1125	*nimO18, pabaA4, yA2*		SWJ 400	
A1126	*nimX2cdc2, F233L, yA2, nicB8, pyroA4*		S059	
A1127	*nimE6, metG1, riboA1, yA2*		S074	
A1128	*nimT23, paba*		nimT	
A1129	*hypA, wA2, pyroA4*		ASK 30	
A1130	*hypB, chaA, paba*		ASK 80	
A1131	*hypC, pyro*		ASK 158	
A1132	*hypD, bi, paba*		ASK 65	
A1133	*hypE, pyro*		ASK 156	
A1134	*biA1; facA303; delta-pscA::pyrG; delta-mcsA::argB; pyrG89; veA1*		RYQ25.4	
A1135	*biA1; delta-pscA::pyrG; delta-mcsA::argB; pyrG89; veA1*		RYQ25.1	
A1136	*biA1; delta-pscA::pyrG; pyrG89; veA1*		TYQ4.24	
A1137	*A. fumigatus pyrG1*		AF293.1	
A1138	*A. fumigatus pyrG1, argB1*		AF293.6	
A1139	*A. fumigatus pyrG1, lys B1*		AF293.7	
A1141	*A. fumigatus*		WVU1943	
A1142	*A. fumigatus*		WVU2026	
A1143	*A niger*		NRRL 3	
A1144	*A. niger*		NRRL 328	
A1145	*pyrG89; pyroA4; nkuA::argB; riboB2*		TN02A7	
A1146	*wA3; pyroA4; argB2 nkuA::argB; riboB2*		TN02	
A1147	*pyrG89; argB2; pabaB22, nkuA::argB; riboB2*		TN02A25	
A1148	*pyrG89; nkuB::A.f riboB; pyroA4, nkuA::argB, riboB2*		TN12	
A1149	*pyrG89; pyroA4; nkuA::argB*		TN02A3	
A1150	*pyroA4; nkuA::argB; riboB2*		TN02A21	
A1151	*A. fumigatus* pyrG^$^{\text{AF::Delta KU80}}$		KU80Delta	
A1152	*A. fumigatus* pyrG		CEA17	
A1153	*yA1 pabaA1 pyroA4 argB2 nkuA::bar*		MH11046	
A1154	*yA1 pabaA1 niiA4 nkuA::bar*		MH11057	
A1155	pyrG89 pyroA4 nkuA::bar		MH11068	
A1156	*A. terreus*		NIH2624	
A1157	*A. fumigatus akuA::ptrA*		Afs28	
A1158	*A. fumigatus akuA::loxP-hygro*$^{R/tk}$		Afs34	
A1159	*A. fumigatus akuA::loxP*		Afs35	
A1160	*A. fumigatus* Δ KU80 *pyrG-*			
A1161	*biA1; argB2; methG1; veA1; phiA1::argB*		PM1	
A1162	*biA1; argB2; methG1; veA1; vmaA1::argB*		PM6	
A1163	*A. fumigatus* Mating type 1-1		CEA10	

VII. *Aspergillus awamori*.

All were obtained from Dr. Renato Bonatelli, Jr.

FGSC #	Genotype	RB Number
A808	*bwnA1;leuA1;proA1*	1784
A809	*ebrA1 greA1;morA1;leuA1;pabA1;proA1*	1785
A810	*bwnA1;morA1;leuA1;pabA1;proA1*	1786
A811	*greA1.morA1 arg2;proA1*	1790
A812	*greA1;proA1*	1792

VIII. *Aspergillus oryzae*

FGSC #	Genotype or characteristics	Obtained from
A815	wild type	T. Uozumi
A816	*ade* (requires adenine)	T. Uozumi

IX. *Aspergillus niger*

FGSC #	Genotype	Other Number	Deposited by
A730	*cspA1 hisD4 lysA7 leuA1 nicA1 pabA1*	N612	CJB
A731	*cspA1 fwnA1 hisD4 lysA7 leuA1 nicA1 pabA1*	N616	CJB
A732	wild type	N400	CJB
A733	*cspA1*	N402	CJB
A734	*cspA1 metB10*	N500	CJB
A735	*cspA1 nicA1 pabA1*	N494	CJB
A736	*cspA1 fwnA1*	N410	CJB
A737	*cspA1 nicA1 bioA1*	N493	CJB
A738	*cspA1 nicA1*	N423	CJB
A739	*cspA1 fwnA1 lysA7*	N436	CJB
A740	*cspA1 hisD4*	N434	CJB
A741	*cspA1 leuA1*	N414	CJB
A742	*cspA1 pyrA5*	N592	CJB
A797	*cspA1 cysA2*	N406	CJB
A798	*cspA1 argL2*	N409	CJB
A799	*cspA1 argA1*	N408	CJB
A801	*cspA1 trpA1*	N469	CJB
A800	*cspA1 nicA1 pdxA2*	N630	CJB
A802	*cspA1 olvA1 argF8*	N474	CJB
A803	*cspA1 fwnA1 trpA1 lysA7 bioA1 leuA1 nicA1 pabA1*	N620	CJB
A804	*cspA1 fwnA1 hisD4 lysA7 bioA1 leuA1 metB1 pabA1*	N655	CJB
A805	*cspA1 fwnA1 trpA1 argB2 leuA1 nicA1 pabA1*	N661	CJB
A806	*cspA1 fwnA1 hisD4 lysA7 bioA1 leuA1 nicA1 pdxA2*	N690	CJB
A807	*cspA1 olvA1 hisD4 lysA7 bioA1 argF8 nicA1 pabA1*	N669	CJB
A875	*cspA1;olvA1;proC9*	N476	KS
A876	*cspA1;cysB3*	N403	KS
A877	*cspA1;proC3*	N404	KS
A878	*cspA1;lysB2*	N425	KS
A879	*cspA1;lysC5*	N428	KS
A880	*cspA1;argD6*	N430	KS
A881	*cspA1 hisA1*	N431	KS
A882	*cspA1;metC3*	N441	KS
A883	*cspA1;gryA1;leuB3;argE5*	N458	KS
A884	*cspA1;argE5*	N459	KS
A885	*cspA1;cysA2;leuA1;argA1*	N462	KS
A886	*cspA1;olvA1;adeA1*	N478	KS
A887	*cspA1;olvA1;argG11*	N479	KS
A888	*cspA1;argB13 nicA1*	N492	KS
A889	*cspA1;adeB2;nicA1*	N495	KS
A890	*cspA1 adeC3*	N499	KS
A891	*cspA1 hisE5;nicA3*	N508	KS
A892	*cspA1;fwnA1;adeD5*	N518	KS
A893	*cspA1;fwnA1;adeE6*	N519	KS
A894	*cspA1;fwnA1 metD12*	N523	KS
A895	*cspA1;ntrA2 fwnA1*	N525	KS
A896	*cspA1;fwnA3;pabB2 trpA1*	N531	KS
A897	*cspA1;brnA2;metB2*	N639	KS
A898	*cspA1;nicA1;proA4*	N681	KS
A900	*cspA1;olvA1;bioB2;niaD2*	N694	KS
A901	*cspA1;olvA1;bioB2;cnxB3*	N699	KS
A902	*cspA1;olvA1;bioB2;cnxC5*	N701	KS
A903	*cspA1;cnxD6;metB10*	N702	KS
A904	*cspA1;olvA1;bioB2;cnxE8*	N704	KS
A905	*cspA1;olvA1;bioB2;nirA3*	N707	KS

