

Fungal Genetics Stock Center Catalogue of Strains, 9th edition

Kevin McCluskey
University of Kansas Medical Center

John A. Kinsey
University of Kansas Medical Center

Follow this and additional works at: <http://newprairiepress.org/fgr>

Recommended Citation

McCluskey, K., and J.A. Kinsey (2002) "Fungal Genetics Stock Center Catalogue of Strains, 9th edition," *Fungal Genetics Reports*: Vol. 49, Article 14. <https://doi.org/10.4148/1941-4765.1196>

This Supplementary Material is brought to you for free and open access by New Prairie Press. It has been accepted for inclusion in Fungal Genetics Reports by an authorized administrator of New Prairie Press. For more information, please contact cads@k-state.edu.

Fungal Genetics Stock Center Catalogue of Strains, 9th edition

Abstract

Catalogue of Strains, 9th edition, 2002, supplement to Fungal Genetics Newsletter No. 49. This catalogue contains lists of materials held by the Fungal Genetics Stock Center.

Creative Commons License



This work is licensed under a [Creative Commons Attribution-Share Alike 4.0 License](https://creativecommons.org/licenses/by-sa/4.0/).

FUNGAL GENETICS STOCK CENTER
CATALOGUE OF STRAINS

9th Edition

2002

Supplement to Fungal Genetics Newsletter No. 49

Kevin McCluskey, Ph.D. Curator

John A. Kinsey, Ph.D. Director

Department of Microbiology

University of Kansas Medical Center

Kansas City, KS 66160-7420

913-588-7044

FAX 913-588-7295

WWW.FGSC.NET

Supported by National Science Foundation Grant DBI 9726962

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: \$20.00 per culture is requested of individuals and nonprofit institutions using the strains for research. All or part of this request can be waived for those without department or grant funding. A maximum contribution of \$200.00 will be asked for shipments of more than 10 strains within reasonable limits. Certain kits of strains, designed to be used together, are available for \$75.00, though each kit contains more than 4 strains. Strains for teaching at the undergraduate or K-12 level are available for \$10. Commercial concerns are charged \$50.00 per strain, and \$200.00 for kits. **There is no price cap for commercial orders.**

Cloned genes or individual cosmids are considered individual strains. Separate pricing schemes exist for gene libraries. The price cap does not include plasmids, cosmid clones or gene libraries. While fees may be waived for individual clones, they are not normally waived for gene libraries.

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 UPS. 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 913-588-7044; the FAX number is 913-588-7295; We encourage the use of E-mail as this assures timely and accurate ordering. The FGSC e-mail address is fgsc@fgsc.net. The FGSC will always be on-line at www.fgsc.net and orders can be placed 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*.

FGSC on the Internet: A site maintained by FGSC can be accessed via the World Wide Web. Included are lists of stocks, genes and libraries available from the Stock Center, research methods, links, a bulletin board, the *Neurospora* and *Aspergillus* compendia, recent reprints from the Fungal Genetics Newsletter, and the FGN mailing list. We try to keep the FGSC web site updated, so recently deposited strains will show in the search areas before they are listed elsewhere. The FGSC can be found at www.fgsc.net.

Nomenclature: Brief sections on nomenclature and symbols have appeared in: *Neurospora* Newsletter 8:23 (Barratt and Perkins, 1965); *Neurospora* Newsletter 14:13 (Barratt, 1969); *Neurospora* Newsletter 20:38 (Perkins and Barratt, 1973) and *Adv. Genetics* (Perkins and Barry, 1977). In the Newsletters, FGSC has made this appeal: "Please do not use the FGSC number as a substitute for the genotype, allele or locus."

With issue 6 of the FGSC catalog we have tried to use correct nomenclature. If you find errors please notify the FGSC.

Format: The 9th edition of the FGSC catalog is marked by a change in format. Molecular materials are now 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

Section A. Cloning tools	5
Section B. Neurospora and relatives	
Molecular tools	
Plasmids	7
Gene Libraries	
Genomic	9
cDNA	11
Neurospora stocks	
Part I. Single mutant stocks	13
Part II. Multiple mutant stocks	63
Part III. Mitochondrial mutants and stocks containing mitochondrial plasmids	83
Part IV. Wild type strains	
<i>Neurospora africana</i>	86
<i>Neurospora crassa</i> :	
Standard reference strains and derived wild types	86
Original <i>N. crassa</i> strains collected from nature	87
<i>Neurospora discreta</i>	90
<i>Neurospora dodgei</i>	90
<i>Neurospora galapagosensis</i>	90
<i>Neurospora intermedia</i> :	
Reference strains, derived wild types	90
Original <i>N. intermedia</i> strains collected from nature	91
<i>N. intermedia</i> mutants	98
<i>Neurospora lineolata</i>	98
<i>Neurospora pannonica</i>	98
<i>Neurospora sitophila</i> :	
Reference strains, derived wild types and mutants	98
Original collected <i>N. sitophila</i> strains	99
<i>Neurospora sublineolata</i>	102
<i>Neurospora terricola</i>	102
<i>Neurospora tetrasperma</i> :	
Reference strains, derived wild types	102
<i>N. tetrasperma</i> wild-collected	103
Miscellaneous <i>N. tetrasperma</i> from Dodge collection	106
<i>N. tetrasperma</i> mutants	107
<i>Neurospora toroi</i> (probably = <i>N. tetrasperma</i>)	108
Neurospora collected from nature, species uncertain	109
Genes transferred between Neurospora species	109
Hybrid strains useful for interspecific gene transfer	110
Other genera related to Neurospora	111
Ascobolus	112
Part V. Aberration Stocks	
A. Reciprocal translocations. Single translocation stocks	113
B. Complex translocations involving more than one linkage group	116
C. Inversions that do not generate viable duplications	116
D. Insertional translocations that do not generate viable duplications	116
E. Rearrangements that produce viable duplications when crossed by normal	117
F. Heteromorphic chromosome stocks	118
G. Mini-chromosome stocks	118

Part VI. Testers and stocks for special purposes

A. Linkage Testers	119
1. Alcoy - follow-up testers for use with alcoy	119
2. Multiply marked centromere testers (Multicent)	119
3. Pairs of strains used as prototrophic heterokaryons in crosses x unmapped mutants	119
4. Testers for linkage in distal regions	120
5. Multiply marked mapping strains with <i>sn cr-1</i> for replication	121
B. Standard <i>N. crassa</i> wild types and mating type testers	121
C. Species testers and reference strains	121
D. Heterokaryon incompatibility testers and reference strains:	
1. Normal sequence testers for <i>het-c, -d, -e</i>	122
2. Testers for het-incompatibility in duplications	122
E. Strains for mutant enrichment and replication	123
F. Cross for molecular mapping	124
G. <i>Multicent-2</i> cross kit with centromere markers	124
H. Strains for obtaining protoplasts or spheroplasts	124
I. Strains for disruption of essential genes	125
J. Strains that produce only microconidia	126
K. Special teaching strains	126
Mutants with <i>eas</i>	126
L. Strains for photobiology and circadian rhythms	126
M. Spore-killer tester strains	127
N. Transport mutants	128
O. Tester set to determine the genotype of <i>ad-3</i> mutants induced in homokaryons or two-component heterokaryons	129
P. Strains used to study the genetic structure of the <i>ad-3</i> region	130
Q. Set of tester strains to determine the nature of damage in individual <i>ad-3^{IR}</i> mutations	130
R. Strains for testing reverse mutation rates	130
S. Strains used as testers to determine the nature of genetic damage in the <i>ad-3</i> and adjacent regions	130
T. Wild-type and repair-deficient strains with markers identical to those used in component II of Heterokaryon 12	130
U. Mutant strains used to distinguish between point mutations and multilocus deletions in the <i>ad-3</i> region	131
V. Strains used as heterokaryon testers in crosses to obtain stocks heterokaryon compatible with 74A	131
W. Two component heterokaryons for studying the effects of repair deficient mutations on mutation induction in the <i>ad-3</i> region	131
X. 2-17 series <i>ad-3</i> mutants	132
Y. 2-15 series <i>ad-3</i> mutants	133
Z. Additional <i>ad-8</i> mutants	133
AA. Dikaryons and trikaryons	134
BB. Additional <i>his-3</i> alleles from Yale	134
CC. <i>leu-2</i> mutants from S.R. Gross	135
DD. Strains for targeted transformation	135
EE. Strains for assaying aneuploidy	135
FF. Stocks maintained as heterokaryons on minimal medium	136
GG. Strains for Forcing and Resolving Heterokaryons	136
HH. Strains for studying MSUD	137
 Part VII. <i>Sordaria fimicola</i>	 138
 Part VIII. Key to symbols	 145

Podospora anserina - see part IV, pg. 111

Sordaria brevicollis - see part IV, pg. 111

Sordaria sp. - see part IV, pg. 111

Section C. *Aspergillus*

Molecular resources

Cloned genes	149
Genomic libraries	150
cDNA libraries	152

Fungal Strains

Part I.	Alphabetical list of genetic loci and alleles	153
Part II.	Aberration strains	166
Part III.	Wild type strains	166
Part IV.	Mitotic and meiotic mapping strains	167
Part V.	Other special purpose strains	167
Part VI.	Numerical listing of stocks	167
Part VII.	<i>Aspergillus awamori</i> mutants	185
Part VIII.	<i>Aspergillus oryzae</i>	185
Part IX.	<i>Aspergillus niger</i> mutants (numerical listing)	185
	<i>Aspergillus niger</i> mutants (listing by gene name)	188
Part X.	<i>Aspergillus flavus</i> mutants	190
Part XI.	<i>Aspergillus heterothallicus</i>	190
Part XII.	<i>Aspergillus fumigatus</i>	190
Part XIII.	Key to symbols and depositors	190

Section D. Plant Pathogenic fungi

<i>Fusarium moniliforme</i>	191
RFLP probes	191
<i>Fusarium proliferatum</i>	191
<i>Fusarium subglutinans</i>	191
<i>Fusarium oxysporum</i> f. sp. <i>asparagi</i>	192
<i>Nectria haematococca</i> (<i>Fusarium solani</i> f.sp <i>pisi</i>)	192
<i>Fusarium oxysporum</i> f. sp. <i>cubense</i>	193

Magnaporthe grisea

RFLP probes	194
Strains	194

<i>Aspergillus nidulans</i> genetic maps (from A.J. Clutterbuck)	196
<i>Neurospora crassa</i> genetic maps (from D.D. Perkins)	199

Section A. Cloning tools

Cloning Vectors

- λ pAn - 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 Genet 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
- Plasmid vectors based on hygromycin or phleomycin resistance:
- | | | |
|-------------|-----------|---|
| pMOcosX | | Orbach 1994. <i>Gene</i> <u>150</u> :159-162 |
| pCSN43 | pCSN44 | Staben <i>et al.</i> 1989. <i>Fungal Genet. Newsl.</i> <u>36</u> :79-81 |
| pES200 | | |
| pCB1003, | pCB1004 | Carroll <i>et al.</i> 1994. <i>Fungal Genet. Newsl.</i> <u>41</u> :22 |
| pCB1636 | pCB1636 | Sweigard <i>et al.</i> 1997. <i>Fungal Genet. Newsl.</i> <u>44</u> :52-53 |
| pCB1490 | pCB1179 | |
| pCB1535 | pCB1538 | |
| cosmid AN26 | | Taylor and Borgmann 1996 <i>Fungal Genet. Newsl.</i> <u>43</u> :52 |
| pMTR::Hyg | | Schroeder <i>et al.</i> 1995 <i>Fungal Genet Newsl</i> <u>42</u> :65-68 |
| pBC-hyg, | pBC-phleo | Silar, 1995 <i>Fungal Genet Newsl</i> <u>42</u> :73 |
- Vectors based on phosphinothricin (Ignite/Basta) resistance:
- | | | |
|-------------------|----------------------|---|
| pBARGEM5-1 | pBARKS1 | Pall and Brunelli 1993. <i>Fungal Genet. Newsl.</i> <u>40</u> :59 |
| pBARGEM7-1 | | |
| pBARGEM7-2 | pBARGPE1 | |
| pBARGRG1 | λ BARGRG1 | Pall and Brunelli 1994. <i>Fungal Genet. Newsl.</i> <u>41</u> :63 |
| λ BARGEM7 | λ BARMTE1 | |
| λ BARGPE1 | λ -IIBARGEM7 | |
| pCB1517 | pCB1635 | Sweigard <i>et al.</i> 1997. <i>Fungal Genet. Newsl.</i> <u>44</u> :52-53 |
| pCB1546 | pCB1524 | |
| pCB1525 | pCB1530 | |
| pCB1531 | pCB1534 | |
| pCB1537 | | |
- Vectors based on Sulfonylurea resistance:
- | | | |
|---------|---------|---|
| pCB1528 | pCB1637 | Sweigard <i>et al.</i> 1997. <i>Fungal Genet. Newsl.</i> <u>44</u> :52-53 |
| pCB1551 | pCB1550 | |
| pCB1532 | pCB1533 | |
| pCB1536 | pCB1539 | |
- Vectors for expression and modification of cDNA in *N. crassa* Campbell *et al.* 1994. *Fungal Genet. Newsl* 41:20-21
- pMYX2, pMYX10

GENE LIBRARIES

The FGSC maintains several gene libraries for *Neurospora crassa* and *Aspergillus nidulans*. 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 \$50 for cDNA or phage libraries and double for ordered libraries. Certain cDNA libraries cannot be sent to commercial organizations.

Fees are current as of 2002 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 cosmid libraries and the YAC library 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.

Fee list:

Neurospora libraries

Lambda J1: \$20, \$40 additional for FedEx
Lambda Bargem7: \$20, \$40 additional for FedEx
pcosAX: \$20, \$40 additional for FedEx
Orbach/Sachs pMOCosX cosmid: \$200 on agar, \$250 frozen
Chromosome specific sub-library: \$100 to \$200 on agar, \$150 to \$250 frozen
pSV50 cosmid: \$200 on agar, \$250 frozen
YAC: \$200 on agar, \$250 frozen
any cDNA or phage library \$20, \$40 additional for FedEx
2-hybrid libraries \$20, \$40 additional for FedEx

Aspergillus libraries

pWE15 and pLORIST2 cosmid \$200 on agar, \$250 frozen
Ordered chromosome specific library \$200 on agar, \$250 frozen
Compressed minimal library \$150 on agar, \$200 frozen
Individual chromosomes from the chromosome specific library \$75
24 Hr cDNA library \$20, \$40 additional for FedEx
Unizap or Lambda GT10 cDNA library \$20, \$40 additional for FedEx
AMA1 genomic libraries \$20, \$40 additional for FedEx

If you anticipate needs other than those described above, please contact the FGSC.
cDNA and phage libraries are \$50 for commercial enterprises and other libraries are double the listed fee.

Fees are subject to change and the most recent fee information can be found on the FGSC web-site.
For detailed listings of the gene libraries, please look at the sections for the individual fungi.

Aspergillus 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						
<i>aaX1</i>	VI	A 279	<i>yA2;pyroA4</i>	A 220		none
ABACUS						
<i>abaA14</i>	VIIIR	A 589, A590	<i>biA1</i>	A 26	NA	none
ACONIDIAL						
<i>acoA49</i>	VII	A 1068, A1071				
<i>acoB202</i>	II	A 075				
<i>acoC193</i>	VII	A 1073, 1076				
<i>aco3</i>		A 1067				
<i>aco14</i>		A 1069				
<i>aco55</i>		A 1072				
<i>aco70</i>		A 1074				
<i>aco445</i>		A 1082				
ACRIFLAVINE RESISTANT						
<i>AcrA1</i>	IIL	A 36, A 204 & others	<i>pabaA1 yA2;coA1</i>	--	S	(VI;VII)
<i>AcrA3</i>	IIL	A 346	<i>biA1;adC1;sC12;pyroA4</i>	A 259	S	none
<i>acrB2</i>	IIR	A 338				
ACTIDIONE RESISTANCE						
<i>ActA1</i>	IIIL	A 231, A412, A607	<i>riboA1 yA1;nicB8</i>	A 122	UV	none
<i>actB2</i>	VII	A 529	<i>biA1;wA2;carA1</i>	--	S	
ACETATE NON-UTILIZATION						
<i>acuD254</i>	VR	A 649	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuE201</i>	IR	A 650	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuF205</i>	VII	A 651	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuG223</i>	VR	A 652	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuH253</i>	V	A 653	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuJ211</i>	IL	A 654	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuK248</i>	I	A 655	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuL217</i>	I	A 656	<i>pabaA1 yA2</i>	A 234	UV	none
<i>acuM301</i>	--	A 953	<i>wA3;pyroA4</i>			
ADENINE REQUIRING						
<i>adA55</i>	IL	A 216, A218	prototroph	--	UV	none?
<i>adB57</i>	VIIIR	A 217	prototroph	--	UV	none?
<i>adC1</i>	IIR	A 259, A346 & others	<i>yA2 (veA⁺)</i>	--	X	<i>T1(III~VIII;IV)</i>
<i>adD3</i>	IIR	A 268, A565 & others				
<i>adE8</i>	IR	A 42	<i>biA1</i>	A 26	UV	none
<i>adE20</i>	IR	A 226, A428 & others	<i>biA1</i>	A 26	UV	none
<i>adF15</i>	IR	A 46	<i>biA1</i>	A 26	UV	none
<i>adF17</i>	IR	A 273, A306				
<i>adG14</i>	IL	A 37, A611 & others	<i>biA1</i>	A 26	UV	none
<i>adH23</i>	IIL	A 239, A382 A 285 <u>et al.</u>	<i>biA1</i>	A 26	UV	none
<i>adI50*</i>	IIIL	A 285 and others	<i>biA1</i>	A 26	UV	none

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

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
AFLATOXIN REGULATION						
<i>aflR</i>	IV	A1052			D	
ASPARTATE HYDROXAMATE RESISTANT						
<i>ahrA3</i>	VIIIR	A680	<i>biA1</i>	A26	NG	none
ALCOHOL DEHYDROGENASE						
<i>alcR125</i>	VII	A752, A952	<i>biA1</i>			
<i>alcΔ500</i>	--	A950	<i>pabaA1;riboB2</i>			
ACETAMIDE UTILIZATION						
<i>amdA7</i>	VIIIR	A749, A752				
<i>amdI18</i>	IIIR	A749, A750				
<i>amdI66</i>	IIIR	A751, A752				
<i>amdR-44</i>	IIR	A746				
<i>amdS1005</i>	IIIR	A752				
ANEURIN REQUIRING						
<i>anA1</i>	IL	A31, A201 & others	<i>biA1</i>	A26	UV	none
<i>anB2</i>	II	A261, A382	<i>biA1;AcrA1 wA3</i>	A123	UV	none
AROMATIC METABOLITE REQUIRING						
<i>aromA1248</i>	VIII	A1066				
ASPARAGINE NON-UTILIZATION						
<i>apnA1</i>	IIIL	A659	<i>pabaA1;fwA1</i>	--	NG	
RAS						
A-ras		A986, A987, A988, A1059				
ARGININE REQUIRING						
<i>argA1</i>	VIR	A230				
<i>argB2</i>	IIIL	A89	<i>biA1</i>	A26	UV	none
<i>argC3</i>	VIIIR	A256	<i>biA1</i>	A26	UV	
<i>argD11</i>	V	A646	<i>biA1</i>	A26	UV	none
BENOMYL RESISTANCE						
<i>benA10</i>	VIIIR	A524	<i>biA1;AcrA1</i>	--	UV	
<i>benA19</i>	VIIIR	A523	<i>biA1;AcrA1</i>	--	UV	
<i>benA33</i>	VIIIR	A820	<i>pabaA1 yA2</i>	--	UV	
<i>benB29</i>	IIR	A565, A566	<i>suA1adE20 yA2 adE20;AcrA1; phenA2;pyroA4;lysB5;nicB8</i>	--	UV	
<i>benC28</i>	VIIIR	A529	<i>biA1;AcrA1</i>	--	UV	
BIOTIN REQUIRING*						
<i>biA1;veA1</i>	IR	A26, many others	wild type (<i>veA</i> ⁺)	A4	X	none
* <i>veA1</i> occurs simultaneously with <i>biA1</i>						
BLOCKED IN MITOSIS						
<i>bimA1</i>	I	A780		A154	UV	
<i>bimB3</i>	III	A1065				
<i>bimC4</i>	VI	A777		A154	UV	
<i>bimD6</i>	IV	A1061 - A1064				
<i>bimE7</i>	VI	A776		A154	UV	
<i>bimG11</i>	VIII	A778	<i>riboA1 yA2;nicB8</i>	A122	UV	

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
BLUE ASCOSPORES						
<i>bla1</i>	IIR	A 268	<i>yA2;wA3;sC12</i>	--	NA	
BRISTLE MORPHOLOGY						
<i>brlA42</i>	VIIIR	A 583, A 729	<i>biA1</i>	A 26	NA	none
<i>alc(p)::brlA</i>		A 107, A 1078				
Δ <i>brlA</i>		A 1079, A 1080				
BROWN CONIDIA						
<i>bwA1</i>	VIR	A 77, A 112-115, A 366 & others	[2n]proA 1 yA2;wA3// <i>adG14 pabaA1 biA1</i>	--	S	<i>T1(III-VIII)</i> <i>T1(VI;VII)?</i>
CARBOXIN RESISTANCE						
<i>carA1</i>	VIIR	A 529	<i>biA1;wA2;ornB7</i>	--	UV	
<i>carB2</i>	VIIIR	A 525	<i>biA1;benA10 fwA1</i>	--	UV	
<i>carC9</i>	IIIR	A 528	<i>biA1;benA10 fwA1</i>	--	UV	
CATALASE						
<i>catA</i>	III	A 1053, A 1055			D	
<i>catB</i>	VIII	A 1054, A 1055			D	
CHARTREUSE CONIDIA						
<i>chaA1</i>	VIIIR	A 23, A 204 & others	<i>biA1;choA1</i>	A 1	S	<i>T1(I;VII)</i>
<i>chaA2</i>	VIIIR	A 372, A 413	<i>biA1;sA2</i>	A 316	S	<i>T1(V;VIII)</i>
CHLORONEB RESISTANCE						
<i>chlA10</i>	IIIL	A 536	<i>biA1;AcrA1</i>	--	UV	none?
CHOLINE REQUIRING						
<i>choA1</i>	VIIR	A 1, A 607 & others	<i>biA1</i>	A 26	UV	none
<i>choC3</i>	VIIIR	A 669	<i>pabaA biA1</i>		NG	
COLORLESS ASCOSPORES						
<i>clA6</i>	IL	A 280				
<i>clB1</i>	IL	A 674	<i>yA2;wA2;sC12</i>		UV	
NITRATE AND HYPOXANTHINE UTILIZATION						
<i>cnxA5</i>	VIIIR	A 555	<i>biA1</i>	A 26	DES	none
<i>cnxB2*</i>	VIIIR	A 381, A 449 & others	<i>AcrA1;wA3;nicB8</i>	--		none
<i>cnxB11</i>	VIIIR	A 557	<i>biA1</i>	A 26	DES	none
<i>cnxB50[†]</i>	VIIIR	A 266	<i>biA1</i>	A 26	UV	none
<i>cnxC[§]</i>	VIIIR	A 558	<i>biA1</i>	A 26	DES	none
<i>cnxE16[‡]</i>	IIR	A 63, A 337, A 462 & many others	<i>biA1;wA3</i>	A 51	UV	<i>T1(III-VIII)</i> <i>T1(VI;VII)</i>
<i>cnxF8</i>	VIIR	A 560	<i>biA1</i>	A 26	DES	none
<i>cnxG</i>	VI	A 559	<i>biA1</i>	A 26	DES	none
<i>cnxH3</i>	IIIL	A 553, A 662 & others	<i>biA1</i>	A 26	DES	none
* also called <i>ni21/11</i>						
[†] also called <i>ni50</i>						
[§] <i>cnxAB</i> & <i>C</i> are one gene that shows intragenic complementation between groups of certain mutants						
[‡] also called <i>ni3</i>						
COMPACT MORPHOLOGY						
<i>coA1</i>	VIIIR	A 29, A 120, A 449	<i>pabaA1 biA1</i>	--	S	<i>T1(VI;VII)</i>
COLONIAL - TEMPERATURE SENSITIVE						
<i>cotA1</i>	V	A 827				