FGSC #	Genotype	Other Number	Deposited by
A906	*cspA1;proB5;metB10*	N714	KS
A907	*cspA1;bioA1;leuA1;nicA1;pabA1; oliC2;nirA1*	N716	KS
A908	*cspA1;nicA1;adeF12*	N717	KS
A909	*cspA1;acrA1 brnA2;nicA1*	N724	KS
A910	*cspA1;cnxG13 fwnA1 metD12;pabA1*	N725	KS
A911	*cspA1 hisD4;adeG13*	N753	KS
A912	*cspA1 hisF6;nicA1*	N734	KS
A913	*cspA1;cysC5;nicA1*	N747	KS
A914	*cspA1;nicA1;argK16*	N748	KS
A915	*cspA1;thiA1;metB10*	N749	KS
A916	*cspA1;fwnA1;pabA1 cnxA1 pyrB4*	N761	KS
A917	*cspA1 pyrC7;metB10*	N766	KS
A918	*cspA1;fwnA1;leuD8 lysC27*	N779	KS
A919	*cspA1 hisG7;metB10*	N786	KS
A920	*cspA1;fwnA1;pyrG5;nicB5*	N814	KS
A921	*cspA1;cnxF12;nicA1*	N819	KS
A922	*cspA1;olvA1;bioB2;crnA11*	N829	KS
A923	*cspA1;bioA1;serA1*	N833	KS
A924	*cspA1;fwnA1;argH12;lysA7;hisC3; pheA1;pdxA2;nicB5;trpB2*	N835	KS
A925	*cspA1;fwnA1;argH12;lysA7; leuA1;hisB2;pdxA2;cnxC5;trpB2*	N837	KS
A926	*cspA1;fwnA1;trpA1;pyrG5;hisC3; pheA1;pdxA2;nicB5;crnB12*	N840	KS
A927	*cspA1;metB10;adeF12 cnxC5*	N850	KS
A928	*cspA1;pdxB3;nicA1*	N853	KS
A929	*cspA1;bioA1;pabC5*	N854	KS
A930	*cspA1;nicA1;pabD6*	N860	KS
A931	*cspA1;bioA1;pyrE9*	N872	KS
A932	*cspA1;bioA1;lysF29*	N873	KS
A933	*cspA1;bioA1 proD6*	N874	KS
A934	*cspA1;bioA1;trpE6*	N880	KS
A935	*cspA1;fwnA1;metB11;proE7*	N883	KS
A936	*cspA1;fwnA1;argH12;pyrG5; leuA1;pheA1;lysD25;oliC2;crnB12*	N890	KS
A937	*cspA1;fwnA1;bioA1 pyrG5 hisH8;pheA1*	N893	KS
A938	*cspA1;olvA1;leuC5;pyrD8*	N894	KS
A939	*cspA1 hisI9;bioA1*	N898	KS
A940	*cspA1;ntrC4;pheA1*	N899	KS
A941	*cspA1;bioA1;ntrD5*	N903	KS
A942	*cspA1;fwnA1;argH12;pyrG5;ntrB3; metB11;lysD25;oliC2;crnB12*	N907	KS
A943	*cspA1;fwnA1;trpA1;bioA1 lysE28;pdxA1;crnB12*	N912	KS
A954	*cspA1;acrA1 brnA2; choA101; nicA1*	EK053	EK
A955	*cspA1;acrA1 brnA2 ;cysA101;nicA1*	EK054	EK
A956	*cspA1; fwnA1;choA101;thiB101;pdxA2*	EK163	EK
A957	*cspA1;fwnA1;choA101;pdxA2;nicB101*	EK164	EK
A958	*cspA1;fwnA1;leuA1;pdxA2;sftC102*	EK211	EK
A959	*cspA1;acrA1 brnA2;choA101; pdxA2;sftB103*	EK217	EK
A960	*cspA1; fwnA1; pyrG5 choA101; nicB5*	EK189	EK
A961	*cspA1;acrA1 brnA2; fpaD19; choA101 lysA14; (+/- ntrB3); metB11; nicB101*	EK196	EK
A962	*cspA1;fwnA1;fpaD19;lysA14; ntrB3 thiB101;oliC2*	EK200	EK
A963	*cspA1;fwnA1;choA101;pdxA2; oliC2 sftC101;crnB12*	EK218	EK
A964	*cspA1;acrA1 brnA2;choA101;niaD2*	EK134	EK
A965	*cspA1; olvA1; bioB2; leu A1; niaD2*	EK140	EK
A966	*cspA1fwnA1;lysA7;pdxA2; niaD2*	EK141	EK
A967	*cspA1;adrA1 brmA2; pyrG5; metB11;cnxC5; crnB12*	EK157	EK

FGSC #	Genotype	Other Number	Deposited by
A968	*cspA1;acrA1 brnA2; pyrG5; pdxA2; nicB5*	EK185	EK
A969	*cspA1;fwnA1;pyrG5; metB10*	EK182	EK
A970	*cspA1;fwnA1;pyrG5 choA101; pdxA2; nicB5*	EK187	EK
A971	*cspA1; brnA2;pyrG5;metB10; nicB5*	EK184	EK
A972	*cspA1;acrA1 brnA2; pyrG5; niaD2*	EK191	EK
A973	*cspA1; fwnA1; fpaD19; lysA14; pdxA2; nicB101*	EK199	EK
A974	*cspA1;fwnA1;leuA1;pdxA2; sftC101*	EK210	EK
A975	*cspA1;acrA1 brnA2;fpaD19; choA101;pdxA2;sftC101;crnB12*	EK219	EK
A976	*cspA1;fwnA1;fpaD19;choA101; pdxA2;sftC101; crnB12*	EK221	EK
A977	*cspA1;fwnA1;leuA1;pdxA2;oliC2 sftC101; crnB12*	EK222	EK
A978	*cspA1;acrA1 brnA2;argH12; choA101;ntrB3;metB11;pdxA2;oliC2;crnB12*	EK138	EK
A979	*cspA1;fwnA1;fpaD19;lysA14;ntrB3; metB11;pdxA2;oliC2;crnB12*	EK192	EK
A980	*cspA1; fwnA1;fpaD19;choA101; ntrB3;metB11;pdxA2;oliC2;crnB12*	EK194	EK
A981	*cspA1;acrA1 brnA2;fpaD19; choA101;thiB101;metB11;pdxA2;oliC2*	EK201	EK
A982	*cspA1;fwnA1 fpaD19;choA101; thiB101;metB11pdxA2;oliC2;crnB12*	EK223	EK
A983	*cspA1;acrA1 brnA2;fpaD19; lysA14;ntrB3 thiB101; metB11;pdxA2;oliC2;crnB12*	EK224	EK
A984	*cspA1;fwnA1;fpaD19;lysA14;ntrB3; metB11;pdxA2;oliC2;crnB12*	EK225	EK
A985	*cspA1;acrA1 brnA2;fpaD19;choA101; thiB101;metB11;pdxA2;oliC2;crnB12*	EK226	EK
A1121	Wild type	NRRL3	
A1143	Wild type	NRRL3	SB
A1144	Wild type	NRRL 328	

***A. niger* strains by gene name**

Gene and allele #	Linkage group	Gene function or phenotype	FGSC number[1]	N#[2]	SFU #[3]
acrA1	I	acrivlavin resistant	A909	N724	036
adeA1	IV	adenine requiring	A886	N478	071
adeB2	III	adenine requiring	A889	N495	050
adeC3	II	adenine requiring	A890	N499	046
adeD5	IV	adenine requiring	A892	N518	047
adeE6	II	adenine requiring	A893	N519	051
adeF12	VII	adenine requiring	A908	N717	048
adeG13	III	adenine requiring	A911	N733	052
argA1	V	argenine requiring	A885	N462	070
argB13	V	argenine requiring	A888	N492	073
argD6	III	argenine requiring	A880	N430	065
argE5	VI	argenine requiring	A884	N459,458	069,068
argF8	IV	argenine requiring	A802	N474	018
argG11	VI	argenine requiring	A887	N479	072
argH12	II	argenine requiring	A925	N837,907	040,106
argK16	VI	argenine requiring	A914	N748	085
argL2 (was B2)	III	argenine requiring	A798	N409	017
			A805	N661	021
bioA1	III	biotin requiring	A737	493912,903	013,105,107
bioB2	III	biotin requiring	A900	N694	032
brnA2	I	brown conidial color	A897, A909	N639,724	037,036
choA101	III	choline requring	A954,A960		053,189
			A964		134
cnxA1	VI	nitrite requiring	A916	N761	029
cnxB3	IV	nitrite requiring	A901	N699	041
cnxC5	VII	(XDH cofactor)	A902	N701	033
cnxD6	III	nitrite requiring	A903	N702	043
cnxE8	VI	nitrite requiring	A904	N704	042
cnxF12	I	nitrite requiring	A921	N819	045
cnxG13	I	nitrite requiring	A910	N725	044
crnA11	VIII	|chlorate resistant	A922	N829	089
crnB12	VIII	|nitrate transporter	A943	N912	107
cspA1	III	adhering conidia	A733	N402	011 (Present in all strains)
cysA2,101	III	cystine requiring	A885	N462	070
cysB3	I	cystine requiring	A876	N403	061
cysC5	IV	cystine requiring	A913	N747	084
fwnA1,3	I	fawn conidial color	A739, A895	N436,531	015,077
gryA1	I	grey (likely fwnA allele)	A883	N458	068
hisA1	II	histidine requiring	A881	N431	066
hisB2	V	histidine requiring	A925	N837	040
hisC3	IV	histidine requiring	A925	N840	091
hisD4	II	histidine requiring	A730	N612	052
hisE5	II	histidine requiring	A891	N508	074
hisF6	II	histidine requiring	A912	N734	083
hisG7	II	histidine requiring	A919	N786	088
hisH8	III	histidine requiring	A937	N893	038
hisI9	II	histidine requiring	A939	N898	103
leuA1	IV	leucine requiring	A885	N462	070
leuB3	III	leucine requiring	A883	N458	068
leuC5	II	leucine requiring	A938	N894	102
leuD8	IV	leucine requiring	A918	N779	087
lysA1,14	III	lysine requiring	A795	N837	040
lysB2	VI	lysine requiring	A878	N425	
lysC5,27	IV	lysine requiring	A879,918	N428,779	064
lysD25		lysine requiring	A942	N907	104
lysE28	IV	lysine requiring	A943	N912	107

Aspergillus niger

Gene and allele #	Linkage group	Gene function or phenotype	FGSC number[1]	N#[2]	SFU #[3]
lysF29	VII	lysine requiring	A932	N873	097
metB2,10,11	V	methionine requiring	A734,915	N500,749	012,035
metC3	I	methionine requiring	A882	N441	067
metD12	I	methionine requiring	A910	N725	044
niaD2	VIII	nitrate requiring	A964		134
		(nitrate reductase)	A900	N694	032
nirA1,3	VIII	N-regulator	A907,905	N716,707	082,080
nicA1,3	V	nicotinic acid requiring	A889	N495	
nicB5	VII	nicotinic acid requiring	A920,926	N814	
nicB101		nicotinic acid requiring	A957		164
ntrA2	I	|nicotinic	A895	N525	076
ntrB3	IV	| acid or	A942	N907	062
ntrC4	IV	| tryptophan	A940	N899	104
ntrD5	IV	| requiring	A941	N903	105
oliC2	VII	oligomycin resistant	A942	N907	106
olvA1	I	olive conidial color	A802,886	N474,770	018,071
pabA1	VI	p-aminobenzoic acid req	A910,907	N725,716	044,082
pabB2	II	p-aminobenzoic acid req	A896	N531	077
pabC5	VI	p-aminobenzoic acid req	A929	N854	094
pabD6	VI	p-aminobenzoic acid req	A930	N860	095
pdxA2	VI	pyridoxine requiring	A926	N 840	091
pdxB3	III	pyridoxine requiring	A928	N853	093
pheA1	V	phenylalanine requiring	A940	N899	104
proA4	VI	proline requiring	A898	N681	078
proB5	III	proline requiring	A906	N714	
proC3	III	proline (±arg) requiring	A877	N404	062
proE7	VI	proline (not arg) req	A935	N883	100
proD6	III	proline (not arg) req	A933	N874	093
pyrB4	VI	pyrimidine (uridine) req	A916	N761	029
pyrC7	II	pyrimidine (uridine) req	A917	N766	086
pyrD8	VIII	pyrimidine (uridine) req	A938	N894	102
pyrE9	VIII	pyrimidine (uridine) req	A931	N872	096
pyrG5,6 (was A)	III	pyrimidine (uridine) req	A742	N592, 593	016,031
serA1	V	serine requiring	A923	N833	090
sftB103		|selenate resistant/	A959		217
sftC101,102	VII	| sulfite requiring	A958		211
thiA1	III	thiamine requiring	A913	N747	035
thiB101	IV	thiamine requiring	A956		163
trpA1	II	tryptophan requiring	A896,943	N531,912	77,107
trpB2	VIII	tryptophan requiring	A925	N837	040
trpE6	VIII	tryptophan requiring	A934	N880	099

Notes:

[1] FGSC number: The listed strains contain the particular lesion in combination with other markers

[2] N# Bos/Debets number from the Netherlands

[3] SFU# Simon Frasier University number, from the collection of Dr. E. Kafer

X. *Aspergillus flavus*

FGSC #	Genotype	Other Number	Origin	Deposited by
A1009	White arg *pyrG* aflatoxin+	86-10	ATCC 60041	G. Payne
A1010	White *leu aflR pyrG*	656-2	650-33 X 656	G. Payne
A1120	Wild Type from EST program	NRRL3357		

XI. *Aspergillus heterothallicus*

FGSC #	Genotype	Other Number	Origin
A251	*A. heterothallicus*	WB5096	Wild types of Raper
A252	*A. heterothallicus*	WB5097	

XI. *Aspergillus fumigatus*

FGSC #	Genotype	Other Number	Origin
A1100		AF293	MA
A1137	pyrG1	AF293.1	GSM
A1138	pyrG1, argB1	AF293.6	GSM
A1139	pyrG1, lys B1	AF293.7	GSM
A1141	*A. fumigatus*	WVU1943	DP
A1142	*A. fumigatus*	WVU2026	DP
A1151	*A. fumigatus* pyrG^$^{\text{AF::Delta KU80}}$	KU80Delta	GHG
A1152	*A. fumigatus* pyrG	CEA17	GHG
A1157	*A. fumigatus akuA::ptrA*	Afs28	SK
A1158	*A. fumigatus akuA::loxP-hygro*$^{R/tk}$	Afs34	SK
A1159	*A. fumigatus akuA::loxP*	Afs35	SK
A1160	*A. fumigatus* Δ KU80 *pyrG-*		GHG
A1163	*A. fumigatus* Mating type 1-1	CEA10	WN

XII. Key to Symbols

Ab	Aberration	DES	diethyl sulfate	S	spontaneous
BC	Back Cross	γ	gamma rays	T	Translocation
C	Cross	INAH	isonicotinic acid hydrazide	UV	ultraviolet
D	Gene Disruption	NA	nitrous acid	X	X-rays
NG	nitrosoguanidine	4-NQO	4-nitroquinoline oxide		

Depositors:

AJC	A.J. Clutterbuck	GSM	Gregory S. May	NRM	N.R. Morris
AP	Andrzej Paszewski	HSK	Hyen-Sam Kang	RB	Renato Bonatelli
BRO	Berl R. Oakley	HNA	Herbert N. Arst	RG	Roy Gravel
BRS	Barry R. Scott	JLA	J.L. de Azevedo	RHP	R.H. Pritchard
BWB	B.W. Bainbridge	JMF	J.M. Foley	RTR	R.T. Rowlands
CFR	C.F. Roberts	JMvT	J.M. van Tuy	RWT	R.W. Tuveson
CJB	C.J. Bos	KS	Klaas Swart	SK	Sven Krappmann
DL	David Laidlaw	M	Montreal (E. Käfer)	TS	Tapan Som
EK	Etta Käfer	MA	Michael Anderson	WM	W. McCullough
EP	E. Pees	MAS	Mary A. Stringer	WN	W. Nierman
GD	Gordon Dorn	MG	M. Grindle	WT	W. Timberlake
GHG	Gustavo H. Goldman	MJH	M.J. Hynes	YP	Yarir Parag
GJOJ	G.J.O Jansen	NK	Nancy Keller		

Section D. Other Fungi

Note: USDA Permit (PPQ 526) needed to receive plant pathogens within the USA. Appropriate import permits required for international orders