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans- location
CARBON REPRESSION						
<i>creA204</i>	IL	A 748	<i>areA217</i>	--	NG	
<i>creB15</i>	IIR	A 747	<i>areA217</i>	--	NG	
<i>creC27</i>	IIR	A 671	<i>areA217</i>	--	NG	
CHOLINE-O-SULFATE NONUTILIZATION						
<i>csuA6</i>	V	A 539	<i>suA1adE20 adE20 biA1 sB3;choA1;chaA1</i>	A 168	NG	
CYSTEINE UTILIZATION						
<i>cysA1</i>	VL	A 756	<i>mecA biA1 anA1</i>	--	UV	
<i>cysB102</i>	IIL	A 753	<i>yA1;pyroA4;metB3</i>	--	S	
<i>cysC103</i>	VL	A 754	<i>yA1;pyroA4;metB3</i>	--	S	
DILUTE CONIDIAL COLOR						
<i>dilA1</i>	IIIL	A 489, A 644 & more	<i>yA2;pyroA4</i>	A 220?	UV	
DARK CONIDIA						
<i>drkA1</i>	VII	A 588	<i>biA1</i>	A 26	NA	none
<i>drkB5</i>	II	A 685			UV	
FLUOROACETATE RESISTANCE (ACETATE NON-UTILIZATION)						
<i>facA303</i>	VR	A 502, A 613 & others	<i>wA3;pyroA4</i>	--	S	<i>T1(VI;VII)</i>
<i>facB101</i>	VIIIR	A 409, A 420 & others	<i>wA3;pyroA4</i>	--	S	<i>T1(VI;VII)</i>
<i>facC102</i>	VIIIR	A 427	<i>wA3;pyroA4</i>	--	S	<i>T1(VI;VII)</i>
<i>fanA3</i>	V	A 675	<i>biA1;facA303</i>	--	S	none?
<i>fanB52</i>	VII	A 676	<i>biA1;facA303</i>	--	S	none?
<i>fanD151</i>	VIII	A 673	<i>biA1;facA303</i>	--	S	none?
<i>fanE7</i>	VI	A 677	<i>biA1</i>	A 26	S	none?
FLUFFY AUTOLYTIC DOMINANT						
<i>fadA</i>		A 1035, A 1036, A 1037, A 1056			D	
FATTY ACID SYNTHASE						
<i>fasA</i>	VIII	A 1038			D	
<i>fasB</i>	VIII	A 1038			D	
FLUFFY LOW br1A						
<i>flbA</i>		A 1034				
FLUFFY MORPHOLOGY						
<i>fluG1</i>	III	A 744	<i>pabaA1 yA2</i>	A 234	NG	none
<i>fluG701</i>		A 1081, A 1084 - A 1087				
FLUOROPHENYLALANINE RESISTANCE						
<i>fpaA1</i>	IL	A 275	<i>biA1</i>	A 26	S	none
<i>fpaA91</i>	IL	A 387, A 439 & others	<i>proA11 yA2;pyroA4</i>	--	NG	
<i>fpaB37</i>	IL	A 422, A 507 & others	<i>riboA1 biA1</i>	A 158	S	none
<i>fpaC43</i>	VII	A 286	<i>riboA1 biA1</i>	A 158	S	none
<i>fpaD11</i>	III	A 273	<i>adF17 pabaA yA2</i>	--	S	?
<i>fpaD43</i>	III	A 582				
<i>fpaI64</i>	IL	A 717				
FRUCTOSE NON-UTILIZATION						
<i>fra1</i>	IVR	A 59, A 276	<i>yA2;pyroA4</i>	A 220	UV	none
FAWN CONIDIA						
<i>fwA1</i>	VIIIR	A 378, A 524 & others	<i>biA1</i>	A 26	S	none
<i>fwA2</i>	VIIIR	A 371, A 440 & others	<i>AcrA2;lysB5</i>	A 205	S	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
GALACTOSE NON-UTILIZATION						
<i>galA1</i>	IIIL	A 211 & many others	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galB3</i> (= <i>araA</i>)	II	A 215	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galC4</i>	VIII	A 291	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galD5</i>	IL	A 212, A 213, A 608	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galE9</i>	IIIL	A 214	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galF2</i>	VIII	A 718	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>galG2</i>	VIIIR	A 714				
GALACTOSE NON-UTILIZATION/MOLYBDATE RESISTANCE						
<i>gamA55</i>	I	A 696	<i>biA1</i>	A 26	S	none
<i>gamB65</i>	VIIIR	A 697	<i>biA1</i>	A 26	S	none
<i>gamC66</i>	?	A 698	<i>biA1</i>	A 26	S	none
GABA TRANSAMINASE						
<i>gatA</i>	VIIIR	A 848				
GLUTAMATE DEHYDROGENASE						
<i>gdhA1</i>	IIIL	A 699	<i>biA1</i>	A 26	NG	none
<i>gdhB2</i>	VI	A 689	<i>biA1</i>	A 26	NG	none
HISTIDINE REQUIRING						
<i>hisA10</i>	IV	A 277	<i>yA2 biA1;AcrA1;riboB2</i>	--	UV	none?
<i>hisB179</i>	I	A 727	<i>proA yA2;chaA1</i>	--	UV	
<i>hisC38</i>	VIIIR	A 257	<i>biA1;AcrA1 wA3;nicB8</i>	--	UV	none
<i>hisG113</i>	II	A 715	<i>proA yA2;chaA1</i>	--	UV	
<i>hisH13</i>	VIII	A 278	<i>yA2 biA1;AcrA1;riboB2</i>	--	UV	none
<i>hisJ122</i>	VIIIR	A 299	<i>biA1;sB3</i>	A 41	NA	none?
HYPOXANTHINE NON-UTILIZATION						
<i>hxA1</i>	VR	A 258, A 554	<i>biA1</i>	A 26	DES	none
<i>hxB13</i>	VII	A 552	<i>biA1</i>	A 26	DES	none
ISOLEUCINE REQUIRING						
<i>ileA1</i>	IIR	A 295	<i>biA1;sB3</i>	A 41	NA	none
<i>ileA3</i>	IIR	A 254, A 505	<i>biA1</i>	A 26	UV	none
IMAZALIL RESISTANCE						
<i>imaA4</i>	VIIIR	A 529	<i>biA1;AcrA1</i>	--	UV	none?
<i>imaB9</i>	V	A 532	<i>biA1;AcrA1</i>	--	S	none?
<i>imaC10</i>	IIR	A 533	<i>biA1;AcrA1</i>	--	S	none?
<i>imaD13</i>	VIIIR	A 534	<i>biA1;AcrA1</i>	--	S	none?
<i>imaG18</i>	IIIL	A 535	<i>biA1;AcrA1</i>	--	NG	none?
<i>imaH19</i>	III	A 537	<i>biA1;AcrA1</i>	--	NG	none?
INOSITOL REQUIRING						
<i>inoA1</i>	IIR	A 678	<i>biA1</i>	A 26	UV	none
<i>inoB2</i>	IVR	A 679	<i>biA1</i>	A 26	NG	none
INTEGRATION OF GABA METABOLISM (=amdR)						
<i>inta^C2</i>	II	A 660	<i>biA1</i>	A 26	NG	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
IODOACETATE RESISTANCE						
<i>IodA1</i>	IIL	A 462, A 492	<i>biA1;wA3;nicB8</i>	--	S	<i>T1(III-VIII)</i>
IVORY CONIDIOPHORES						
<i>ivoA1</i>	IIIL	A 687			S	
<i>ivoB63</i>	VIIIR	A 729			S	
LACTOSE NON-UTILIZATION						
<i>lacA1</i>	VIR	A 58, A 349 & others	<i>yA2;pyroA4</i>	A 220	UV	none
<i>lacB3</i>	IIR	A 292	<i>biA1;wA3</i>	A 51	UV	<i>T1(III-VIII)</i>
						<i>T1(VI;VII)</i>
LEUCINE REQUIRING						
<i>luA1</i>	IL	A 55, A 406	<i>biA1</i>	A 26	UV	none
LYSINE REQUIRING						
<i>lysA1</i>	VIR	A 38, A 350*	<i>wA1(veA⁺)</i>		X	Ab VI?
<i>lysB5</i>	VL	A 66, A 205 & others	<i>biA1</i>	A 26	UV	none
<i>lysD7</i>	VIIIR	A 300	<i>biA1;sB3</i>	A 41	NA	none?
<i>lysD18</i>	VIIIR	A 294, A 606	<i>biA1;sB3</i>	A 41	NA	none?
<i>lysD20</i>	VIIIR	A 418, A 645	<i>biA1;sB3</i>	A 41	UV	<i>T1(III;VIII)</i>
<i>lysE13</i>	VR	A 296	<i>biA1;sB3</i>	A 41	UV	none?
<i>lysE14</i>	VR	A 298	<i>biA1;sB3</i>	A 41	UV	none?
<i>lysE231</i>	VR	A 301	<i>biA1;sB3</i>	A 41	UV	none?
<i>lysF51</i>	IR	A 297	<i>biA1;sB3</i>	A 41	UV	none?
<i>lysF88</i>	IR	A 293, A 376	<i>biA1;sB3</i>	A 41	UV	none?
* Contains Ab VI (Inversion?)						
MALTOSE NON-UTILIZATION						
<i>malA1</i>	VIIIR	A 57, A 461 & others	<i>yA2;pyroA4</i>	A 220	UV	none
MANNOSE NON-UTILIZATION						
<i>manA1</i>	VIIIR	A 670				
MONOAMINE UTILIZATION						
<i>mauA2</i>	IVR	A 681	<i>yA2;pyroA4 meaA8</i>		NG	
<i>mauB4</i>	IIR	A 682	<i>yA2;pyroA4 meaA8</i>		NG	
METHYLAMMONIUM RESISTANCE						
<i>meaA8</i>	IVR	A 672	<i>biA1</i>	A 26	DES	none
<i>meaB6</i>	IIIL	A 451, A 496 & others	<i>biA1</i>	A 26	DES	none
METHIONINE INHIBITION						
<i>mecB10</i>	IL	A 758, A 759	<i>biA1 anA1</i>	A 31?	UV	
<i>mecC13</i>	?	A 703	<i>biA1 anA1</i>	A 31?	UV	none
MEDUSA						
<i>medA15</i>	IL	A 586	<i>biA1</i>	A 26	NA	none
MELANIN PRODUCTION						
<i>melA1</i>	VII	A 657				
<i>melB⁰2</i>	VIIIR	A 667				
METHIONINE REQUIRING						
<i>methA17</i>	IIL	A 757	<i>adF9 yA1</i>	--	UV	
<i>methB3</i>	VIR	A 272	<i>yA2;pyroA4</i>	A 220	UV	none
<i>methD10</i>	IIIL	A 755	<i>adF9 biA1</i>	--	UV	
<i>methE6</i>	VIIIR	A 719	<i>biA1</i>	A 26	UV	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
METHIONINE REQUIRING, continued						
<i>methG1</i>	IVL	A 219 & many others	<i>biA1</i>	A 26	UV	none
<i>methH2</i>	IIIL	A 34, A 644	<i>biA1</i>	A 26	UV	none
MORPHOLOGICALLY ABNORMAL						
<i>moC96</i>	III	A 232			P	
MOLYBDATE RESISTANT						
<i>molA67</i>	VIR	A 707	<i>biA1</i>	A 26	S	none
<i>molB35</i>	II	A 716	<i>biA1</i>	A 26	S	none
MUTAGEN SENSITIVE						
<i>musK228</i>	VIIIR	A 840, A 1031	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
<i>musL222</i>	IR	A 841	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
<i>musM225</i>	VIR	A 828	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
MUTAGEN SENSITIVE, continued						
<i>musN227</i>	VIIIR	A 842, A 1030	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
<i>musO226</i>	III or VIIIR		A 843	<i>biA1;acrA1;nicA2</i>		A 605
γ		T2(IL;IIIL)				
<i>musP234</i>	II or VII	A 844	<i>pabaA1 yA2</i>	A 610	UV	none
<i>musQ230</i>	IIR	A 845	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
<i>musR223</i>	IIIL	A 846	<i>biA1;acrA1;nicA2</i>	A 605	γ	T2(IL;IIIL)
<i>musS224</i>	III or VIIIR		A 847	<i>biA1;acrA1;nicA2</i>		A 605
γ		T2(IL;IIIL)				
NITRATE NON-UTILIZATION						
<i>niaD15</i>	VIIIR	A 691	<i>biA1</i>	A 26	NA	none
NICOTINAMIDE REQUIRING						
<i>nicA2</i>	VL	A 495, A 605 & others	wild type (<i>veA</i> ⁺)	A 4	X	
<i>nicB8</i>	VIIIR	A 122, A 317 & others	<i>biA1</i>	A 26	UV	none
<i>nicC10</i>	VI	A 11	<i>biA1;AcrA1; wA3</i>	--	UV	none
NITRITE NON-UTILIZATION						
<i>niiA4</i>	VIIIR	A 713				
NEVER IN MITOSIS						
<i>nimA5</i>	III	A 781		A 154	UV	
NITRATE PATHWAY REGULATOR						
<i>nirA14</i>	VIIIR	A 260, A 472 & others	<i>biA1;phenA3</i>	--	S	T1(I;IV)
NUCLEAR DISTRIBUTION						
<i>nudA1</i>	--	A 944-A 948				
<i>nudA (snfC1524)</i>		A 1011	<i>nudF6 pyrG89</i>			UV
<i>nudA (snfC1232)</i>		A 1019, A 1020	<i>nudF6 pyrG89</i>			UV
<i>nudC3</i>	--	A 779	<i>wt x pabaA1 pyrG89;fwA1 uaY9</i>	A 4 x A 154	UV	
<i>nudF6</i>		A 1011 & others				
OLIGOMYCIN RESISTANT						
[<i>oliA6</i>]	cyto.	A 666	<i>pabaA1 yA2</i>	A 234	S	none
<i>oliC2</i>	VIIIR	A 450, A 453 & others	<i>pabaA1 yA2</i>	A 234	S	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
ORNITHINE REQUIRING						
<i>ornA4</i>	IVR	A 43, A358	<i>biA1</i>	A 26	UV	none
<i>ornB7</i>	VIIIIR	A 379				
<i>ornB9</i>	VIIIIR	A 353				
<i>ornB20</i>	VIIIIR	A 263	<i>biA1</i>	A 26	UV	none
<i>ornC31</i>	IIIR	A 668				
PALE CONIDIA						
<i>pA2</i>	VR	A 35, A460, A495	<i>adG14 biA1</i>	A 37	S	none
P-AMINOBENZOIC ACID REQUIRING						
<i>pabaA1</i>	IR	A 610	<i>biA1</i>	A 26	X	none
<i>pabaA6</i>	IR	A 28, A 595 & others	<i>biA1</i>	A 26	UV	none
<i>pabaA18</i>	IR	A 305, A308, A309	<i>biA1</i>	A 26		none
<i>pabaA108</i>	IR	A 333, A334	<i>biA1</i>	A 26?	UV	none?
<i>pabaA125</i>	IR	A 335, A336, A571	<i>biA1</i>	A 26?	UV	none?
<i>pabaB22</i>	IVR	A 426, A493 & others	<i>biA1</i>	A 26	UV	none
ACID PHOSPHATASE DEFICIENT						
<i>pacA1</i>	IV	A 241	<i>rA1 biA1</i>	--	UV	none
<i>pacC5</i>	VI	A 242	<i>biA1</i>	A 26	UV	none
ALKALINE PHOPHATASE DEFICIENT						
<i>palA1</i>	IIIL	A 243, A287	<i>rA1 biA1</i>	--	UV	none
<i>palB7</i>	VIIIIR	A 244, A381 & others	<i>rA1 biA1</i>	--	UV	none
<i>palC4</i>	IVR	A 250, A497 & others	<i>rA1 biA1</i>	--	UV	none
<i>palD8</i>	VIIR	A 245, A581 & others	<i>rA1 biA1</i>	--	UV	none
<i>palF15</i>	VIIR	A 247, A400 & others	<i>rA1 biA1</i>	--	UV	none
ACID & ALKALINE PHOSPHATASE DEFICIENT						
<i>palcA1</i>	IIL	A 248	<i>rA1 biA1</i>	--	UV	none
<i>palcC4</i>	VIIIIR	A 712				
PANTOTHENIC ACID REQUIRING						
<i>pantoA1</i>	VIIIIR	A 340	<i>yA2;thiA1 (veA⁺)</i>	--	X	<i>T(III-VII;IV)</i>
<i>pantoA10</i>	VIIIIR	A 665				
<i>pantoB100</i>	VIIR	A 397, A453 & others			UV?	
<i>pantoC3</i>	IIIL	A 662				
PYRUVATE DEHYDROGENASE						
<i>pdhA4</i>	IR	A 637	<i>yA2 pabaA1</i>	A 234	UV	none
<i>pdhB2(ts)</i>	V	A 628	<i>yA2 pabaA1</i>	A 234	UV	none
<i>pdhB4</i>	V	A 634	<i>yA2 pabaA1</i>	A 234	UV	none
<i>pdhC1</i>	VIIIL	A 627, A635(ts)	<i>yA2 pabaA1</i>	A 234	UV	none
PHENYLALANINE REQUIRING						
<i>phenA2</i>	IIIR	A 498, many more	<i>biA1</i>	A 26	UV	none
<i>phenA3</i>	IIIR	A 260, A402	<i>biA1</i>	A 26	S	none
<i>phenB6</i>	VIIR	A 394, many more	<i>biA1</i>	A 26	UV	none
PIMARICIN RESISTANCE						
<i>pimA1</i>	IVR	A 530	<i>biA1;AcrA1</i>	--	UV	none?
<i>pimB10</i>	IL	A 531	<i>biA1;AcrA1</i>	--	S	none?
PYRUVATE KINASE						
<i>pkiA2(ts)</i>	V	A 630	<i>yA2 pabaA1</i>	A 234	UV	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
PENTOSE PHOSPHATE PATHWAY						
<i>pppA1</i>	II	A 690	<i>biA1</i>	A 26		none
<i>pppB1</i>	III	A 688	<i>biA1</i>	A 26	NG	none
PRECOCIOUS						
<i>pre1</i>		A 1089				
PROLINE REQUIRING						
<i>proA1</i>	I	A 32, many more	<i>biA1</i>	A 26	UV	none
<i>proA2</i>	IL	A 792, A 793				
<i>proA5</i>	I	A 45	<i>biA1</i>	A 26	UV	none
<i>proA11</i>	I	A 387	<i>yA2;pyroA4</i>	A 220	UV	none
<i>proB3</i>	I	A 692	<i>biA1</i>	A 26	UV	none
<i>proB4</i>	I	A 658	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII);</i> <i>T1(VI;VII)</i>
<i>proB94</i>	IL	A 386, A 453	wild type (<i>veA</i> ⁺)	A 4	UV	none
PUTRESCINE REQUIRING						
<i>puA1</i>	IIR	A 338, A 341	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
<i>puA2</i>	IIR	A 682, A 701	<i>biA1</i>	A 26	NG	none
PUTRESCINE NON-UTILIZATION						
<i>punA11</i>	IIR	A 700	<i>biA1</i>	A 26	UV	none
PYRUVATE CARBOXYLASE						
<i>pycA2</i>	V	A 632	<i>yA2 pabaA1</i>	A 234	UV	none
<i>pycA12(ts)</i>	V	A 625	<i>yA2 pabaA1</i>	A 234	UV	none
<i>pycB4</i>	V	A 624	<i>yA2 pabaA1</i>	A 234	UV	none
PYRIMIDINE REQUIRING						
<i>pyrD23</i>	VIIIR	A 723, A 724	<i>biA1</i>	A 26	NG	none
<i>pyrF11</i>	IL	A 721				NG
<i>pyrG89</i>	IL	A 722, A 767 & others	<i>pabaA1;fwA1 uaY9</i>	--		NG
<i>pyrN25</i>	VIII	A 813, A 814				NG
PYRIDOXINE REQUIRING						
<i>pyroA4</i>	IVR	A 33, A 220 & others	<i>biA1</i>	A 26	UV	none
<i>pyroB12</i>	IL	A 693	<i>biA1;wA3</i>	A 51	UV	<i>T1(III→VIII)</i> <i>T1(VI;VII)</i>
RECOMBINATION DEFICIENT						
<i>rec-402</i>		A 543(dp), A 597(hap)	duplication YP 511	A 542	NG	
<i>rec-408</i>		A 546(dp), A 598(hap)	duplication YP 511	A 542	NG	
<i>rec-412</i>		A 549(dp)	duplication YP 511	A 542	NG	
<i>rec-444</i>		A 548(dp), A 599(hap)	duplication YP 511	A 542	NG	
<i>rec-469</i>		A 544(dp), A 600(hap)	duplication YP 511	A 542	NG	
<i>rec-471</i>		A 547(dp), A 562(hap)	duplication YP 511	A 542	NG	
RIBOFLAVIN REQUIRING						
<i>riboA1</i>	IL	A 158, many more	<i>biA1</i>	A 26	UV	none
<i>riboB2</i>	VIIIR	A 353, A 612 & others	<i>biA1;AcrA1 wA3</i>	A 123	UV	none
<i>riboC3</i>	V	A 311	<i>yA2;pyroA4</i>	A 220	UV	
<i>riboD5</i>	VR	A 258, A 504 & others	<i>biA1</i>	A 26	UV	none
<i>riboE6</i>	IIR	A 64	<i>biA1;wA3</i>	A 51	UV	<i>T1(VI;VII)</i> <i>T1(III→VIII)</i>
<i>riboF8</i>	I	A 726	<i>biA1</i>	A 26	NA	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
RODLETLESS						
<i>rodA</i>	IIIR	A 849	<i>pabaA1 yA2; ΔargB::trpCΔB; veA1 trpC801</i>	A 851	D	
SULPHATE NON UTILIZATION						
<i>sA1</i>	IIIL	A 40, A 417 & others	<i>biA1</i>	A 26	UV	none
<i>sA2</i>	IIIL	A 316, A 368 & others	<i>biA1</i>	A 26	UV	none
<i>sA4</i>	IIIL	A 2, A 339 & others	<i>biA1</i>	A 26	UV	none
<i>sA49</i>	IIIL	A 404	<i>biA1</i>	A 26	NG	none
<i>sA91</i>	IIIL	A 405	<i>biA1</i>	A 26	NG	none
<i>sA130</i>	IIIL	A 602	<i>biA1</i>	A 26	NG	none
<i>sB3</i>	VIR	A 41, many more	<i>biA1</i>	A 26	UV	none
<i>sB25</i>	VIR	A 383	<i>riboA1;AcrA1;chaA1</i>	--	NG	none
SULPHATE NON UTILIZATION (continued from previous page)						
<i>sC12</i>	IIIL	A 24, many more	<i>wild type (veA⁺)</i>	A 4	NM	none
<i>sC22</i>	IIIL	A 384	<i>riboA1 yA2</i>	A 361	NG	none
<i>sC63</i>	IIIL	A 603	<i>biA1</i>	A 26	NG	none
<i>sC84</i>	IIIL	A 604	<i>biA1</i>	A 26	NG	none
<i>sD50</i>	VIIIR	A 249, A 398, A 431, A 434	<i>biA1</i>	A 26	UV	none
<i>sD85</i>	VIIIR	A 419, A 421 & others	<i>biA1</i>	A 26	NG	none
<i>sD157</i>	VIIIR	A 420	<i>biA1</i>	A 26	NG	none
<i>sE15</i>	VIIIR	A 385, A 399 & others	<i>biA1</i>	A 26	NG	none
<i>sF211</i>	VIIIR	A 388, A 403 & others	<i>biA1;pyroA4</i>	A 33	NG	none
SORBITOL NON-UTILIZATION						
<i>sbA3</i>	VIR	A 500, A 510 & others	<i>biA1;wA3</i>	A 51	UV	T1(III-VIII)
T1(VI;VII)						
SALT SENSITIVITY						
<i>sltA1</i>	VIR	A 702	<i>biA1</i>	A 26	NG	none
SMALL COLONIAL SIZE						
<i>smA1</i>	IIIL	A 66, A 436, A 501	<i>biA1</i>	A 26	UV	none
SUPPRESSOR OF MMS SENSITIVITY						
<i>smsA61</i>	VR	A 395	<i>biA1;sB3</i>		UV	none
SUPPRESSOR OF NUCLEAR DISTRIBUTION						
<i>snaA26</i>		A 945	<i>pyrG89;chaA1;nudA1</i>		UV	
<i>snaB76</i>		A 946	<i>pyrG89;chaA1;nudA1</i>		UV	
<i>snaC108</i>		A 947	<i>pyrG89;chaA1;nudA1</i>		UV	
<i>snaD385</i>		A 944	<i>pyrG89;chaA1;nudA1</i>		UV	
<i>snaE285</i>		A 948	<i>pyrG89;chaA1;nudA1</i>		UV	
SUPPRESSOR OF <i>nudF</i>						
<i>snfC1524 (nudA)</i>		A 1011, A 1012	<i>nudF6 pyrG89</i>		UV	
<i>snfC1232 (nudA)</i>		A 1019, A 1020	<i>nudF6 pyrG89</i>		UV	
<i>snfE798</i>		A 1013	<i>nudF6 pyrG89</i>		UV	
<i>snfA890 (tubA22)</i>		A 1014, A 1015, A 1016	<i>nudF6 pyrG89</i>		UV	
<i>snfB1267</i>		A 1017	<i>nudF6 pyrG89</i>		UV	
<i>snfD860</i>		A 1018	<i>nudF6 pyrG89</i>		UV	
<i>snfD1468</i>		A 1021	<i>nudF6 pyrG89</i>		UV	
<i>snfD1292</i>		A 1022, A 1023	<i>nudF6 pyrG89</i>		UV	
<i>snfD1555</i>		A 1024, A 1025	<i>nudF6 pyrG89</i>		UV	
<i>snf1364</i>		A 1026, A 1028	<i>nudF6 pyrG89</i>		UV	
<i>snf1062</i>		A 1027	<i>nudF6 pyrG89</i>		UV	
<i>snf1422</i>		A 1029	<i>nudF6 pyrG89</i>		UV	

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
SORBOSE RESISTANCE						
<i>sorA2</i>	I	A 705	<i>biA1;adH23 AcrA1 wA3;nicB8</i>	--	S	
<i>sorB11</i>	IIIL	A 728	<i>biA1;adH23 AcrA1 wA3;nicB8</i>	--	S	
SPERMIDINE SENSITIVITY						
<i>spsA1</i>	IIIL	A 701	<i>biA1;puA2</i>	--	NA	
SUPPRESSOR OF <i>sbA3</i>						
<i>sbA1</i>	IV	A 1	<i>biA1</i>	A 26	UV	
STERIGMATOCYSTIN CLUSTER						
<i>stcB</i>	IV	A 1048			D	
<i>stcE</i>	IV	A 1041			D	
<i>stcF</i>	IV	A 1049			D	
<i>stcI</i>	IV	A 1051			D	
<i>stcJ</i>	IV	A 1040			D	
<i>stcK</i>	IV	A 1039			D	
<i>stcL</i>	IV	A 1046, A 1047			D	
<i>stcN</i>	IV	A 1042			D	
<i>stcP</i>	IV	A 1043, A 1044			D	
<i>stcQ</i>	IV	A 1045			D	
<i>stcU</i>	IV	A 1047			D	
<i>stcW</i>	IV	A 1050			D	
STUNTED CONIDIOPHORES						
<i>stuA1</i>	IL	A 584, A 585	<i>biA1</i>	A 26	NA	
SUPPRESSORS						
<i>suA1adE20</i>	IL	A 47, many more	<i>adE20;pyroA4</i>	A 227	S	
<i>suC11adE20</i>	IVL	A 443, A 486 A 517, A 639	<i>pabaA1 yA2 adE20 AcrA1; coA1 cnxB2</i>	--	S	none
<i>suA1palB7</i>	VIIIR	A 281	<i>biA1;palB7</i>	A 244	S	none?
<i>suB2palB7</i>	VI	A 284	<i>biA1;palB7</i>	A 244	S	none?
<i>suC6palF15</i>	V	A 282	<i>biA1;palF15</i>	A 247		none?
<i>suD2palA1</i>	I	A 287	<i>biA1;palA1</i>	A 243		
<i>suB4pro</i>	IIIR	A 423, A 441, A 454 and others	<i>proA biA1</i>	A 45	S	
SUCCINATE NON-UTILIZATION						
<i>sucA1</i>	?	A 694	<i>biA1;wA3</i>	A 51	UV	<i>T1(III-VIII)</i> <i>T1(VI;VII)</i>
SULPHANILAMIDE RESISTANT						
<i>SulA1</i>	IL	A 507, A 511 & others	<i>yA2;pyroA4</i>	A 220	UV	none
AMMONIUM REGULATION						
<i>tamA200</i>	VIR	A 822, A 823	<i>biA1</i>	A 26	UV	none
MOUND SHAPED COLONY						
<i>telA1</i>	VIIIR	A 695	<i>biA1</i>	A 26	S	none
THIAZOLE REQUIRING						
<i>thiA1</i>	IIR	A 14	<i>yA2 (veA⁺)</i>	A 647?	X	<i>T(III-VIII;IV)</i>
<i>thiA4</i>	IIR	A 52, A 337	<i>biA1</i>	A 26	UV	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
TRYPTOPHAN REQUIRING						
<i>trypA69</i>	II(R?)	A 235	<i>pabaA1 yA2</i>	A 234	UV	none
<i>trypB403</i>	I(L?)	A 236	<i>pabaA1 yA2</i>	A 234	UV	none
<i>trypC801</i>	VIII	A 237	<i>pabaA1 yA2</i>	A 234	UV	none
<i>trypD432</i>	II(R?)	A 238	<i>pabaA1 yA2</i>	A 234	UV	none
TEMPERATURE SENSITIVE						
<i>tsB5</i>	VIR	A 708	<i>biA1</i>	A 26	UV	none
<i>tsC17</i>	IIR	A 720	<i>biA1</i>	A 26	UV	none
<i>tsD15</i>	VIII	A 269	<i>biA1</i>	A 26	UV	none
<i>tsE6</i>	V	A 725	<i>adF15 biA1</i>	A 46	EMS	
TUBULIN						
<i>tubA4</i>	VIIIR	A 821			UV	
<i>tubA22 (snfA890)</i>		A 1014, A 1015, A 1016	<i>nudF6 pyrG89</i>		UV	
UREA NON-UTILIZATION						
<i>uY5</i>	VII	A 262	<i>biA1</i>	A 26	DES	none
URIC ACID NON-UTILIZATION						
<i>uaX10</i>	VI	A 264	<i>biA1</i>	A 26	DES	none
<i>uaY9</i>	VIIIR	A 551, A 729, A 722	<i>biA1</i>	A 26	DES	none
UREASE DEFICIENT						
<i>ureA1 (uruA)</i>	VIIIR	A 683				
<i>ureB3 (uX)</i>	VIIIR	A 684				
<i>ureD4 (uZ)</i>	VIIIR	A 648				
ULTRAVIOLET SENSITIVE						
See Kafer and Mayor 1986 Mutation Res. <u>161</u> :119-134 for original designations of <i>uvs</i> mutants.						
<i>uvs-5</i>	--	A 327	<i>adE20 biA1;wA3;methG pyroA4</i>	A 139	UV	none
<i>uvsA101</i>	IR	A 579, A 831	<i>pabaA108 biA1</i>	--	UV	
<i>uvsB110</i>	IVC	A 333, A 577, A 832	<i>pabaA108 biA1</i>	--	UV	
<i>uvsB312</i>	IVC	A 573	<i>yA2;AcrA1;pyroA4</i>		UV	none
<i>uvsB413</i>	IVC	A 561, A 609	<i>pabaA6 yA2 adE8 biA⁺</i> <i>Dp(I-II)yA⁺ adE20 biA1</i>	A 542	NG	
<i>uvsB504</i>	IVC	A 827	<i>suA1 adE20 adE20</i>	A 168	UV	
<i>uvsB505</i>	IVC	A 826	<i>biA1;ssbA3;sB3;choA1;chaA1</i> <i>suA1 adE20 adE20</i>	A 168	4-NQO	
<i>uvsC114</i>	VIIIR	A 334, A 570, A 833	<i>pabaA108 biA1</i>	--	UV	
<i>uvsD153</i>	V(L?)	A 335, A 571, A 834	<i>proA1 pabaA125 biA1;pyroA4</i>	--	UV	
<i>uvsD308</i>	V(L?)	A 574	<i>biA1;niiB1</i>	--	UV	
<i>uvsE182</i>	VR	A 572, A 835	<i>proA1 pabaA125 biA1;pyroA4</i>	--	UV	
<i>uvsF201</i>	IL	A 389, A 567, A 836	<i>riboA1 yA2</i>	A 361	UV	none
<i>uvsH77</i>	IVL	A 330, A 568, A 837	<i>adE20 biA1;wA3;methG</i>	A 139	UV	none
<i>uvsH304</i>	IVL	A 329, A 576	<i>yA2;AcrA1;pyroA4</i>	--	UV	none
<i>uvsH311</i>	IVL	A 575	<i>yA2;AcrA1;pyroA4</i>	--	UV	none
<i>uvsI501</i>	IIIL	A 838				
<i>uvsJ1</i>	VL	A 569, A 578, A 839	<i>adE20? biA1;methG?</i>	--	UV	none
VELVET-LOOKING CONIDIA						
<i>veA1</i>	VIIIR	in most strains, exceptions indicated by <i>veA⁺</i>	X of A4-A26 (<i>biA1;veA1</i>)		X	none

Locus	Linkage group	Present in FGSC #	Strain of origin genotype	FGSC#	Mutagen	Trans-location
WHITE CONIDIA						
<i>wA1</i>	IIL	A 38	wild type of Yuill(1936)	--	S	none
<i>wA2</i>	IIL	A 75, A 344 & others	<i>yA2(veA⁺)</i>	A 647?	X	
T1(III-VIII;IV)						
<i>wA3</i>	IIL	A 191 & many others	<i>pabaA1 biA1</i>	--	S	T1(VI;VII)
<i>wA4</i>	IIL	A 69, A 436, A 439	<i>biA1;smA1;lysB5</i>	A 66	S	none
<i>wB1</i>	VII	A 824	<i>proA1 pabaA6 adE20 biA1; Dp(IR-IIR)yA2</i>	--	INAH	
WET-WHITE CONIDIA						
<i>wetA6</i>	VIIR	A 580, A 581	<i>biA1</i>	A 26	UV	none
EXTRACELLULAR PROTEASE						
<i>xprD1(areA1)</i>	IIIR	A 661	<i>pabaA1 biA1;trypC801 hisC38</i>		UV	
YELLOW CONIDIA						
<i>yA2</i>	IR	A 71, A 83, many more	wild type (<i>veA⁺</i>)	A 4	X	none
<i>y^oA91</i>	IR	A 425, A 445 & others	<i>biA1;phenA2</i>	A 498	S	none?
YELLOW-GREEN CONIDIA						
<i>ygA1</i>	IIR	A 270, A 706	<i>biA1</i>	A 26	S	none

II. Aberration Strains

1. Translocation strains

<i>T2(I;III)</i>	: A605, A828	<i>T2(III;VII)</i>	: A843
<i>T1(I;IV)</i>	: A260	<i>T3(III;VII)</i>	: A847
<i>T1(I;VII)</i>	: A1, A129, A354, A430, A438	<i>T1(III-VIII)</i>	: A309, A212
<i>T2(I;VII)</i>	: A355	<i>T1(III-VIII;IV)</i>	: A647
<i>T1(I;VIII)</i>	: A125, A304, A352	<i>T1(IV;VIII)</i>	: A250, A276, A435, A470
<i>T2(I;VIII)</i>	: A398, A431, A434	<i>T1(V;VI)</i>	: A40, A370, A373, A518, A521
<i>T1(II;III)</i>	: A111, A414	<i>T2(V;VI)</i>	: A333
<i>T1(II;IV)</i>	: A345	<i>T1(V;VIII)</i>	: A316, A372, A413
<i>T1(II;VII)</i>	: A50, A429	<i>T1(VI;VII)</i>	: A27, A29, A36, A482, A519, A520
<i>T1(III;VII)</i>	: A395, A418, A447	<i>T2(VII-II)</i>	: A844

2. Other aberration strains

a. aberration induced simultaneously with <i>adE20</i> and <i>T1(II;VII)</i> ?	: A50, A428, A429
b. <i>T1(VI;VII)</i> <i>T1(III-VIII)</i> strains	: A3, A64, A215, A291, A292, A693, A694, A718
c. intrachromosomal aberrations	: A261, A382
d. <i>T1(I;V;VII;VIII)</i> - possibly related to <i>T2(I;VII)</i>	: A347* A348
e. <i>Ab(VI)</i>	: 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

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

III. Wild Type Strains

<u>FGSC no.</u>	<u>Description</u>	<u>FGSC no.</u>	<u>Description</u>
A4	Glasgow wild type	A96	Grindle wild isolate #44
A90	Grindle wild isolate #2	A251	<i>A. heterothallicus</i> A #W B5096
A94	Grindle wild isolate #26	A252	<i>A. heterothallicus</i> a #W B5097
A96	Grindle wild isolate #36	A732	<i>A. niger</i> N400 (=ATCC 9029)
A815	<i>A. oryzae</i>	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	Com post, 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	<i>A. niger</i> Lem ore
A1100	<i>A. fumigatus</i> (AF293)		

IV. 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 *TI(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 Strains

1. Combinations of color mutants: *yA2*, *wA3*, *chaAI*, *bwAI*
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) *TI(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, <i>TI(V;VI)/T</i>	:A518/A370 or A521
Linkage Group VI	:A464/A377
Linkage Group VII, <i>TI(VI;VII)/T</i>	:A519/A520
7. Strains for teaching meiotic recombination: *w*, *cha* and green strains \pm *AcrAI*:
A188, A205, A222, A356, A359, A360, A452
8. Strains for mutant selection by biotin starvation with *biAI*:
A26, A194, A357, A378, A391, A392

9. Back cross strains:

Standard in Montreal

a. (<i>veA</i> ⁺)	BC VIII	A 17, A 18, A 80, A 81 A 82, A 83, A 126	a. = back crosses of <i>adG14 proA1 pabaA1 yA2;wA3</i>
	BC IX	A 343	
b. (<i>veA1</i>)	BC V	A 360, A 365	b. = back crosses of <i>yA2;AcrA1;lysB5;chaA1</i>
	BC IV	A 204, A 205	
c. (<i>wA3;chaA1</i>)	BC V	A 222, A 223	c. = crosses between strains of a. and b.
(<i>wA3;cha</i> ⁺)		A 221	

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

<u><i>rec</i>⁻ mutants</u>	Original		Derived spontaneous haploids	
	<u>Duplication strains</u>			
<i>rec-402</i> YP 2(3)	YP528	A 543	M2826	A 597
<i>rec-408</i> YP 8(3)	YP529	A 546	M2827	A 598
<i>rec-412</i> YP B2	YP533	A 549	--	--
<i>rec-444</i> YP44(3)	YP530	A 548	M2828	A 599
<i>rec-469</i> YP69(3)	YP531	A 544	M2829	A 600
<i>rec-471</i> YP71(3)	YP532	A 547	YP532y	A 562
Hyper- <i>rec</i> mutant				
<i>uvsB413</i> YP <i>popB13</i>	YP511A (lost)	--	YP511Ay	A 561

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.