Strains from various sequencing programs

FGSC #	Description	Other Stock #	Citation	Depositor
8958	*Magnaporthe grisea*	70-15		RD
9002	*Phanerochaete chrysosporium*	RP-78	AEM 66: 1629-1633	DC
9003	*Coprinus cinereus*	130; Okayama 7	Genetics 128: 529-538	PJP
9021	*Ustilago maydis* a1 b1	UM521		JK
9075	*Fusarium graminearum*	NRRL 31084	Mycologia 92:130-138	FT
9013	OR74A used by WICGR	A N150	Nature 422:859 - 868	EUS
A1100	*Aspergillus fumigatus*	AF293		MA
A1120	*A. flavus*	NRRL3357		JY
A1121	*A. niger*	NRRL 3		JY
A1143	*A niger*	NRRL 3		SB
A1144	*A. niger*	NRRL 328		SB
9487	*Cryptococcus neoformans*	H99		JH
9543	*Rhizopus oryzae*	RA99880		AI
9596	*Nectria haematococca*	77-12-4		HDV
10151	*Chaetomium globosum*	NRRL 1870		KOD
9923	*Ashbya gossypii*	ATCC 10895		PP
9935	*F. oxysporum* fsp *lycopersici*	NRRL 34936, 4287		KOD
10004	*Phycomyces blakesleeanus*	NRRL1555		LC
10005	*Phycomyces blakesleeanus*	A56		LC
10135	*Batrachochytrium dendrobatidis*	JEL423		JEL
10136	*Verticillium albo-atrum*	VaMs102		GV
10137	*V.dahliae*	VdLs17		GV
10138	*V. dahliae*	VdBob70		GV
A1163	*A. fumigatus*	CEA10		WN

Other strains

FGSC #	Description	Other Stock #	Citation	Depositor
9461	*Coprinus cinereus*	Java6		MZ
9926	*Ustilago maydis* a2b2	2/9		SG
9924	*Ashbya gossypii Δleu2 Δthr4*			PP

Pichia pastoris

FGSC#	Foreign gene	FGSC#	Foreign gene	FGSC#	Foreign gene
9925	AN1542.2	10078	AN2385.2	10104	AN6352.2
10060	AN0393.2	10079	AN2528.2	10105	AN6395.2
10061	AN0452.2	10080	AN2569.2	10106	AN6427.2
10062	AN0494.2	10081	AN2612.2	10107	AN6470.2
10063	AN0712.2	10082	AN3044.2	10108	AN7135.2
10127	AN8761.2	10083	AN3049.2	10109	AN7152.2
10128	AN9035.2	10084	AN3201.2	10110	AN7180.2
10129	AN9045.2	10085	AN3294.2	10111	AN7345.2
10130	AN9134.2	10086	AN3297.2	10112	AN7349.2
10131	AN9286.2	10087	AN3337.2	10113	AN7413.2
10132	Afu8g06890	10088	AN3358.2	10114	AN7505.2
10133	NCU09102.7	10089	AN3368.2	10115	AN7533.2
10064	AN0741.2	10090	AN3390.2	10116	AN7541.2
10065	AN0787.2	10091	AN3418.2	10117	AN7624.2
10066	AN0941.2	10092	AN3613.2	10118	AN7646.2
10067	AN1277.2	10093	AN3777.2	10119	AN7908.2
10068	AN1285.2	10094	AN4372.2	10120	AN7950.2
10069	AN1551.2	10095	AN4700.2	10121	AN8007.2
10070	AN1571.2	10096	AN4843.2	10122	AN8138.2
10071	AN1602.2	10097	AN5176.2	10123	AN8149.2
10072	AN1804.2	10098	AN5214.2	10124	AN8327.2
10073	AN1818.2	10099	AN5267.2	10125	AN8401.2
10074	AN2206.2	10100	AN5282.2	10126	AN8453.2
10075	AN2227.2	10101	AN5361.2	10134	AN3556.2
10076	AN2331.2	10102	AN5727.2		
10077	AN2359.2	10103	AN6093.2		

These strains are described in Bauer S, Vasu P, Mort AJ, Somerville CR. 2005 Cloning, expression, and characterization of an oligoxyloglucan reducing end-specific xyloglucanobiohydrolase from *Aspergillus nidulans*. Carbohydr Res. Dec 12;340(17):2590-7.

Fusarium

The FGSC has chosen to list strains as they were deposited. Current taxonomy may supercede names used here.

Gibberella fujikuroi anamorphs:

FGSC#	JFL#	Mating type	VCG	Origin; other markers
Fusarium moniliforme				
7598*	A-102	A+	A1	sorghum, San Joaquin Co. California (Sk^K)
7599	A-148	A-	A2	corn, Visalia California
7600*	A-149	A-	A7	corn, Visalia California (Sk^S)
7601	A-171	A+	?	rice, Italy
7602	A-411	A-	?	corn; *hsi1* (heterokaryon self-incompatible)
7603*	A-999	A+	A17	corn, Knightstown Indiana (Sk^K)
7604	A-2903	A-	A48	corn, Red Spring North Carolina; *pal1* (albino perithecia)
7605	A-2949	A-	A49	corn, Crowder Mississippi; *pal1* (albino perithecia)
7606	A-4516	A+	?	corn, Kathmandu Nepal; *fum1* (no fumonisin mycotoxins) (Sk^S)
7607	A-5113	A-	?	cross 7600 x 7606; *fum1* (no fumonisin mycotoxins) (Sk^S)
7054*	F-4091	F-	?	cross 7619 x 7620
7055*	F-4092	F+	?	cross 7619 x 7620
7056*	F-4093	F-	?	cross 7619 x 7620
7057*	F-4094	F+	?	cross 7619 x 7620
7618	F-966	F-	?	sorghum, Zeandale Kansas
7619	F-1377	F+	?	sorghum, WaKeeney Kansas
7620	F-1540	F-	?	cross 7618 x 7619
8078	A-04643	F+	?	cross A00149 x A04522

7950-8070 Progeny of cross 8078 x 7607. For molecular mapping. See Xu and Leslie, Genetics **143**:175-189 and Xu and Leslie, FGN **43**:61-65. RFLP Mapping probes for *Gibberella fujikuroi* mating population A are also available.

Fusarium proliferatum

7612	D-502	D+	?	corn, Rossville Kansas
7613	D-2945	D-	?	sorghum, Holcomb Mississippi
7614*	D-4853	D+	?	cross 7612 x 7613
7615*	D-4854	D-	?	cross 7612 x 7613

Fusarium subglutinans

7608	B-278	B+	B1	sugar cane, Hsingying Taiwan
7609	B-281	B-	B2	sugar cane, Hsingying Taiwan
7610*	B-3852	B+	?	cross 7608 x 7609
7611*	B-3853	B-	?	cross 7608 x 7609
7616*	E-990	E-	E14	corn, St. Elmo Illinois
7617*	E-2192	E+	E13	corn, St. Elmo Illinois

* - Standard mating type testers for each mating population

Strains from Anne Desjardins (See Appl Environ Microbiol 66:1020-1025)

FGSC #	Designation	Other number	Origin	Alternate Designation
8381	MP C MATC-1	HKM35	1997, Kavre Nepal	*Fusarium fujikuroi*
8382	MP C MATC-1	HKM41	1997, Lalitpur Nepal	*Fusarium fujikuroi*
8383	MP D MATD-1	HKM28	1997, Lalitpur Nepal	*Fusarium proliferatum*

Fusarium moniliforme auxotrophs

Nitrate non-utilizing strains.
Klittich and Leslie 1988. Genetics **118**:417-423

Mutant locus	Vegetative compat. grp.	Mating type	FGSC number
nit1	A1	A+	5955
nit1	A4	A-	5956
nit2	A1	A+	5965
nit2	A4	A-	5960
nit3	A1	A+	5966
nit3	A4	A-	5958
nit4	A1	A+	5964
nit4	A7	A-	5954
nit5	A3	A+	5961
nit5	?	A-	5967
nit6	A5	A+	5963
nit6	A4	A-	5959
nit7	A3	A+	5962
nit7	A4	A-	5957

Other mutants.
Puhalla & Spieth 1983. Exp. Mycol. **7**:328-335
and/or 1985. Exp. Mycol. **9**:39-47.