FGSC#	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 1	<i>biA1;ssbA1;choA1 T1(I;VII)</i>		M 7	UV of A26
A 2	<i>biA1;sA4</i>	none	M 27	UV of A26
A 3	<i>biA1;wA3;sA6 T1(III→VIII);T1(VI;VII)?</i>		M 29	UV of A51
A 4	Glasgow wild type (<i>veA</i> ⁺)	none	M 139	Yuill, 1950
A 11	<i>biA1;AcrA1 wA3;nicC10</i>		G 0119	UV of A123
A 14	<i>yA2;thiA1 T(III→VIII;IV) (veA</i> ⁺)		M 420	X of yA2, <i>veA</i> ⁺ <i>T(III→VIII;IV)</i>
A 17	<i>adG14;(veA</i> ⁺)		M 635	BC VIII[1]
A 18	<i>adG14 yA2(veA</i> ⁺)		M 640	BC VIII[1]
A 23	<i>pabaA1 yA2;chaA1</i>	none	M 755	Cross 507
A 24	<i>sC12;(veA</i> ⁺)		M 801	NM of A4
A 26	<i>biA1;veA1</i>	none	M 804	X of A4
A 27	<i>pabaA1 biA1;wA3 T1(VI;VII)</i>		M 805	X of A26 and S
A 28	<i>pabaA6 biA1</i>	none	M 807	UV of 26
A 29	<i>pabaA1 biA1;coA1 T1(VI;VII)</i>		M 809	X of A26 and S
A 31	<i>anA1 biA1*</i>	none	M 812	UV of A26
A 32	<i>proA1 biA1</i>	none	M 813	UV of A26
A 33	<i>biA1;pyroA4</i>	none	M 815	UV of A26
A 34	<i>biA1;methH2*</i>	none	M 818	UV of A26
A 35	<i>adG14 biA1;pA2</i>	none	M 820	S in A37
A 36	<i>pabaA1 yA2;AcrA1;coA1 T1(VI;VII)</i>		M 822	*S in <i>pabaA1</i> *yA2;coA1;T1(VI;VII)
A 37	<i>adG14 biA1</i>	none	M 823	UV of A26
A 38	<i>wA1;lysA1 AbVI? (veA</i> ⁺)		M 829	X of wA1
A 40	<i>biA1;sA1 T1(V;VI)</i>		M 837	UV of A26
A 41	<i>biA1;sB3</i>	none	M 834	UV of A26
A 42	<i>adE8 biA1*</i>	none	M 851	UV of A26
A 43	<i>biA1;ornA4</i>	none	M 232	UV of A26
A 44	<i>suA1adE20 adE20 biA1;AcrA1;phenA2; pyroA4;lysB5;sB3;choA1;coA1 chaA1</i>	none	M 857	Cross 474[2]
A 45	<i>proA5 biA1</i>	none	M 861	UV of A26
A 46	<i>adF15 biA1</i>	none	M 862	UV of A26
A 47	<i>suA1adE20 adE20;pyroA4</i>	none	M 864	S in A227
A 50	<i>adE20 biA1 T(II;VII) Ab?</i>		M 871	UV of A26
A 51	<i>biA1;wA3 T(III;VIII); T(VI;VII)</i>		M 879b	yA2;adC1x pabaA1biA1;wA3
A 52	<i>biA1;thiA4</i>	none	M 882	UV of A26
A 55	<i>luA1 biA1</i>	none	M 892	UV of A26
A 56	<i>biA1;ornB9</i>	none	M 893	
A 57	<i>yA2;pyroA4;malA1</i>	none	M 895	UV of A220
A 59	<i>yA2;frA1 pyroA4 T1(IV;VIII)</i>		M 897	UV of A220
A 64	<i>biA1;wA3 riboE6 T1(III→VIII);T1(VI;VII)</i>		M 903b	UV of A51
A 66	<i>biA1;smA1;lysB5</i>	none	M 905	UV of A26
A 68	<i>suA1adE20 yA2 adE20;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;riboB2</i>	none	M 911	Cross of Forbes:MSD
A 69	<i>biA1;wA4;smA1;lysB5</i>	none	M 912	S in A66
A 70	<i>suA1adE20 adE20 biA1;AcrA1;phenA2; pyroA4;lysB5;sB3;nicB8;chaA1</i>	none	M 915	C 434 [2]
A 71	<i>suA1adE20 riboA1 pabaA1 yA2 adE20;AcrA1 wA2</i>	none	M 59	C K K[3]
A 72	<i>adG14 proA1 pabaA1 yA2;wA3</i>	none	M 140	BC I [1]
A 74	<i>adG14 proA1 pabaA1 yA2;wA3;(veA</i> ⁺)	none	M 387	BC II of A72
A 75	<i>suA1adE20 adE20 biA1;wA2;ssbA1;choA1;chaA1</i>	none	M 391	C 362 [2]
A 77	<i>suA1adE20 yA2;methG1;bwA1;chaA1</i>		M 544	C 314 [2]
A 78	wA3 (may carry <i>suA1adE20</i> , yA2 and/or <i>chaA1</i>)	none	M 552	C 419 [1]

* Contain UV induced morphological mutation

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 79	<i>suA1adE20 pabaA1 yA2 adE20;cnxE16;sC12;pyroA4;nicA2;sB3;choA1;chaA1</i>	none	M 626	C 400 (4)
A 80	<i>adG14 proA1 pabaA1;(veA⁺)</i>	none	M 632	BC VIII[1]
A 81	<i>adG14 pabaA1 yA2;(veA⁺)</i>	none	M 639	BC VIII[1]
A 82	<i>pabaA1 yA2;(veA⁺)</i>	none	M 641	BC VIII[1]
A 83	<i>yA2;(veA⁺)</i>	none	M 643	BC VIII[1]
A 84 [†]	<i>yA2;chaA1</i>	none	M 701	C 419 [1]
A 87	<i>riboA1 adG14 proA1 pabaA1 yA2</i>	none	M 841	C X [2]
A 89	<i>biA1;argB2</i>	none	G 034	UV of A26
A 90	Grindle wild isolate 2		2 (MG)	
A 91	Grindle white spores		2w (MG)	UV of A90
A 92	Grindle wild type 26		26 (MG)	
A 93	Grindle yellow spores		26y (MG)	UV of A92
A 94	Grindle wild type 36		36 (MG)	
A 95	Grindle white spores		36w (MG)	UV of A94
A 96	Grindle wild type 44		44 (MG)	
A 97	Grindle yellow spores		44y (MG)	UV of A96
A 104	<i>yA2 adE20;AcrA1;phenA2;pyroA4;lysB5;sB3;nicB8;coA1</i>	none	M 301	C 282 (4)
A 105	<i>biA1;AcrA1 wA3;phenA2;pyroA4;lysB5;sB3;nicB8;coA1</i>	none	M 276	C 280 (4)
A 108	<i>adE20 biA1;wA2 cnxE16;sC12;methG1;nicA2;choA1;chaA1</i>	none	M 455	C 349
A 111	<i>proA2 biA1 T1(II;III)</i>		M 233	UV of A26
A 112 [†]	<i>yA2;bwA1</i>	none	M 545	*set of
A 113 [†]	<i>bwA1</i>	none	M 546	*prototroph
A 114 [†]	<i>bwA1;chaA1</i>	none	M 547	*(not <i>veA⁺</i>)
A 115 [†]	<i>wA3;bwA1</i>	none	M 548	*color mutants
A 116 [†]	<i>yA2</i>	none	M 549	*from C 419
A 117 [†]	prototroph, wild type color (no <i>veA⁺</i>)	none	M 550	*(includes A78
A 118 [†]	<i>chaA1</i>	none	M 551	* A84 and A36)
	[†] May contain <i>suA1adE20</i>			
A 120	<i>pabaA1 yA2 adE20;AcrA1;coA1</i>	none	M 286	C 281 (4)
A 121	<i>suA1adE20 riboA1 proA1 pabaA1 adE20;chaA1</i>	none	M 310	C 300
A 122	<i>riboA1 yA2;nicB8</i>	none	M 15a	C 4
A 123	<i>biA 1;A cr 1;w A 3</i>		M 74	C 69
A 125	<i>riboA1 biA1;AcrA1;pyroA4;sB3;nicB8 T1(I;VIII)</i>		M 78	C 62 [6]
A 126	<i>pabaA1 yA2;wA3;(veA⁺)</i>	none	M 740	BC VIII [1]
A 129	<i>pabaA1 yA2 adE20;choA1 T1(I;VII)</i>		M 260=M 96	C 103
A 139	<i>adE20 biA1;wA3;methG1 pyroA4</i>	none	M 180	C 235
A 146	<i>pabaA1;AcrA1;phenA2;pyroA4;lysB5;sB3;nicB8;riboB2 chaA1</i>	none	M 927	C 434 [2]
A 147	<i>AcrA1;lysB5;sB3;chaA1</i>	none	M 940	C 434 [2]
A 148	<i>suA1adE20 pabaA1 yA2 adE20;lysB5</i>	none	M 951	C 461 [2]
A 154	<i>adE20 biA1;wA2 cnxE16;sC12;methG1;nicA2;lacA1;choA1;chaA1</i>	none	M 1043	C 500
A 155	<i>suA1adE20 pabaA1 yA2 adE20;AcrA1;phenA2;</i>	none	M 1056	C 474 [2]
A 158	<i>riboA1 biA1 (abnormal for penicillin synthesis)</i>	none	M 827	UV of A26
A 159	<i>suA1adE20 pabaA1 yA2 adE20;AcrA1;phenA2;pyroA4;lysB5;sB3;nicB8;riboB2</i>	none	M 1295	C 283 (4)
A 163	<i>suA1adE20 yA2 adE20;AcrA1;phenA2;pyroA4;lysB5;sB3;nicB8;coA1</i>	none	M 300	C 282 (4)
A 168	<i>suA1adE20 adE20 biA1;ssbA3;sB3;choA1;chaA1</i>	none	M 878	C 75
A 173	<i>suA1adE20 pabaA1 yA2 adE20;phenA2;nicB8</i>	none	M 947	C 461 [2]
A 183	<i>riboA1 pabaA1 yA2;wA3</i>	none	M 1072	C 630 [1]
A 186	<i>riboA1 pabaA1 biA1</i>	none	M 1078	C 630 [1]
A 187	<i>pabaA1 yA2</i>	none	M 1079	C 630 [1]
A 188	<i>riboA1;wA3</i>	none	M 1085	C 640 [1]
A 191	<i>wA3</i>	none	M 1088	C 640 [1]
A 192	<i>adG14</i>	none	M 1090	C 639 [1]
A 193	<i>riboA1 adG14 pabaA1 yA2;wA3</i>	none	M 1202	C 637 [1]

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 194	<i>yA2 biA1</i>	none	M 1205	C 638 [1]
A 201	<i>anA1</i>	none	M 1243	C 758 [1]
A 202	<i>riboA1 anA1</i>	none	M 1244	C 758 [1]
A 204	<i>AcrA1;chaA1</i>	none	M 1240	C 751 [1]
A 205	<i>AcrA1;lysB5</i>	none	M 1241	C 751 [1]
A 206	<i>riboA1 adG14 yA2</i>	none	M 1250	C 758 [1]
A 208	<i>suA1adE20 riboA1 proA1 pabaA1 adE20; choA1;chaA1</i>	none	M 279	C 300
A 211	<i>biA1;wA3;galA1</i>	none	RR-10	Cross by Roberts
A 212	<i>galD5 biA1;wA3; (T1 III → VIII)</i>		RR-6	Cross by Roberts
A 213	<i>galD5 biA1;wA3; (T1(VI;VII))</i>		RR-7	Cross by Roberts
A 214	<i>biA1;wA3;galE9</i>	none	RR-31	Cross by Roberts
A 215	<i>biA1;wA3;galB3; T1(III→VIII);T1(VI;VII)</i>		RR-13	UV of A51
A 216	<i>adA55</i>		AM-55 (RG)	* UV of green pro-
A 217	<i>adB57</i>		AM-57 (JMF)	*totroph from cross * A82 ⁺⁺ X A34
A 218	<i>adA55 yA2 biA1;AcrA1;riboB2</i>		A-201	Cross of A216 of JMF
A 219	<i>biA1;methG1</i>	none	M 800	UV of A26
A 220	<i>yA2;pyroA4</i>	none	M 1105	<i>yA2;sC12</i> X A33
A 222	<i>AcrA1 wA3;lysB5;chaA1</i>	none	M 1251	Cross 762
A 223	<i>wA3;lysB5;chaA1</i>	none	M 1252	Cross 762
A 227	<i>adE20;pyroA4</i>		P78 (RHP)	Cross AAA
A 228	<i>adE⁺biA⁺ Dp1(I→II) adE20 biA1</i>		P575 (RHP)	*Duplication from
A 229	<i>yA2 adE⁺ biA⁺Dp1(I→II)yA⁺ adE20 biA1 pyroA4</i>		P529 (RHP)	* <i>adE20</i> cross
A 230	<i>yA2;wA2;argA1;(veA⁺)</i>		B 66 (BWB)	*Cross of A344 X * <i>biA1;argA1</i> (T?)
A 231	<i>riboA1 yA2;ActA1;nicB8</i>	none likely	B 115 (BWB)	UV of A122
A 232	<i>yA2;adD3;sA1 moC96</i>		B 172 (BWB)	
A 234	<i>pabaA1 yA2</i>	none	A 148 (CFR)	from cross by JMF
A 235	<i>pabaA1 yA2;trypA69</i>		A 148 (CFR)	UV of A234
A 236	<i>trypB403 pabaA1 yA2</i>		A 148 (CFR)	UV of A234
A 237	<i>pabaA1 yA2;trypC801</i>		A 148 (CFR)	UV of A234
A 238	<i>pabaA1 yA2;trypD432</i>		A 148 (CFR)	UV of A234
A 239	<i>biA1;adH23 AcrA1 wA3;nicB8</i>	none	M 6	Cross 59
A 241	<i>biA1;pacA1</i>		(GD)	Recomb. as A243
A 242	<i>biA1;pacC5</i>	none	(GD)	UV of A26
A 243	<i>biA1;palA1</i>		(GD)	*Recombinants,
A 244	<i>biA1;palB7</i>		(GD)	*UV induced in
A 245	<i>biA1;palD8</i>		(GD)	* <i>rA1 biA1</i> &
A 247	<i>biA1;palF15</i>		(GD)	* separated from
A 248	<i>biA1;palcA1</i>		(GD)	* <i>rA1</i> in crosses
A 249	<i>biA1;sD50 T2(I;VIII)</i>		(GD)	
A 250	<i>yA2;frA1 palC4 pabaB22 pyroA4 T1(IV;VIII)</i>		(GD)	Cross by GD
A 251	<i>A. heterothallicus</i>		WB5096	*Wild types
A 252	<i>A. heterothallicus</i>		WB5097	* of Raper
A 254	<i>biA1;AcrA1 wA3 ileA3 cnxE16 adD3</i>	none likely	(GD)	Cross of E. Forbes
A 256	<i>pabaA1;wA3;argC3 facB101 riboB2</i>		(GD)	Cross of E. Forbes
A 257	<i>biA1;AcrA1 wA3;nicB8;hisC38</i>		(GD)	*UV of T-free strain * of J. Foley
A 258	<i>nicA2 hxA1 riboD5</i>		(GD)	Cross of Darlington
A 259	<i>biA1;adC1;sC12;pyroA4</i>	none	(GD)	Cross R (2)
A 260	<i>biA1;phenA3;nirA14 T1(I;IV)</i>		(GD)	S in <i>biA1;phenA3;T1(I;IV)</i>
A 261	<i>biA1;AcrA1 wA3 anB2 (Ab likely)</i>		(GD)	UV of A123
A 262	<i>biA1;uY5</i>		(GD)	DES of A26
A 263	<i>biA1;ormB20</i>	none	(GD)	UV of A26
A 264	<i>biA1;uaX10</i>		(GD)	DES of A26
A 266	<i>biA1;cnxB50</i>	none	(GD)	UV of A26
A 268	<i>yA2;wA2 thiA4 cnxE16 adD3 bla1</i>		(GD)	Cross of Apirion
A 269	<i>pabaA1;tsD15 fwA2 facB101 riboB2</i>		(GD)	Cross of Forbes
A 270	<i>biA1;ygA1</i>	none	(GD)	S in A26
A 272	<i>yA2;pyroA4;methB3</i>		(GD)	UV of A220(CFR)