Mutant locus	Vegetative compat. grp.	Mating type	FGSC number
cys1	A1	A+	6887
nic1	A1	A+	6888
ora1	A1	A+	6889
pdx1	A2	A-	6890
met1	A2	A-	6891
lys1	A2	A-	6892
pro1	?	A+	6893
leu1	A3	A+	6894
arg1 nic1	A1	A+	6895
pdx1 nic1 ste1 (Sk^K)	?	A+	7597

Other references:

Chaisrisook and Leslie 1990. J. Heredity **81**:189-192 (*pal1*). Correll, Klittich, and Leslie 1989. Mycol. Res. **93**:21-27 (*hsi1*). Desjardins et al. 1992. Appl. Environ. Microbiol. **58**:2799-2805 (Fumonisin). Klittich and Leslie 1992. Mycologia **84**:541-547 (Mating population F). Leslie 1991. Phytopathology **81**:1058-1060 (Mating populations). Leslie et al. 1992. Mycopathologia **117**:37-45 (Fumonisin). Leslie et al. 1990. Phytopathology **80**:343-350 (wild-collected *Fusarim* spp.). Leslie et al. 1992. Phytopathology **82**:341-345 (Fumonisins in different mating populations)

Fusarium oxysporum f. sp. *asparagi* All strains from W.H. Elmer. See Elmer and Stephens 1989 Phytopathology 79:88-93 Each vegetative compatibility group is represented by one wild strain and one *nitM* strain. *nitM* = nitrate non-utilizing due to deficiency of molybdenum containing cofactor of nitrate reductase

VCG	Wildtype	FGSC#	Mutant	FGSC#
1001WE	MA25	6607	MA25M	6608
1002WE	MA16	6609	MA16M	6610
1003WE	MA24	6611	MA24M	6612
1004WE	MA43	6613	MA43M	6614
1005WE	MA54	6615	MA54M	6616
1006WE	MA9	6617	MA9M	6618
1007WE	MA6	6619	MA6M	6620
1008WE	MA23	6621	MA23M	6622

Nectria haematococca MP VI (= *Fusarium solani* f sp *pisi*)
All strains from H. D. Van Etten. Some have been characterized with regard to detoxification of other phytoalexins and cutinase activity.

Genotype	FGSC #	Other #	Reference
Pda1	8119	77-2-3	Maloney and VanEtten, Mol Gen Genet 243:506-514
Pda1	9596	77-13-4	Miao et al, Mol Gen Genet 226: 214-223, US DOE JGI strain
Pda2	8120	96-17	Miao et al, Mol Gen Genet 226: 214-223
Pda3	8121	62-22	Miao et al, Mol Gen Genet 226: 214-223
Pda4	8122	196-10-7	Miao et al, Mol Gen Genet 226: 214-223
Pda5	8123	55-5-1	Miao et al, Mol Gen Genet 226: 214-223
Pda6.1	8124	156-30-6	Miao et al, Appl Environ Micrbiol 58:801-808
Pda6.2	8125	24-1-1	Miao et al, Mol Gen Genet 226: 214-223
Pda1	9596	77-13-4	

Fusarium oxysporum f. sp. *cubense* (all from Randy Ploetz, Univ of Florida)

FGSC #	Other number	VCG	Origin
8353	K5	01215	South Africa
8354	4S1	0126	Honduras
8355	BLUG	0124	Honduras
8356	RPML39	"01223"	Malaysia
8357	01221	0129	Queensland, Australia
8358	II 5	01213	Sulawesi
8359	01219	0120	Queensland, Australia
8360	PH2	0122	Philipines
8361	8611	0125	Currumbin, Queensland
8362	RPTH56	01221	Chiang Rai, Thailand
8363	MAL11	01216	Malaysia
8364	RPTH28	01218	Yala province, Thailand
8365	MW42	01214	Karonga, Malawi
8366	RPML4	"01222"	Malaysia
8367	22994	0128	South Johnstone, Queensland
8368	F9130	0121	Taiwan
8369	SH3142	01211	Queensland, Australia
8370	STNP2	01212	Bukava Station, Tanzania
8371	RPML45	"01224"	Malaysia
8384	A1-1	01210	Florida, USA
8385	JLTH5	0123	Smoeng Hwy, Thailand

See Phytopathology (1997) 87:915-923, Fruits (1996) 51:387-395

Fusarium verticillioides auxotrophs

Genotype	FGSC #	JFL#
nit1$^-$ MatA-2	8908	A-00924
nit1$^-$ Fum$^-$ MatA-1	8909	A-04644

Fusarium konzum

Genotype	FGSC #	JFL#
Female Fertile MAT-1	8910	KSU 11616
Female Fertile MAT-2	8911	KSU 11615
Female Sterile MAT-2	8912	KSU 10595
Weakly FertileMAT-1	8913	KSU 10653

Fusarium graminearum

FGSC #	Other #	Designation	Depositor
9075	NRRL 31084	Genome Program WT	FT
8630	Z-3693	parent	JFL
8631	Z-5047	parent	JFL
8632	Z-11570	nit-	JFL
8633	Z-11572	nit-	JFL
9602	PH-1 hyg2-1	parent	HCK
9603	00-676	parent	HCK
8733	16A	Wild Type	MU
8734	CAM1	DMAP1	MU
8735	CAM2	DMAP1	MU
8736	CAM8	Hyg::MAP1^{E}	MU
8959	*F. graminearum*	R5317	JY
9084	*F. graminearum* Lineage 8	NRRL 29306	KOD
9085	*F. graminearum* Lineage 7	NRRL 5883	KOD
9086	*F. graminearum* Lineage 6	NRRL 13818	KOD
9087	*F. graminearum* Lineage 5	NRRL 26752	KOD
9088	*F. graminearum* Lineage 4	NRRL 29148	KOD
9089	*F. graminearum* Lineage 3	NRRL 29020	KOD
9090	*F. graminearum* Lineage 2	NRRL 28436	KOD
9091	*F. graminearum* Lineage 1	NRRL 28585	KOD
9488	Tri3	11	SM
9489	Tri8b	26	SM
9490	Tri8b	3	SM
9491	Tri8b	29	SM
9492	Tri8b	4	SM
9493	Tri8b	2	SM
9494	Tri8b	1	SM
9495	Tri8b	37	SM
9496	Tri11D	12	SM
9497	LH1	41	SM
9498	LH1	65	SM
9499	LH1	72	SM
9500	LH1	44	SM
9501	LH1	3	SM
9502	LH1	47	SM
9503	LH1	59	SM
9553	tri5-3 HygB	GZ3R1	RHP
9554	tri5-3 HygB	GZ3R7	RHP
9555	tri5-3 HygB	GZ4R1	RHP
9556	tri5-3 HygB	GZ4R2	RHP
9557	tri5-3 HygB	GZ4R3	RHP
9558	tri5-3 HygB	GZ4R4	RHP
9559	tri5-3 HygB	GZT40	RHP
9560	tri5-2 HygB	GZT33	RHP
9561	tri5-1 HygB	GZT106	RHP
9562	tri5-1 HygB	GZT108	RHP
9563	Fum1-1, Fum2-1, Fum3-1	M-3125	RHP
9564	Fum1-1, Fum 2-2, fum3-1	109-R-7	RHP
9565	Fum1-1, Fum2-2, fum3-1	109-R-14	RHP
9566	FUM1 HygB	GfA2364	RHP
9569	FUM1 HygB	GfA2556	RHP

The parents and progeny strains from a cross of 8632 and 8633 were deposited by Dr. John Leslie.
The progeny are 8634 (Z-10879) through 8732 (Z-10977)
The progeny from a cross of 9602 and 9603 were deposited by Dr. H. Corby Kistler. They are FGSC #'s 9604- 9715.

Other Fusarium strains

FGSC #	Designation	Other #	Depositor
8931	*G. fujikuroi*	FGC M-1148	DG
8932	*G. fujikuroi*	FRC M-1150	DG
8933	*F. nygamai*	FRC M-7491	DG
8934	*F. nygamai*	FRC M-7492	DG
8960	*F. sporotrichioides*	T0348	JY
8961	*Fusarium verticillioides*	M3125	JY
9022	H-(MAT-1)	MRC 7488	JFL
9023	H+ (MAT2)	MRC 6213	JFL
9092	*F. lumulosporum*	NRRL 13393	KOD
9093	*F. cerealis*	NRRL 25491	KOD
9094	*F. culmorum*	NRRL 25475	KOD
9095	*F. pseudograminearum*	NRRL 28062	KOD
9463	*F. verticillioides* fdb1, fdb2	AEG1-1-57	AEG
9464	*F. verticillioides* FDB1, fdb2	AEG3-A3-1	AEG
9465	*F. verticillioides* fdb1, fdb2, fph1	AEG3-A3-2	AEG
9466	*F. verticillioides* FDB1, FDB2	AEG3-A3-3	AEG
9467	*F. verticillioides* FDB1, FDB2	AEG3-A3-4	AEG
9468	*F. verticillioides* fdb1, FDB2, fph1	AEG3-A3-5	AEG
9469	*F. verticillioides* fdb1, FDB2, fph1	AEG3-A3-6	AEG
9470	*F. verticillioides* FDB1, fdb2	AEG3-A3-7	AEG
9471	*F. verticillioides* fdb1, fdb2, fph1	AEG3-A3-8	AEG
9476	fdb1, fdb2	AEG3-1-6	AEG
9477	FDB1, FDB2	AEG73-A4-1	AEG
9478	FDB1, fdb2	AEG73-A4-2	AEG
9479	fdb1, FDB2	AEG73-A4-3	AEG
9480	fdb1, fdb2	AEG73-A4-4	AEG
9481	fdb1, FDB2	AEG73-A4-5	AEG
9482	FDB1, FDB2	AEG73-A4-6	AEG
9483	FDB1, fdb2	AEG73-A4-7	AEG
9935	*F. oxysporum* fsp *lycopersici*	NRRL 34936, 4287	KOD

Gene Libraries

The FGSC holds the fosmid and BAC libraries used in sequencing the *Fusarium graminearum* genome at the Broad Institute as well as additional cDNA and genomic libraries for several Fusarium species. Please visit the FGSC web-site for additional details.

Magnaporthe grisea

The FGSC holds a number of wild type Magnaporthe strains. Most are from genetic mapping populations.

FGSC #	Other #	Depositor	Comment
8958	70-15	RD	Used in genome program
9462	Guy-11	MO	Mating partner for RFLP

Below are strains used in making the RFLP map. A copy of a permit to receive the strains is required before we can send them. They were deposited by Mark Farman (MF) or Barbara Valent (BV).

FGSC #	Other #	Depositor
8417	5982	MF
8418	6000	MF
8419	6003	MF
8420	6604	MF
8421	6005	MF
8422	6007	MF
8423	6008	MF
8424	6022	MF
8425	6023	MF
8426	6024	MF
8427	6025	MF
8428	6026	MF
8429	6027	MF
8430	6028	MF
8431	6029	MF
8432	6039	MF
8433	6047	MF
8434	6050	MF
8435	6051	MF
8436	6052	MF
8437	6054	MF
8438	6055	MF
8439	6058	MF
8440	6059	MF
8441	6061	MF
8442	6062	MF
8443	6063	MF
8444	6066	MF
8445	6068	MF
8446	6069	MF
8447	6071	MF
8448	6072	MF
8449	6075	MF
8450	6076	MF
8451	6077	MF
8452	6079	MF
8453	6080	MF
8454	6081	MF
8455	6082	MF
8456	6085	MF
8457	6086	MF
8458	6087	MF
8459	6089	MF
8460	6090	MF
8461	6092	MF
8462	6093	MF
8463	6094	MF

FGSC #	Other #	Depositor
8464	6095	MF
8465	6099	MF
8466	6100	MF
8467	6101	MF
8468	6102	MF
8469	6103	MF
8470	6106	MF
8471	6109	MF
8472	6111	MF
8473	6112	MF
8474	6115	MF
8475	10058	MF
8476	10077	MF
8477	4360-R-1	BV
8478	4360-R-2	BV
8479	4360-R-7	BV
8480	4360-R-8	BV
8481	4360-R-9	BV
8482	4360-R-10	BV
8483	4360-R-12	BV
8484	4360-R-13	BV
8485	4360-R-14	BV
8486	4360-R-15	BV
8487	4360-R-16	BV
8488	4360-R-17	BV
8489	4360-R-18	BV
8490	4360-R-19	BV
8491	4360-R-20	BV
8492	4360-R-21	BV
8493	4360-R-22	BV
8494	4360-R-23	BV
8495	4360-R-24	BV
8496	4360-R-25	BV
8497	4360-R-26	BV
8498	4360-R-27	BV
8499	4360-R-28	BV
8500	4360-R-29	BV
8501	4360-R-30	BV
8502	4360-R-31	BV
8503	4360-R-32	BV
8504	4360-R-34	BV
8505	4360-R-35	BV
8506	4360-R-36	BV
8507	4360-R-37	BV
8508	4360-R-39	BV
8509	4360-R-40	BV
8510	4360-R-41	BV

Magnaporthe grisea, continued.

FGSC #	Other #	Depositor
8511	4360-R-42	BV
8512	4360-R-43	BV
8513	4360-R-44	BV
8514	4360-R-45	BV
8515	4360-R-46	BV
8516	4360-R-47	BV
8517	4360-R-48	BV
8518	4360-R-49	BV
8519	4360-R-50	BV
8520	4360-R-51	BV
8521	4360-R-52	BV
8522	4360-R-53	BV
8523	4360-R-54	BV
8524	4360-R-56	BV
8525	4360-R-57	BV
8526	4360-R-58	BV
8527	4360-R-59	BV
8528	4360-R-60	BV
8529	4360-R-61	BV
8530	4360-R-62	BV
8531	4360-R-63	BV
8532	4360-R-64	BV
8533	4360-R-65	BV
8534	4360-R-66	BV
8535	4360-R-67	BV
8536	4360-R-68	BV
8537	4360-R-69	BV
8538	4360-R-70	BV
8539	4360-R-71	BV
8540	4360-R-72	BV
8541	4360-R-73	BV
8542	4360-R-80	BV
8543	4360-R-83	BV
8544	6043	BV
8545	422-7-8	BV
8546	0-135	BV
8547	0-137	BV
8595	6074	MF

Magnaporthe grisea RFLP probes

We have received a set of 182 RFLP probes for Magnaporthe from Dr. S.A. Leong. These are described in Theor. Appl. Genet. 95:20-32, 88:901-908 and 87:545-557, and Genetics 140:479-492. They are available as individual clones or as a set of microtitre plates. Please contact the FGSC for details.

Gene Libraries

The FGSC holds the BAC library used in sequencing the *Magnaporthe grisea* genome at the Broad Institute as well as additional cDNA and genomic libraries for Magnaporthe. Please visit the FGSC web-site for additional details.

Schizophyllum commune
Please refer to Raper, C. and Fowler, T., Fungal Genetics Newsletter 51 for more information on these strains.