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 273	<i>adF17 pabaA1 yA2;fpaD11</i>		(GD)	mutant of Sinha
A 275	<i>fpaA1 adG14 pabaA1 yA2</i>		(GD)	Cross of McCully
A 276	<i>yA2;frA1 pabaB22 pyroA4 T1(IV;VIII)</i>		(GD)	Cross of Siddiqi
A 277	<i>yA2 biA1;AcrA1;hisA10;riboB2</i>		(GD)	*UV induced in T-
A 278	<i>yA2 biA1;AcrA1;riboB2 hisH13</i>		(GD)	*free strain of JMF
A 279	<i>yA2;pyroA4;aaX1</i>		(GD)	*induced in A 220(?)
A 280	<i>clA6 proA1 pabaA1 yA2;palB7</i>		(GD)	Cross of Apirion
A 281	<i>biA1;suA1palB7 palB7</i>		(GD)	S in A244
A 282	<i>biA1;suC6palF15;palF15</i>	none?	(GD)	S in A247
A 283	<i>suA1adE20 yA2 adE20;AcrA1;galA1; pyroA4;facA303;sB3;nicB8;riboB2</i>	none	(GD)	MSF of McCully
A 284	<i>biA1;suB2palB7;palB7</i>	none?	(GD)	S in A244
A 285	<i>biA1;adI50</i>	none	(GD)	UV of A26
A 286	<i>riboA1 biA1;fpaC43</i>	none likely	(GD)	S in A158
A 287	<i>biA1 suD2palA1;palA1</i>	none?	(GD)	S in A243
A 288	<i>suA1adE20 yA2 adE20;wA3;galA1;pyroA4; facA303;sB3;nicB8;riboB2</i>	none	(GD)	MSE of McCully
A 291	<i>biA1;wA3;galC4 T1(III-VIII);T1(VI;VII)</i>		(CFR)	UV of A51
A 292	<i>biA1;wA3 lacB3 T1(III-VIII);T1(VI;VII)</i>		(CFR)	NA of A51
A 293	<i>lysF88 biA1;sB3</i>	none likely	(GD)	NA of A41, Pees
A 294	<i>biA1;sB3;lysD18</i>	none likely	1B (GD)	NA of A41, Pees
A 295	<i>biA1;ileA1;sB3</i>	none likely	IVC10 (EP)	NA of A41
A 296	<i>biA1;lysE13;sB3</i>	none likely	ID1 (EP)	NA of A41
A 297	<i>lysF51 biA1;sB3</i>	none likely	IE1 (EP)	NA of A41
A 298	<i>biA1;lysE14;sB3</i>	none likely	ID2 (EP)	NA of A41
A 299	<i>biA1;sB3;hisJ122</i>	none likely	IIC2 (EP)	NA of A41
A 300	<i>biA1;sB3;lysD7</i>	none likely	IB2 (EP)	NA of A41
A 301	<i>biA1;lysE231;sB3</i>	none likely	(EP)	NA of A41
A 303	<i>proA1 yA2;AcrA1 T1(VI;VII)</i>		P129 (RHP)	Cross of RHP
A 304	<i>proA1 pabaA1 yA2;phenA2 T1(I;VIII)</i>		P97 (RHP)	Cross 2(6)
A 305	<i>proA2 pabaA18 biA1;phenA2;lysB5</i>		P138 (RHP)	Cross of RHP
A 306	<i>adF17 pabaA1 yA2</i>		P112 (RHP)	Cross of RHP?
A 307	<i>proA1 pabaA1;nicB8</i>		P87 (RHP)	Cross of RHP?
A 308	<i>pabaA18 biA1</i>	none?	P115 (RHP)	UV of A26?
A 309	<i>proA2 pabaA18 yA2 T1(III-VIII)</i>		P117 (RHP)	Cross of?
A 310	<i>proA1 biA1;AcrA1;pyroA4</i>	none	P254 (RHP)	Cross 38 (3)
A 311	<i>adE20 biA1;wA2;nicA2 riboD3</i>		P12 (RHP)	Cross of RHP
A 312	<i>suA1adE20 yA2 adE20;AcrA1;phenA2;lysB5</i>		P20 (RHP)	Cross of RHP?
A 314	<i>proA1 pabaA1 yA2;wA3 adC1;(veA⁺)</i>	none	M821	C M811 x M813
A 315	<i>adG14 pabaA1 yA2</i>	none	M825	Cross V (2) of Pontecorvo
A 316	<i>biA1;sA2 T1(V;VIII)</i>		M845	UV of A26
A 317	<i>biA1;nicB8 (Contains UV induced morphological mutation)</i>	none	M873	UV of A26
A 319	<i>anA1 yA2;wA3 adC1;sC12</i>	none	M1128	Cross n, EK
A 320	<i>suA1adE20 riboA1 proA1 adE20 biA1;pyroA4</i>		(GD)	Cross g, EK
A 326	<i>biA1;methG1;flA1</i>		(JLA)	mutant in A219?
A 327	<i>adE20 biA1;wA3;methG1 pyroA4;uvs-5</i>	none?	(RWT)	UV of A139
A 329	<i>adE20 biA1;wA3;uvsH4 methG1 pyroA4</i>	none?	(RWT)	UV of A139
A 330	<i>adE20 biA1;wA3;uvsH77 methG1 pyroA4</i>	none?	(RWT)	UV of A139
A 333	<i>pabaA108 biA1;uvsB110 T2(V;VI)</i>		UT501 (GJOJ)	UV of <i>pabaA108 biA1</i>
A 334	<i>pabaA108 biA1;uvsC114</i>		UT503 (GJOJ)	UV of <i>pabaA108 biA1</i>
A 335	<i>proA1 pabaA125 biA1;pyroA4;uvsD153</i>		UT517 (GJOJ)	UV of <i>proA1 pabaA125 biA1;pyroA4</i>
A 337	<i>riboA1 biA1;wA3 thiA4 cnxE16</i>	none	M23	C 50
A 338	<i>yA2;wA3 puA1 cnxE16 adC1 acrB2</i>		M94	C 85
A 339	<i>suA1adE20 pabaA1 yA2 adE20;sA4</i>	none	M146	C 136
A 340	<i>proA1 biA1;phenA2;pantoA1 T1(III-VIII;VII)</i>		M347	C 243
A 341	<i>suA1adE20 proA1 pabaA1 yA2 adE20;</i>	none	M426	C 347
A 342	<i>suA1adE20 adE20 biA1;AcrA1;choA1 chaA1</i>	none	M771	C 365
A 343	<i>adG14 proA1 pabaA1 yA2;wA3;(veA⁺)</i>	none	M799	BC IX of A72
A 344	<i>yA2;wA2 adC1;sC12;(veA⁺)</i>	none	M814	C J (2)
A 345	<i>biA1;sC12;pyroA4 T1(II;IV)</i>		M854	Cross (2)

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 346	<i>biA1;AcrA3 adC1;sC12;pyroA4</i>	none	M 875	S in A259
A 347	<i>anA1 adE20 biA1;wA2;lysB5 T(I;V;VII;VIII)</i>		M 900	S in A348
A 348	<i>anA1 adE20 biA1;wA2;lysB5</i>	none	M 921	C 512
A 349	<i>adE20 biA1;lacA1;choA1;chaA1</i>	none	M 917	C 496
A 350	<i>biA1;phenA2;lysA1 (Ab VI) sB3</i>		M 918	C 346
A 352	<i>riboA1 adG14 yA2;phenA2 T1(I;VIII)</i>		M 962	C 2 (6)
A 353	<i>biA1;ornB9 riboB2</i>		M 966	C 494
A 354	<i>AcrA1;lysB5;T1(I;VII)</i>		M 1014	C 515
A 355	<i>anA1 adE20 biA1;wA2;lysB5;T2(I;VII)</i>		M 1054	C 542b
A 356	<i>riboA1 biA1</i>	none	M 1076	C 630 [1]
A 357	<i>biA1;wA3</i>	none	M 1089	C 640 [1]
A 358	<i>riboA1 adG14 proA1 yA2;ornA4</i>		M 1101	C 3
A 359	<i>pabaA1;wA3</i>	none	M 1231	C 639 [1]
A 360	<i>AcrA1;lysB5;chaA1</i>	none	M 1239	C 752 (BC V)
A 361	<i>riboA1 yA2</i>	none	M 1265	C 630 [1]
A 362	<i>riboA1 anA1 adG14 proA1 pabaA1 yA2</i>	none	M 1267	C 773
A 363	<i>suA1adE20 riboA1 anA1 luA1 pabaA1 yA2 adE20 biA1;AcrA1</i>	none	M 1274	C 792
A 364	<i>suA1adE20 proA2 yA2 adE20;AcrA1 wA2</i>	none	M 1277	Dipl. 629
A 365	<i>yA2;AcrA1;lysB5;chaA1</i>	none	M 1279	C 752 (BC V)
A 366	<i>yA2;bwA1;chaA1</i>	none likely	M 1282	C 789
A 367	<i>suA1adE20 proA1 yA2 adE20;AcrA1 wA2</i>	none likely	M 1285	Dipl. 628
A 368	<i>riboA1 yA2;sA2</i>	none	M 1301	C 785
A 369	<i>pabaA1 biA1;sB3</i>	none	M 1303	C 788
A 370	<i>adG14;sA1;pyroA4;chaA1;T1(V;VI)</i>		M 1309	C 838
A 371	<i>AcrA1;lysB5;fwA2</i>	none	M 1318	S in A205
A 372	<i>biA1;sA2;chaA2 T1(V;VIII)</i>		M 1319	S in A316
A 373	<i>anA1;sA1;lysB5;chaA1;T1(V;VI)</i>		M 1324	C 838
A 374	<i>suA1adE20 yA2 adE20;AcrA1;sA4;pyroA4; pA2;lacA1;nicB8;riboB2</i>	none	M 1335	C 569
A 375	<i>suA1adE20 adE20 biA1;AcrA1;sA4;pyroA4; pA2;lacA1;nicB8;riboB2</i>	none	M 1343	C 569
A 376	<i>suA1adE20 lysF88 pabaA1 yA2 adE20</i>	none	M 1346	C 841
A 377	<i>riboA1 yA2 adE20</i>	none	M 1368	C 847
A 378	<i>biA1;fwA1</i>	none	M 1370	S in A26
A 379	<i>ornB7 fwA1(veA⁺)</i>		M 1371	Cross of AJC
A 380	<i>lysB5;fwA2 cnxB2 facB101 palB7 chaA1</i>	none	M 1373	C 804
A 381	<i>cnxB2 palB7</i>	none	M 1376	C 804
A 382	<i>yA2;adh23 AcrA1 wA3 anB2</i>	none	M 1383	Cross of AJC
A 383	<i>riboA1;AcrA1;sB25;chaA1</i>		M 1398	NG of M1421
A 384	<i>riboA1 yA2;sC22</i>	none?	M 1400	NG of riboA1;yA2
A 385	<i>biA1;sE15</i>	none?	M 1402	NG of A26
A 386	<i>proB94;(veA⁺)</i>	none?	M 1414	UV of A4
A 387	<i>fpaA91 proA11 yA2;pyroA4</i>		M 1415	NG of orig <i>proA11</i>
A 388	<i>biA1;pyroA4;sF211</i>	none?	M 1433	NG of A33
A 389	<i>uvsF201 pabaA1</i>	none	M 1444	C 915
A 390	<i>fpaA91 pabaA1 biA1;pyroA4</i>	none	M 1447	C 883
A 391	<i>biA1;chaA1</i>	none	M 1466	C 843
A 392	<i>yA2 biA1;chaA1</i>	none	M 1469	C 843
A 393	<i>suA1adE20 proB94 yA2 adE20;AcrA1 wA2</i>	none	M 1474	Dipl 860
A 394	<i>biA1;phenB6</i>	none?	M 1490	UV of A26
A 395	<i>biA1;smsA61;sB3;lysD20 T1(III;VII)</i>		M 1493	UV of A41
A 397	<i>pantoB100</i>		M 1498	UV?(BMR)
A 398	<i>biA1;lysB5;sD50 T2(I;VIII)</i>		M 1500	C 980
A 399	<i>facB101 riboB2 sE15</i>	none	M 1503	C 898
A 400	<i>yA2 adE20;AcrA1;sF211 palF15 choA1</i>	none?	M 2281	C 2116
A 401	<i>facB101 riboB2 palB7 chaA1 sE15</i>	none likely	M 1581b	C 1932
A 402	<i>phenA3;palB7 chaA1 nirA14</i>	none likely	M 1626	C 1045
A 403	<i>pabaA1;wA3;pyroA4;sF211</i>	none likely	M 1631	C 966
A 404	<i>biA1;AcrA1 wA3;sA49;lysB5</i>	none likely	M 1641	C 1164

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 405	<i>pabaA1 yA2; sA91</i>	none likely	M 1643	C 1166
A 406	<i>luA1 yA2</i>	none	M 1824	C 1605
A 407	<i>adE20 biA1; AcrA1; phenA2; pyroA4; lysB5; lacA1; choA1; riboB2 chaA1</i>	none	M 1832	C 1608
A 408	<i>pabaA1 yA2; wA3</i>	none	M 1849	C 1621
A 409	<i>pabaA1; facB101 chaA1</i>	none?	M 1854	C 1701
A 410	<i>pabaA1 biA1; riboB2 chaA1</i>	none	M 1869	C 434
A 411	<i>proA1 pabaA1 yA2</i>	none	M 1885	C 1709
A 412	<i>pabaA1 yA2; ActA1</i>	none	M 1897	C 1649
A 413	<i>pabaA1; sA2; chaA2 T1(V; VIII)</i>		M 1907	C 1708
A 414	<i>riboA1 proA2 yA2; ActA1 T1(II; III)</i>		M 1937	C 1760
A 415	<i>riboA1 proA2 biA1; ActA1</i>	none	M 1940	C 1760
A 416	<i>riboA1; chaA1</i>	none	M 1941	C 1754
A 417	<i>pabaA1; sA1; chaA1</i>	none	M 1942	C 1754
A 418	<i>pabaA1 yA2; lysD20 T1(III; VII)</i>		M 1944	C 1732
A 419	<i>biA1; sD85</i>	none	M 1951	NG of A26
A 420	<i>pabaA1; sD157 facB101</i>	none	M 1986	C 1801
A 421	<i>riboA1; sD85</i>	none	M 1987	C 1794
A 422	<i>fpaB37 riboA1 biA1</i>	none	M 1990	S in A158
A 423	<i>riboA1 proA1 yA2; sC12 phenA2 suB4pro</i>	none	M 1998	C 1846
A 424	<i>suA1adE20 riboA1 proA1 pabaA1 yA2 adE20; AcrA1; pyroA4; phenB6 sF211 malA1 nicB8; chaA1</i>	none	M 2006	C 1530
A 425	<i>y^oA91 biA1; phenA2</i>	none	M 2012	S in A498
A 426	<i>yA2; pabaB22 pyroA4</i>	none	M 2023	C 1783
A 427	<i>pabaA1; AcrA1; sD85 facC102</i>	none	M 2027	C 1802
A 428	<i>pabaA1 adE20 biA1</i>	none, other Ab?	M 2032	C 1716
A 429	<i>pabaA1 adE20 biA1 T(II; VII) Ab?</i>		M 2033	C 1716
A 430	<i>suA1adE20 riboA1 proA1 pabaA1 yA2 adE20; pyroA4; phenB6 sF211 malA1; chaA1 T1(I; VII)</i>		M 2039	C 1530
A 431	<i>galD5 suA1adE20 riboA1 adE20 biA1; sD50 T2(I; VIII) fwA2 facC102</i>		M 2054	C 1808
A 432	<i>galD5 suA1adE20 riboA1 adE20 biA1; AcrA1; fwA2 facB101</i>	none	M 2055	C 1809
A 433	<i>fpaB37 SulA1 anA1 pabaA1 yA2 adE20; pyroA4; cnxB2 chaA1 T1(VI; VII)?</i>		M 2056	C 1822
A 434	<i>fpaB37 anA1 pabaA1 yA2 adE20; sD50 T2(I; VIII) cnxB2 chaA1 (galC7?)</i>		M 2057	C 1822
A 435	<i>frA1 T1(IV; VIII) palC4 pabaB22 pyroA4; chaA1</i>		M 2070	C 1911
A 436	<i>adE20 biA1; wA4; smA1; lysB5</i>	none	M 2071	C 1914
A 437	<i>proA1; wA3; nicA2; malA1</i>	none	M 2072	C 1923
A 438	<i>fpaA91 anA1 adE20 biA1; wA2; lysB5; chaA1 T1(I; VII)</i>		M 2074	C 1519
A 439	<i>fpaA91 anA1 adE20 biA1; AcrA1 wA4; ActA1; choA1</i>	none	M 2076	C 1518
A 440	<i>riboA1 yA2; AcrA1; fwA2</i>	none	M 2102	C 1844
A 441	<i>riboA1 proA1 biA1; wA3; sC12 galA1 ActA1 phenA2 suB4pro</i>	none	M 2108	C 1838
A 442	<i>facB101 riboB2 chaA1 sE15 nirA14</i>	none	M 2113	C 1932
A 443	<i>pabaA1 yA2 adE20; AcrA1; suC11adE20; coA1 cnxB2</i>	none	M 2131	S in rec. from 1799
A 444	<i>suA1adE20 yA2 adE20; AcrA1; phenB6 sF211 malA1 choA1 nicB8</i>	none?	M 2132	C 1942
A 445	<i>riboA1 y^oA91</i>	none	M 2136	C 1903
A 447	<i>anA1 yA2; wA3; adI50 galA1 ActA1; sF211 lysD20 T1(III; VII) choA1 nicB8</i>		M 2150	C 1736
A 448	<i>proA1; AcrA1; galE9 sA1 adI50 ActA1; chaA1</i>	none	M 2151	C 1868
A 449	<i>AcrA1; lysB5; coA1 cnxB2</i>	none	M 2152	C 1799
A 450	<i>pabaA1 yA2; oliC2</i>	none?	M 2153	S in A187
A 451	<i>pabaA1; meaB6 cnxH3 sC12</i>	none	M 2158	C 332
A 452	<i>SulA1 anA1 pabaA1; wA3; ssbA1 chaA1</i>	none	M 2162	C 1950
A 453	<i>oliC2 pantoB100</i>	none	M 2165	C 1945
A 454	<i>riboA1 proA1 yA2; ActA1 suB4pro</i>	none	M 2167	C 1846
A 456	<i>proA1 yA2; galE9 adI50 methH2 dilA1</i>	none	M 2176	C 1969
A 457	<i>proA1 biA1; galE9 sC12 dilA1 phenA2; choA1</i>	none	M 2186	C 1973