FGSC #	Characteristics	Other Stock #
9098	Old A-Factor # 2, A alpha 4, A beta 7, Old B-	H1-2
9099	Old A-Factor # 3, A alpha, A beta, Old B-Factor	H1-3
9100	Old A-Factor # 5, A alpha 1, A beta 1, Old B-	H1-5
9101	Old A-Factor # 6, A alpha 9, A beta 22, Old B-	H1-6
9102	Old A-Factor # 8, A alpha, A beta, Old B-Factor	H1-7
9103	Old A-Factor # 8, A alpha, A beta, Old B-Factor	H1-8
9104	Old A-Factor # 9, A alpha 1, A beta 11, Old B-	H1-9
9105	Old A-Factor # 10, A alpha, A beta, Old B-	H1-10
9106	Old A-Factor # 13, A alpha 3, A beta 4, Old B-	H1-13
9107	Old A-Factor # 14, A alpha, A beta, Old B-	H1-14
9108	Old A-Factor # 16, A alpha 1, A beta 9, Old B-	H1-15
9109	Old A-Factor # 15, A alpha, A beta, Old B-	H1-16
9110	Old A-Factor # 17, A alpha, A beta, Old B-	H1-17
9111	Old A-Factor # 18, A alpha, A beta, Old B-	H1-18
9112	Old A-Factor # 19,20, A alpha, A beta, Old B-	H1-19
9113	Old A-Factor # 25, A alpha, A beta, Old B-	H1-25
9114	Old A-Factor # 26, A alpha, A beta, Old B-	H1-26
9115	Old A-Factor # 27, A alpha, A beta, Old B-	H1-27
9116	Old A-Factor # 28, A alpha, A beta, Old B-	H1-28
9117	Old A-Factor # 32, A alpha, A beta, Old B-	H1-32
9118	Old A-Factor # 35, A alpha 3, A beta 20, Old B-	H1-34
9119	Old A-Factor # 36, A alpha, A beta, Old B-	H1-35
9120	Old A-Factor # 37, A alpha, A beta, Old B-	H1-36
9121	Old A-Factor # 38, A alpha, A beta, Old B-	H1-37
9122	Old A-Factor # 39, A alpha, A beta, Old B-	H1-38
9123	Old A-Factor # 39,40, A alpha, A beta, Old B-	H1-39
9124	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H1-40
9125	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H1-41
9126	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H1-42
9127	Old A-Factor # 46, A alpha 1, A beta 3, Old B-	H1-44
9128	Old A-Factor # 47, A alpha 3, A beta 4, Old B-	H1-45
9129	Old A-Factor # 48, A alpha 7, A beta 26, Old B-	H1-46
9130	Old A-Factor # 49, A alpha 2, A beta 3, Old B-	H1-47
9131	Old A-Factor # 47,48, A alpha 3,7, A beta 4,26,	H1-48
9132	Old A-Factor # 49,50, A alpha, A beta, Old B-	H1-49
9133	Old A-Factor # 51, A alpha 2, A beta 2, Old B-	H1-50
9134	Old A-Factor # 53, A alpha, A beta, Old B-	H1-52
9135	Old A-Factor # 55,56, A alpha 7,?, A beta 21,?,	H1-53
9136	Old A-Factor # 57, A alpha, A beta, Old B-	H1-54
9137	Old A-Factor # 58, A alpha, A beta, Old B-	H1-55
9138	Old A-Factor # 59, A alpha, A beta, Old B-	H1-56
9139	Old A-Factor # 59,60, A alpha, A beta, Old B-	H1-57
9140	Old A-Factor # 61, A alpha, A beta, Old B-	H1-58
9141	Old A-Factor # 62, A alpha 1, A beta 5, Old B-	H1-59
9142	Old A-Factor # 64(=61), A alpha, A beta, Old B-	H1-61
9143	Old A-Factor # 65,66, A alpha 3,?, A beta 20,?,	H1-62
9144	Old A-Factor # 66, A alpha, A beta, Old B-	H1-63
9145	Old A-Factor # 67, A alpha, A beta, Old B-	H1-64
9146	Old A-Factor # 68, A alpha 3, A beta 5, Old B-	H1-65
9147	Old A-Factor # 70, A alpha, A beta, Old B-	H1-66
9148	Old A-Factor # 71, A alpha 2, A beta 13, Old B-	H1-67
9149	Old A-Factor # 72, A alpha 3, A beta 22, Old B-	H1-68
9150	Old A-Factor # 75, A alpha 3, A beta 1, Old B-	H1-71
9151	Old A-Factor # 76, A alpha, A beta, Old B-	H1-72
9152	Old A-Factor # 77, A alpha 5, A beta 24?, Old B-	H1-73
9153	Old A-Factor # 78, A alpha 5, A beta 24?, Old B-	H1-74
9154	Old A-Factor # 81, A alpha, A beta, Old B-	H1-76
9155	Old A-Factor # 82, A alpha, A beta, Old B-	H1-77
9156	Old A-Factor # 85, A alpha, A beta, Old B-	H1-80

FGSC #	Characteristics	Other Stock #
9157	Old A-Factor # 86, A alpha 3, A beta 7, Old B-	H1-81
9158	Old A-Factor # 87, A alpha 9, A beta 15, Old B-	H1-82
9159	Old A-Factor # 88, A alpha 5, A beta 25, Old B-	H1-83
9160	Old A-Factor # 89, A alpha 5, A beta 10, Old B-	H1-84
9161	Old A-Factor # 74, A alpha 5, A beta 7, Old B-	H1-86
9162	Old A-Factor # 92, A alpha 4, A beta 16, Old B-	H1-87
9163	Old A-Factor # 93, A alpha, A beta, Old B-	H1-88
9164	Old A-Factor # 94, A alpha 5, A beta 18, Old B-	H1-89
9165	Old A-Factor # 96, A alpha, A beta, Old B-	H1-91
9166	Old A-Factor # 97, A alpha, A beta, Old B-	H1-92
9167	Old A-Factor # 98, A alpha 9, A beta 7, Old B-	H1-93
9168	Old A-Factor # 97,98, A alpha ?,9, A beta ?,7,	H1-94
9169	Old A-Factor # 99, A alpha 3, A beta 17, Old B-	H1-95
9170	Old A-Factor # 100?, A alpha, A beta, Old B-	H1-96
9171	Old A-Factor # 101, A alpha, A beta, Old B-	H1-97
9172	Old A-Factor # 102, A alpha 5, A beta 18, Old B-	H1-98
9173	Old A-Factor # 103, A alpha, A beta, Old B-	H1-99
9174	Old A-Factor # 107, A alpha 1, A beta 15, Old B-	H1-103
9175	Old A-Factor # 108, A alpha, A beta, Old B-	H1-104
9176	Old A-Factor # 109, A alpha, A beta, Old B-	H1-105
9177	Old A-Factor # 111, A alpha, A beta, Old B-	H1-107
9178	Old A-Factor # 112, A alpha 9, A beta 7, Old B-	H1-108
9179	Old A-Factor # 114, A alpha 7, A beta 3, Old B-	H1-110
9180	Old A-Factor # 117, A alpha 1, A beta 7, Old B-	H1-113
9181	Old A-Factor # 118, A alpha 5, A beta 24, Old B-	H1-114
9182	Old A-Factor # 119, A alpha, A beta, Old B-	H1-115
9183	Old A-Factor # 120, A alpha 7, A beta 3, Old B-	H1-116
9184	Old A-Factor # 121122, A alpha, A beta, Old B-	H1-117
9185	Old A-Factor # 123, A alpha 5, A beta 25, Old B-	H1-118
9186	Old A-Factor # N/A, A alpha 1, A beta 2, Old B-	H2-1
9187	Old A-Factor # N/A, A alpha 1, A beta 4, Old B-	H2-2
9188	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H2-3
9189	Old A-Factor # N/A, A alpha 1, A beta 12, Old B-	H2-5
9190	Old A-Factor # N/A, A alpha 1, A beta 13, Old B-	H2-6
9191	Old A-Factor # N/A, A alpha 1, A beta 14, Old B-	H2-7
9192	Old A-Factor # N/A, A alpha 1, A beta 15, Old B-	H2-8
9193	Old A-Factor # N/A, A alpha 1, A beta 16, Old B-	H2-9
9194	Old A-Factor # N/A, A alpha 1, A beta 17, Old B-	H2-10
9195	Old A-Factor # N/A, A alpha 1, A beta 18, Old B-	H2-11
9196	Old A-Factor # N/A, A alpha 1, A beta 20, Old B-	H2-13
9197	Old A-Factor # N/A, A alpha 1, A beta 21, Old B-	H2-14
9198	Old A-Factor # N/A, A alpha 1, A beta 25, Old B-	H2-17
9199	Old A-Factor # N/A, A alpha 2, A beta 1, Old B-	H2-19
9200	Old A-Factor # N/A, A alpha 6, A beta 1, Old B-	H2-21
9201	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H3-2
9202	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H3-3
9203	Old A-Factor #, A alpha, A beta, Old B-	H3-4
9204	Old A-Factor # 4, A alpha 8, A beta 12, Old B-	H3-5
9205	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H3-6
9206	Old A-Factor #, A alpha, A beta, Old B-	H3-7
9207	Old A-Factor #, A alpha, A beta, Old B-Factor #	H3-9
9208	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H4-3
9209	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H4-5
9210	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H4-8
9211	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H4-11
9212	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H4-12
9213	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H4-13
9214	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	H4-14
9215	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H4-31