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 458	<i>riboA1 proA1 yA2;AcrA1; adI50 methH2 galA1 ActA1 suB4pro</i>	none	M 2187	C 1972
A 459	<i>suA1adE20 pabaA1 yA2 adE20;AcrA1; lacA1 bwA1 sbA3;sF211</i>	none	M 2198	C 1952
A 460	<i>AcrA1;lysB5 pA2</i>	none	M 2200	C 2128
A 461	<i>proA1 biA1;phenA2;malA1;riboB2</i>	none	M 2204	C 1975
A 462	<i>pabaA1 y^oA91;IodA1 cnxE16</i>	none	M 2205	C 1976
A 463	<i>suA1adE20 proB94 lysF88 pabaA1 yA2 adE20;wA2</i>	none	M 2207	C 1985
A 464	<i>suA1adE20 pabaA1 yA2 adE20;AcrA1; lacA1 bwA1 sB3 sbA3</i>	none	M 2209	C 1952
A 466	<i>galD5 suA1adE20 riboA1 anA1 proB94 lysF88 pabaA1 yA2 adE20</i>	none	M 2213	C 2113
A 467	<i>yA2 adE20;lacA1;phenB6 oliC2 sF211 palF15 malA1 choA1 nicB8</i>	none likely	M 2214	C 2116
A 468	<i>SulA1;AcrA1 wA3;galA1;pyroA4;facA303; lacA1 sB3;choA1;riboB2 chaA1</i>	none	M 2216	C 1987
A 469	<i>AcrA1;lysB5;sD85 fwA2</i>	none likely	M 2218	C 1983
A 470	<i>proA1 biA1;methG1 frA1 T1(IV;VIII);chaA1</i>		M 2219	C 1929
A 471	<i>proA1 yA2;meaB6 sC12 methH2 dilA1</i>	none likely	M 2220	C 2108
A 472	<i>riboB2 nir14</i>	none	M 2221	C 1932
A 474	<i>SulA1 adE20;AcrA1;ActA1;choA1;chaA1</i>	none	M 2234	C 2112
A 475	<i>fpaB37 galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1;sD85 fwA2</i>	none	M 2235	Dipl. 2195
A 476	<i>SulA1 adE20;AcrA1 wA3;ActA1; lysB5;choA1;chaA1</i>	none likely	M 2239	C 2112
A 477	<i>SulA1 adE20;AcrA1 wA3;ActA1;pyroA4; lysB5;sB3;choA1;chaA1</i>	none	M 2240	C 2125
A 478	<i>SulA1 adE20;AcrA1 wA3;ActA1;pyroA4 sB3;lysB5;sB3;choA1;riboB2 chaA1</i>	none	M 2242	C 2125
A 479	<i>galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1</i>	none	M 2243	C 1523
A 480	<i>proA1 y^oA91;IodA1;phenA2;methG1; nicA2;sbA3;malA1;riboB2</i>	none likely	M 2246	C 1974
A 481	<i>yA2 adE20; phenB6 oliC2 sF211 malA1 choA1 nicB8</i>	none likely	M 2247	C 2120
A 482	<i>bwA1 sbA3;phenB6 oliC2;riboB2 T1(VI;VII)</i>		M 2248	C 2121
A 483	<i>fpaB37 galD5 suA1adE20 SulA1 riboA1 anA1 pabaA1 yA2 adE20 biA1</i>	none likely	M 2255	C 1523
A 484	<i>AcrA1;lysB5;sD85 fwA2 facC102</i>	none likely	M 2256	C 1983
A 485	<i>riboA1 adE20;fwA2</i>	none	M 2259	C 2105
A 486	<i>riboA1 yA2 adE20;methG1 suC11adE20</i>	none	M 2303	C 2134
A 488	<i>pabaA1 yA2;sC12</i>	none	M 2270	C 1762
A 489	<i>riboA1 biA1;dilA1;choA1</i>		M 2271	C 1967
A 490	<i>proA1;meaB6 cnxH3 adI50 dilA1</i>	none likely	M 2272	C 2108
A 491	<i>AcrA1;lysB5 pA2 facA303 hxA1 riboD5</i>	none	M 2310	C 2133
A 492	<i>pabaA1 y^oA91;IodA1</i>	none	M 2274	C 1978
A 493	<i>pabaB22</i>	none likely	M 2276	C 1907
A 494	<i>galD5 suA1adE20 riboA1 yA2 adE20;AcrA1</i>	none	M 2277	C 1951
A 495	<i>lysB5 nicA2 pA2</i>	none	M 2278	C 2127
A 496	<i>pabaA1 yA2;meaB6 adI50</i>	none likely	M 2279	C 2108
A 497	<i>AcrA1;palC4 pabaB22;chaA1</i>	none	M 2280	C 1911
A 498	<i>biA1;phenA2</i>	none likely	M 2013	C 1632
A 499	<i>suA1adE20 pabaA1 yA2 adE20;phenB6 sF211</i>	none	M 2282	C 1951
A 500	<i>biA1;methG1;nicA2;sbA3;malA1</i>	none	M 2283	C 1977
A 501	<i>adE20 biA1;smA1 ActA1</i>	none	M 2284	C 1935
A 502	<i>SulA1;AcrA1;lysB5 facA303;sB3;chaA1</i>	none	M 2285	C 2125
A 503	<i>proA1 yA2;methH2 dilA1</i>	none	M 2286	C 1969
A 504	<i>AcrA1;lysB5 pA2 riboD5</i>	none	M 2287	C 2127
A 505	<i>pabaA1 yA2;AcrA1 wA3 ileA3</i>	none likely	M 2288	C 1642

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 506	<i>AcrA1;phenB6 oliC2 sF211 malA1 choA1 nicB8</i>	none	M 2289	C 2120
A 507	<i>fpaB37 SulA1 anA1 pabaA1</i>	none	M 2295	C 1950
A 508	<i>AcrA1;nicA2 facA303 hxA1 riboD5;sB3;chaA1</i>	none	M 2309	C 2133
A 509	<i>riboA1 adE20</i>	none	M 2203	C 2110
A 510	<i>pabaA1 yA2 adE20;AcrA1;nicA2;sB3</i>	none	M 2298	C 1955
A 511	<i>SulA1;ActA1;choA1;chaA1</i>	none	M 2325	C 2107
A 512	<i>AcrA1;palC4 pabaB22 pyroA4;chaA1</i>	none likely	M 2307	C 1911
A 514	<i>anA1 adE20 biA1;AcrA1;ActA1;sB3;fwA2</i>	none	M 2356	C 2216
A 515	<i>fpaB37 galD5 suA1adE20 riboA1 yA2 adE20;pyroA4;facA303;chaA1</i>	none likely	M 2313	C 2217
A 516	<i>galE9 meaB6 adI50 ActA1; chaA1 sE15 nirA14</i>	none?	M 2328	C 2124
A 517	<i>riboA1 yA2 adE20;methG1 suC11adE20 palC4 pabaB22 pyroA4</i>	none	M 2316	C 2135
A 518	<i>AcrA1;lysB5 facA303 hxA1;lacA1 sB3 sbA3 T1(VR;VIR)</i>		M 2318	C 2131
A 519	<i>suA1adE20 riboA1 proA1 pabaA1 yA2 adE20; wA2;oliC2 malA1 choA1 nicB8 T1(VIR;VIIR)</i>		M 2319	Dipl. 1955
A 520	<i>pabaA1;AcrA1;sB3 sbA3;phenB6;riboB2 T1(VIR;VIIR)</i>		M 2320	Dipl. 1998
A 521	<i>suA1adE20;AcrA1;galA1;pyroA4; pA2 facA303 riboD5;sbA3 T1(VR;VIR)</i>		M 2321	C 2131
A 522	<i>pabaA1 yA2 adE20;AcrA1;facA303; lacA1 sB3 T1(VR;VIR)</i>		M 2322	C 2131
A 523	<i>biA1;AcrA1;benA17</i>		33 (JM vT)	UV of <i>biA1;AcrA1</i>
A 524	<i>biA1;benA10 fwA1</i>		5 (JM vT)	Cross <i>biA1;AcrA1;benA10 X fwA1 ornB7</i>
A 525	<i>suA1adE20 yA2 adE20;phenA2;pyroA4; lysB5;nicB8;benA10 fwA1 carB2</i>		10 (JM vT)	from diploid of Jm vT
A 526	<i>suA1adE20 yA2 adE20;wA3;galA1;pyroA4; facA303;sB3;nicB8;benA10 fwA1 carB2</i>		321 (JM vT)	from diploid of Jm vT
A 528	<i>biA1;phenA2 carC9</i>		125 (JM vT)	JM vT cross
A 529	<i>biA1;AcrA1;ActB2 oliC13 imaA4 benC28 choA1 carA1</i>		218 (JM vT)	
A 530	<i>biA1;AcrA1;pimA1</i>		181 (JM vT)	UV of <i>biA1;AcrA1</i>
A 531	<i>pimB10 proA1 pabaA1 yA2</i>		313 (JM vT)	JM vT cross
A 532	<i>biA1;AcrA1;imaB9</i>		146 (JM vT)	S in <i>biA1;AcrA1</i>
A 533	<i>biA1;AcrA1 imaC10</i>		147 (JM vT)	S in <i>biA1;AcrA1</i>
A 534	<i>biA1;AcrA1;imaD13</i>		250 (JM vT)	S in <i>biA1;AcrA1</i>
A 535	<i>biA1;AcrA1;imaG18</i>		248 (JM vT)	NG of <i>biA1;AcrA1</i>
A 536	<i>biA1;AcrA1;chlA10 imaG18</i>		305 (JM vT)	UV of <i>biA1;AcrA1</i>
A 537	<i>biA1;AcrA1;imaH19</i>		247 (JM vT)	NG of <i>biA1;AcrA1</i>
A 538	<i>yA2;csuA6;sB3;choA1</i>	none likely		H. Arst cross 255
A 539	<i>biA1 adE20;csuA6;sB3;chaA1</i>	none likely		H. Arst cross 213
A 542	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1</i>		YP 511 (YP)	Cross of YP 156 X Dp
A 543	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-402</i>		YP 528 (YP)	NG in YP 511
A 544	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-469</i>		YP 531 (YP)	NG in YP 511
A 546	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-408</i>		YP 529 (YP)	NG in YP 511
A 547	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-471</i>		YP 532 (YP)	NG in YP 511
A 548	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-444</i>		YP 530 (YP)	NG in YP 5113/20/1998
A 549	<i>pabaA6 yA2 adE8 biA⁺ Dp(I-II)yA⁺adE20 biA1;rec-412</i>		YP 533 (YP)	NG in YP 511
A 550	<i>anA1 adE20 biA1;AcrA1;ActA1;sB3;choA1;fwA2</i>	none	M 2358	C 2216
A 551	<i>uaY9</i>		Black 3 (BRS)	
A 552	<i>hxB13</i>		Black 4 (BRS)	
A 553	<i>biA1;cnxH3</i>		Black 5 (BRS)	DES of A26

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 554	<i>hxA1</i>		Black 7 (BRS)	
A 555	<i>biA1;cnxA5</i>		Black 29(BRS)	DES of A26
A 556	<i>biA1;cnxE14</i>		Black 30(BRS)	DES of A26
A 557	<i>biA1;cnxB11</i>		Black 31(BRS)	DES of A26
A 558	<i>biA1;cnxC</i>		Black 32(BRS)	DES of A26
A 559	<i>biA1;cnxG</i>		Black 33(BRS)	DES of A26
A 560	<i>cnxF8</i>		Black 34(BRS)	
A 561	<i>pabaA6 yA2 adE8;uvsB413</i>		YP 511 Ay	Loss of duplicated segment from A 545
A 562	<i>pabaA6 yA2 adE8;rec-471</i>	none likely	YP 532y	Loss of duplicated segment from A 547
A 563	<i>proA1 pabaA6 yA⁺adE20 biA1 (Del IR); Dp(I-II) yA2 adE⁺biA⁺uvsB110;nicA2 riboD5</i>		YP 300/2	UV of <i>Dp(I-II) YP300</i>
A 564	<i>suA1adE20 yA2 adE20;wA3;galA1; uvsB413;facA303;sB3</i>	none likely	YP 524	
A 565	<i>yA2;adD3 benB29</i>		C 1465 (HNA)	Strain 309 of JMvT
A 566	<i>pabaA1;benB29</i>		C 1605 (HNA)	*Cross <i>yA2;adD3 benB29</i> * <i>pabaA1;AcrB14 creB304</i>
A 567	<i>uvsF201 riboA1 yA2</i>	none	M 1392	UV of A361
A 568	<i>yA2;uvsH77</i>	none likely	M 2346	C 2407
A 569	<i>riboA1;AcrA1;uvsJ1;chaA1</i>	none likely	M 2382	C 2431
A 570	<i>pabaA108 biA1;uvsC114</i>	none likely	M 2393	C 2408
A 571	<i>pabaA125 biA1;uvsD153;fwA2</i>	none likely	M 2398	C 2409
A 572	<i>anA1 biA1;pyroA4;uvsE182</i>	none likely	M 2403	C 2410
A 573	<i>AcrA1;uvsB312 pyroA4;riboB2</i>		M 2435	C 2442
A 574	<i>riboA1 biA1;uvsD308;chaA1</i>	none likely	M 3628	C 2219
A 575	<i>anA1 yA2;AcrA1;uvsH311;fwA2</i>	none likely	M 2457	C 2445
A 576	<i>AcrA1;uvsH304;chaA1</i>	none likely	M 2503	C 2444
A 577	<i>yA2;AcrA1;uvsB110;riboB2 chaA1</i>	none likely	M 2506	diploid 2449
A 578	<i>pabaA1 yA2;uvsJ1</i>	none likely	M 2522	C 2496
A 579	<i>uvsA101;adD3</i>		M 2527	UV of <i>adD3</i>
A 580	<i>biA1;wetA6</i>	none likely	G 0241	UV of <i>biA1</i>
A 581	<i>yA2;wetA6 malA1 palD8 nicB8</i>		G 712	Cross Glasgow 0241 X 71
A 582	<i>yA2;niaD15 brlA42 fpaD43</i>		G 816	*Cross Glasgow 0248 X * <i>yA2;niaD15 fpaD43</i>
A 583	<i>biA1;brlA42</i>	none	G 0248	NA of A26
A 584	<i>luA1 stuA1 proA1 yA2</i>		G 134	
A 585	<i>stuA1 biA1</i>	none	G 0256	NA of A26
A 586	<i>medA15 biA1</i>	none	G 0255	NA of A26
A 587	<i>medA15 galD5 riboA1;nicB8</i>			
A 588	<i>biA1;drkA1</i>	none	G 070	NA of A26
A 589	<i>adH23;abaA14 chaA1</i>		G 830	Cross Glasgow 01 X 82
A 590	<i>biA1;abaA14</i>	none	G 01	NA of A26
A 591	<i>fpaB37 suA1adE20 riboA1 pabaA1 yA2 adE20; AcrA1;galA1 ActA1;pyroA4;facA303;sB3; oliC2 malA1;fwA2</i>	none	M 2626	diploid 2340a
A 592	<i>SulA1 anA1 biA1;wA2 cnxE16;methG1; nicA2;sbA3;choA1;chaA1</i>	none	M 2461	diploid 2477
A 593	<i>fpaB37 suA1adE20 riboA1 pabaA1 yA2 adE20; AcrA1;galA1 ActA1;pyroA4;facA303;sB3; oliC2 malA1;fwA2</i>	none	M 2627	diploid 2340b
A 594	<i>adE20 biA1;wA2 cnxE16;methG1;nicA2; sbA3;choA1;chaA1</i>	none	M 2492	diploid 2478
A 595	<i>pabaA6 yA2 adE8</i>		M 2824	haploid from A 542
A 596	<i>pabaA6;yA⁺ adE20 biA1(on II?)</i>		M 2831	haploid from A 542
A 597	<i>pabaA6 yA2 adE8;rec-402</i>		M 2826	haploid from A 543
A 598	<i>pabaA6 yA2 adE8;rec-408</i>		M 2827	haploid from A 546
A 599	<i>pabaA6 yA2 adE8;rec-444</i>		M 2828	haploid from A 548
A 600	<i>pabaA6 yA2 adE8;rec-469</i>		M 2829	haploid from A 544
A 601	<i>biA1;sA31</i>	none?	M 1456	NG of A26