FGSC #	Characteristics	Other Stock #
9216	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H4-39
9217	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H4-40
9218	Old A-Factor #, A alpha 1 or 4, A beta 1(1), Old	H4-44
9219	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H5-1
9220	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H5-2
9221	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H5-3
9222	Old A-Factor #, A alpha, A beta, Old B-Factor	H5-4
9223	Old A-Factor #, A alpha, A beta, Old B-Factor #	H5-5
9224	Old A-Factor #, A alpha, A beta, Old B-Factor #	H5-6
9225	Old A-Factor # dik, A alpha 4,1, A beta 6,6, Old	H5-8
9226	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H5-10
9227	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-1
9228	Old A-Factor #, A alpha, A beta, Old B-Factor #	H6-2
9229	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-4
9230	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H6-5
9231	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H6-6
9232	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H6-9
9233	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H6-11
9234	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-12
9235	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-13
9236	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H6-14
9237	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H6-15
9238	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-16
9239	Old A-Factor # 23?, A alpha 1, A beta 5?, Old B-	H6-17
9240	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H6-18
9241	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-20
9242	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-21
9243	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-22
9244	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H6-23
9245	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H6-24
9246	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H6-25
9247	Old A-Factor # N/A, A alpha 4, A beta 1(1-0^2),	H6-27
9248	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H6-28
9249	Old A-Factor # N/A, A alpha 4, A beta 1, Old B-	H6-29
9250	Old A-Factor # N/A, A alpha 4, A beta 1, Old B-	H6-30
9251	Old A-Factor # N/A, A alpha 1, A beta 6?, Old B-	H6-31
9252	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H7-5
9253	Old A-Factor # N/A, A alpha 1, A beta 1(1)sup1,	H7-35
9254	Old A-Factor # N/A, A alpha 4, A beta 1(1)sup2,	H7-36
9255	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-1
9256	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H8-3
9257	Old A-Factor # 11, A alpha, A beta, Old B-	H8-6
9258	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-7
9259	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-8
9260	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-9
9261	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H8-10
9262	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-11
9263	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H8-12
9264	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H8-13
9265	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H8-14
9266	Old A-Factor #, A alpha, A beta, Old B-Factor	H8-16
9267	Old A-Factor # 41 or 43, A alpha, A beta, Old	H8-17
9268	Old A-Factor # 41 or 43, A alpha, A beta, Old	H8-19
9269	Old A-Factor # 41 or 43, A alpha, A beta, Old	H8-25
9270	Old A-Factor #, A alpha, A beta, Old B-Factor	H8-26
9271	Old A-Factor #, A alpha, A beta, Old B-Factor	H8-27
9272	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H8-28
9273	Old A-Factor # 4, A alpha 8, A beta 12, Old B-	H8-29
9274	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	H9-1,frt

FGSC #	Characteristics	Other Stock #
9275	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	H9-1,non frt
9276	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H9-3
9277	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	H9-4
9278	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H9-5
9279	Old A-Factor # 9, A alpha, A beta, Old B-Factor	H9-6
9280	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H9-7
9281	Old A-Factor # 2, A alpha, A beta, Old B-Factor	H9-8
9282	Old A-Factor #, A alpha 4, A beta 1, Old B-	H9-10
9283	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	H9-12
9284	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	H10-1
9285	Old A-Factor #, A alpha 4, A beta 1, Old B-	H11-1
9286	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H11-3
9287	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	H11-7
9288	Old A-Factor # N/A, A alpha 4 or 1, A beta 1(1),	H11-11
9289	Old A-Factor # N/A, A alpha 4 or 1, A beta 1(1),	H11-12
9290	Old A-Factor # N/A, A alpha 4 or 1, A beta 1(1),	H11-13
9291	Old A-Factor # N/A, A alpha 4 or 1, A beta 1(1),	H11-14
9292	Old A-Factor # N/A, A alpha 4 or 1, A beta 1(1),	W1-14
9293	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	W4-19
9294	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	W5-12
9295	Old A-Factor # 14, A alpha, A beta, Old B-	W6-33
9296	Old A-Factor # 51, A alpha 2, A beta 2, Old B-	W7-22
9297	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	12-43
9298	Old A-Factor #, A alpha 4, A beta 1, Old B-	T-11
9299	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	T-12
9300	Old A-Factor #, A alpha 7, A beta 1, Old B-	T-26
9301	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	72(2)
9302	Old A-Factor #, A alpha 5, A beta 7, Old B-	72-4
9303	Old A-Factor # N/A, A alpha 1, A beta 6, Old B-	V11-20
9304	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	V14-40
9305	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	V16-4
9306	Old A-Factor # 41, A alpha 1, A beta 1, Old B-	V28-2
9307	Old A-Factor # N/A, A alpha 4, A beta 1(1), Old	V46-48
9308	Old A-Factor # N/A, A alpha 4, A beta 1(1), Old	V51-15
9309	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	V63-41
9310	Old A-Factor # N/A, A alpha 1, A beta 1(1), Old	V63-50
9311	Old A-Factor #, A alpha 5, A beta 7, Old B-	V112-3
9312	Old A-Factor # 3, A alpha, A beta, Old B-Factor	V112-17
9313	Old A-Factor # 35, A alpha 3, A beta 20, Old B-	V113-9
9314	Old A-Factor # 35, A alpha 3, A beta 20, Old B-	V113-17
9315	Old A-Factor # 37, A alpha, A beta, Old B-	V114-3
9316	Old A-Factor # 37, A alpha, A beta, Old B-	V114-25
9317	Old A-Factor #, A alpha 5, A beta 7, Old B-	V115-3
9318	Old A-Factor # 15, A alpha, A beta, Old B-	V115-4
9319	Old A-Factor # 51, A alpha 2, A beta 2, Old B-	V118-4
9320	Old A-Factor #, A alpha 5, A beta 7, Old B-	V118-7
9321	Old A-Factor #, A alpha 5, A beta 7, Old B-	V119-19
9322	Old A-Factor #, A alpha 5, A beta 7, Old B-	V119-32
9323	Old A-Factor #, A alpha 5, A beta 7, Old B-	V121-5
9324	Old A-Factor # 87, A alpha 9, A beta 15, Old B-	V123-18
9325	Old A-Factor # 87, A alpha 9, A beta 15, Old B-	V123-29
9326	Old A-Factor # 89, A alpha 5, A beta 10, Old B-	V124-5
9327	Old A-Factor # 86, A alpha 3, A beta 7, Old B-	V125-8
9328	Old A-Factor #, A alpha 5, A beta 7, Old B-	V125-20
9329	Old A-Factor #, A alpha 8, A beta 12, Old B-	V131-5
9330	Old A-Factor #, A alpha 5, A beta 7, Old B-	V131-16
9331	Old A-Factor #, A alpha 7 or 3, A beta 1 or 5,	V140-24
9332	Old A-Factor #, A alpha 7 or 3, A beta 1 or 5,	V140-27
9333	Old A-Factor # 23?, A alpha 1 or 3, A beta 5, Old	V141-6

FGSC #	Characteristics	Other Stock #
9334	Old A-Factor # 23?, A alpha 1 or 3, A beta 5, Old	V141-11
9335	Old A-Factor # 2, A alpha 4, A beta 7, Old B-	V142-3
9336	Old A-Factor #, A alpha 4, A beta 1, Old B-	V142-5
9337	Old A-Factor #, A alpha 5, A beta 7, Old B-	V147-1
9338	Old A-Factor # 118, A alpha 5, A beta 24, Old B-	V147-6
9339	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	V150-21
9340	Old A-Factor #, A alpha, A beta, Old B-Factor #	V150-24
9341	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	V151-18
9342	Old A-Factor # N/A, A alpha 4, A beta 7, Old B-	V151-20
9343	Old A-Factor # 41 or 42, A alpha 1 or 3, A beta 1	V153-14
9344	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	V153-21
9345	Old A-Factor #, A alpha 5, A beta 7, Old B-	V187-13
9346	Old A-Factor # 1, A alpha 7, A beta 12, Old B-	V187-29
9347	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	V201-13
9348	Old A-Factor # 43, A alpha 4, A beta 6, Old B-	V201-36
9349	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	V201-37
9350	Old A-Factor # 42, A alpha 3, A beta 5, Old B-	V201-106