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 602	<i>biA1;saI30</i>	none?	M 1853	NG of A26
A 603	<i>biA1;sC63</i>	none?	M 2880	NG of A26
A 604	<i>biA1;sC84</i>	none?	M 2881	NG of A26
A 605	<i>biA1;AcrA1;nicA2 T2(I;III)</i>		M 2499	C 2439
A 606	<i>AcrA1;lysD18;riboB2</i>	none likely	M 2750	C 2580
A 607	<i>yA2;ActA1;choA1</i>	none	M 2878	diploid 2600b
A 608	<i>galD5 suA1adE20 anA1 biA1;chaA1</i>	none	M 1996	C 1791
A 609	<i>uvsB413;riboB2 chaA1</i>	none?	M 2838	C 2658
A 610	<i>pabaA1 yA2</i>	none	M 2600	C 1621
A 611	<i>adG14 biA1</i>	none likely	M 2601	C 1621
A 612	<i>AcrA1;riboB2 chaA1</i>	none likely	M 2386	C 2464
A 613	<i>AcrA1;nicA2 pA2 facA303 hxA1 riboD5</i>	none	M 2697	C 2468b
A 614	<i>SulA1 adE20;AcrA1 wA3;ActA1;methG1; nicA2;sbA3;choA1;riboB2 chaA1</i>	none	M 2843	diploid 2365
A 615	<i>SulA1 adE20;AcrA1 wA3;ActA1;methG1; nicA2;lacA1 sB3;choA1;riboB2 chaA1</i>	none	M 2844	diploid 2365
A 616	<i>SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;nicA2;sbA3;choA1;riboB2 chaA1</i>	none	M 2485	diploid 2478
A 617	<i>anA1 adE20 biA1;AcrA1;ActA1;pabaB22 pyroA4;nicA2;sbA3;choA1;fwA2</i>	none	M 2848	diploid 2358
A 618	<i>SulA1 adE20;AcrA1;ActA1 galA1;pyroA4; nicA2;sB3;oliC2 malA1;fwA2</i>	none	M 2851	diploid 2349
A 624	<i>yA2 pabaA1;pycB4</i>	none?	WG 135 (CJB)	UV of A234
A 625	<i>yA2 pabaA1;pycA12</i>	none?	WG 257 (CJB)	UV of A234
A 626	<i>wA3;pyroA4;pdhC2</i>	none?	WG 195 (CJB)	CJB cross
A 627	<i>yA2 pabaA1;pdhC1</i>	none?	WG 107 (CJB)	UV of A234
A 628	<i>yA2 pabaA1;pdhB2</i>	none?	WG 206 (CJB)	UV of A234
A 629	<i>yA2 pabaA1 pycB5</i>	none?	WG 218 (CJB)	UV of A234
A 630	<i>biA1;pkiA2(ts) nicA2 riboD5</i>	none?	WG 256 (CJB)	CJB cross
A 631	<i>biA1;wA3;pycB4</i>	none?	WG 136 (CJB)	CJB cross
A 632	<i>yA2 pabaA1;pycA2</i>	none?	WG 102 (CJB)	UV of A234
A 633	<i>yA2 pabaA1;pkiA9</i>	none?	WG 193 (CJB)	UV of A234
A 634	<i>yA2 pabaA1;pdhB4</i>	none?	WG 228 (CJB)	UV of A234
A 635	<i>yA2 pabaA1;pdhC2(ts)</i>	none?	WG 194 (CJB)	UV of A234
A 636	<i>pdhA4(ts);wA3;pyroA4</i>	none?	WG 143 (CJB)	UV of A234
A 637	<i>yA2 pabaA1 pdhA1</i>	none?	WG 097 (CJB)	CJB cross
A 638	<i>yA2;lysA1 (Ab VI)</i>	Ab VI	M 2558	A350 X A 187
A 639	<i>yA2 adE20 biA1;AcrA1;methG1 suC11adE20 pyroA4;chaA1</i>	none?	M 2477	C 2467
A 640	<i>phenB6 pantoB100 sF211 malA1 nicB8</i>	none?	M 2251	C 2120
A 641	<i>suA1adE20 yA2 adE20;AcrA1;galA1;pyroA4; nicA2;sB3;choA1;riboB2</i>	none	M 2574	diploid 2350
A 642	<i>biA1;AcrA1;ActA1;nicA2;sbA3;choA1;chaA1</i>	none?	M 2902	diploid 2344
A 643	<i>proA2 yA2;AcrA1;ActA1;pabaB22 pyroA4; nicA2;sbA3;choA1;riboB2 chaA1</i>	none	M 2974	C 2703
A 644	<i>riboA1 yA2;methH2 dilA1</i>	none?	M 2652	C 2561
A 645	<i>biA1;AcrA1;lysD20 T(III;VII);chaA1</i>		M 2724	C 2586
A 646	<i>biA1 argD11</i>	none?	G 036	UV of A26
A 647	<i>yA2;ve⁺ T1(III-VIII;IV)</i>		G 0257	
A 648	<i>biA1;ureD4</i>		G 0286	
A 649	<i>pabaA1 yA2;acuD254</i>	none?	G 0300	UV of A234
A 650	<i>pabaA1 yA2;acuE201</i>	none?	G 0301	UV of A234
A 651	<i>pabaA1 yA2;acuF205</i>	none?	G 0302	UV of A234
A 652	<i>pabaA1 yA2;acuG223</i>	none?	G 0303	UV of A234
A 653	<i>pabaA1 yA2;acuH253</i>	none?	G 0304	UV of A234
A 654	<i>acuJ211 pabaA1 yA2</i>	none?	G 0305	UV of A234
A 655	<i>pabaA1 yA2;acuK248</i>	none?	G 0306	UV of A234
A 656	<i>pabaA1 yA2;acuL217</i>	none?	G 0307	UV of A234
A 657	<i>pabaA1 biA1;melA1</i>		G 0315	
A 658	<i>proB4 pabaA1 biA1</i>		G 137	
A 659	<i>yA2;AcrA1 apnA1 wA3;choA1</i>		G 247	cross 1297 of Arst

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 660	<i>pabaA1;intA^{C2}</i>		G248	cross 445 of Arst
A 661	<i>pabaA1 yA2;xprD1</i>		G332	
A 662	<i>pantoC3 cnxH3 sC12</i>		G338	cross 1126 of Arst
A 663	<i>yA2 xprD1 sC250 cnxH3;pantoB100</i>		G344	
A 665	<i>pantoA10</i>	none	G853	cross 961 of Arst
A 666	<i>[oliA6] pabaA1 yA2</i>		G0274	S in R 21
A 667	<i>pabaA1 biA1;melB⁰²</i>		G0316	UV of <i>pabaA1 biA1</i>
A 668	<i>ornC31</i>		G345	cross 1432 of Arst
A 669	<i>pyroA4;choC3 fwA1</i>		G852	cross after NG of <i>pabaA1biA1</i>
A 670	<i>pabaA1 biA1;AcrA1;facA303;manA1</i>		G851	NG of <i>mnrA455</i>
A 671	<i>biA1;wA7 creC27</i>		G245	
A 672	<i>yA2;meaA8 pyroA4</i>		G420	cross after DES of A26
A 673	<i>biA1;facB302 fanD151</i>	none?	G085	S in <i>biA1 facB302</i>
A 674	<i>clB1 yA2;wA2;sC12</i>		G064	UV of <i>yA2;wA2;sC12</i>
A 675	<i>biA1;facA303 fanA3</i>	none?	G083	S in <i>biA1 facA303</i>
A 676	<i>biA1;facA303 fanB52</i>	none?	G084	S in <i>biA1 facA303</i>
A 677	<i>biA1;fanE7</i>	none	G083	S in A26
A 678	<i>biA1;inoA1</i>		G0101	UV of A26
A 679	<i>biA1;wA5;inoB2</i>		G0102	NG of A26
A 680	<i>biA1 ahrA3</i>		G0275	NG of A26
A 681	<i>luA1 biA1;mauA2</i>		G0278	NG of <i>yA2;pyroA4 meaA8</i>
A 682	<i>wA3 puA2 mauB4</i>		G0279	NG of <i>yA2;pyroA4 meaA8</i>
A 683	<i>biA1;ureA1</i>		G0283	
A 684	<i>biA1;ureB3</i>		G0284	
A 685	<i>biA1;drkB5</i>	none?	G234	UV of A26
A 686	<i>yA2;methH2 gdhA1 galA1</i>		G323	A699 X G33
A 687	<i>yA2;wA3;sC12 ivoA1 methH2 argB2 galA1</i>		G324	
A 688	<i>biA1;pppB1</i>		G325	NG of A26
A 689	<i>pabaA1 yA2;gdhB1 pyroA4</i>		G416	NG of A26-X G158
A 690	<i>yA2;pyroA4;lacA1;pppA1</i>		G840	
A 691	<i>biA1;niaD15</i>		G0125	NG of A26
A 692	<i>proB3 biA1</i>		G0165	UV of A26
A 693	<i>pyroB12 biA1;wA3 T1(III-VIII);T1(VI;VII)</i>		G0187	UV of A51
A 694	<i>biA1;wA3;sucA1 T1(III-VIII) T1(VI;VII)</i>		G0212	UV of A51
A 695	<i>biA1;telA1</i>		G0223	S in A26
A 696	<i>biA1;gamA55</i>		G0265	S in A26
A 697	<i>biA1;gamB65</i>		G0266	S in A26
A 698	<i>biA1;gamC66</i>		G0267	S in A26
A 699	<i>biA1 gdhA1</i>		G0268	NG of A26
A 700	<i>biA1;punA11</i>		G0277	UV of A26
A 701	<i>biA1;puA2;spsA1</i>		G0280	NA of <i>biA1;puA2</i>
A 702	<i>pabaA1 yA2;sltA1</i>		G0281	NA of A26-X G158
A 703	<i>anA1 biA1;mecC13</i>		G0282	UV of <i>anA1 biA1</i>
A 705	<i>biA1 sorA2</i>		G186	
A 706	<i>AcrA1 punA11 ygA6</i>		G242	G0277 X G233
A 707	<i>biA1;mola67</i>		G616	S in A26
A 708	<i>wA3;tsB5 sB3 sbA3</i>		G62	
A 710	<i>yA2; telA1 malA1 palD8 nicB8</i>		G71	G158 X G617
A 711	<i>yA2;phenB6 pantoB100 malA1 wetA6 methE6 palD8 nicB8</i>		G716	
A 712	<i>pabaA1 yA2;galH7;palcC4 facB101 riboB2</i>		G820	
A 713	<i>yA2;pyroA4;niiA4</i>		G833	
A 714	<i>biA1;fwA1 galG2 facC307</i>		G836	G835 X G813
A 715	<i>proA1 yA2;hisG113;chaA1</i>		G0296	UV of <i>proA1 yA2;chaA1</i>
A 716	<i>biA1;molB35</i>		G0271	S in A26
A 717	<i>riboA1 fpaI64 biA1</i>		G0297	
A 718	<i>biA1;wA3;galF2 T1(III-VIII);T1(VI;VII)</i>		G097	UV of A51
A 719	<i>biA1;methE6</i>		G0114	UV of A26
A 720	<i>biA1;tsC17</i>		G0224	UV of A26
A 721	<i>anA1 pyrF11 luA1 yA2;cnxH4</i>		G190	

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 722	<i>pyrG89 pabaA1;fwA1 uaY9</i>		G 191	NG of <i>pabaA1;fwA1 uaY9</i>
A 723	<i>biA1;pyrD23</i>		G 846	NG of A26
A 724	<i>yA2;wA3;pyroD9 araA1</i>		G 848	
A 725	<i>wA3;pyroA4;tsE6</i>		G 0272	
A 726	<i>biA1;riboF8</i>		G 0196	NA of A26
A 727	<i>proA1 hisB179 yA2;chaA1</i>	none?	G 0294	UV of <i>proA1 yA2;chaA1</i>
A 728	<i>yA2;sorB11 cnxH14;pyroA4</i>		G 328	G 321 X G 319
A 729	<i>pabaA1;brlA42 uaY9 ivoB63</i>		G 841	NG of <i>biA1 abaA6→X G839</i>
A 732-A 742 Section IX, <i>A. niger</i> mutants				
A 743	<i>riboA1 pabaA1 yA2;AcrA1;galA1 ActA1; pyroA4;lysB5;sB3;oliC2 malA1;fwA2</i>		M 3207	diploid 2720
A 744	<i>pabaA1 yA2;fluG1</i> NG of A234	none?	WM 355 (WM)	
A 745	<i>SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;nicA2;sbA3;malA1;riboB2 chaA1</i>	none?	M 2486	diploid 26
A 746	<i>biA1;pyroA4;niiA4;amdR4</i>		MH 345 (MJH)	
A 747	<i>biA1;creB15</i>		MH 532 (MJH)	
A 748	<i>biA1;niiA4;creA204</i>		MH 664 (MJH)	
A 749	<i>biA1;niiA4;amdA7;amdI18</i>		MH 767 (MJH)	
A 750	<i>biA1;niiA4;amdI93</i>		MH 1176 (MJH)	
A 752	<i>pabaA1;sB43;alcR125 amdA7; amdI66 amdS1005</i>		MH 2238 (MJH)	
A 753	<i>mecB10 anA1 yA2;cysB102</i>		AP	S in <i>yA2;pyroA4;methB3</i>
A 754	<i>mecB10 anA1 yA2;cysC103</i>		AP	S in <i>yA2;pyroA4;methB3</i>
A 755	<i>yA2;methD10;pyroA4</i>		AP	UV of <i>adF9 yA2</i>
A 756	<i>mecB10 anA1 yA2;cysA1</i>		AP	UV of <i>mecA biA1 anA1</i>
A 757	<i>yA2;methA17;pyroA4</i>		AP	UV of <i>adF9 yA2</i>
A 758	<i>mecB10 proA2 pabaA2 yA2</i>		AP	UV of <i>biA1 anA1</i>
A 759	<i>mecB10 anA1 biA1;AcrA1;phenA2</i>		AP	UV of <i>biA1 anA1</i>
A 760	<i>pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;chaA1</i>	none	M 3171	diploid 2793
A 761	<i>pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;riboB2 chaA1</i>	none	M 3172	diploid 2793
A 762	<i>pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3;choA1;fwA2</i>	none	M 3271	diploid 2800
A 763	<i>pyrG89;AcrA1;ActA1;pabaB22;nicA2;sB3; malA1;fwA2</i>	none	M 3272	diploid 2800
A 764	<i>pyrG89;AcrA1;ActA1;nicA2;sB3;malA1;chaA1</i>	none	M 3174	diploid 2793
A 765	<i>pyrG89 biA1;AcrA1;ActA1;pyroA4;sbA3; choA1;riboB2 chaA1</i>	none	M 3223	diploid 2775
A 766	<i>pyrG89 biA1;AcrA1;ActA1;pyroA4;nicA2;sbA3; riboB2 chaA1</i>	none	M 3224	diploid 2775
A 767	<i>pyrG89;nicA2</i>	none	M 3376	C 2870
A 768	<i>pyrG89 yA2;riboB2 chaA1</i>	none	M 3091	C 2794
A 769	<i>pyrG89;AcrA1;pabaB22;chaA1</i>	none	M 3097	C 2794
A 770	<i>pyrG89;pabaB22;riboB2</i>	none	M 3098	C 2794
A 771	<i>pyrG89 riboA1;wA3;pyroA4</i>	none	M 3104	C 2781
A 772	<i>galD5 pyrG89;AcrA1;chaA1</i>	none	M 3268	C 2795
A 773	<i>pyrG89;wA3;pyroA4</i>	none	M 3338	GR 5 of R. Morris
A 774	<i>fpaB37 galD5 pyrG89 yA2 adE20;AcrA1;pyroA4;facA303;chaA1</i>	none	M 3317	C 2819
A 775	<i>fpaB37 galD5 pyrG89 riboA1 anA1;nicA2;sD85</i>	none	M 3361	C 2874
A 776	<i>pabaA1;AcrA1;bimE7;riboB2 chaA1</i>		DBE 1 (NRM)	UV of A154
A 777	<i>adE20 biA1;wA2 cnxE16;sC12;methG1;nicA2; bimC4 lacA1;choA1;chaA1</i>		244 (NRM)	UV of A154
A 778	<i>pyrG89 riboA1;pyroA4;nicB8;bimG11</i>		JD04 (NRM)	UV of A122
A 779	<i>nudC3 pyrG89 pabaA1;wA2;nicA2</i>			UV A4→x A722
A 780	<i>bimA1;wA2</i>		50-10 (NRM)	UV of A154
A 781	<i>nimA5;wA2</i>		507 (NRM)	A 154 x A 722 x A 4
A 782	<i>yA2;AcrA1;ActA1;pabaB22;nicA2;sbA3;choA1; riboB2 chaA1</i>	none	M 3080	diploid 2707

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 783	<i>SulA1;AcrA1;ActA1;pabaB22;nicA2;sbA3;choA1;riboB2 chaA1</i>	none	M 3081	diploid 2707
A 784	<i>yA2;wA3;ActA1;pabaB22;nicA2;sbA3;choA1;riboB2 chaA1</i>	none	M 3082	diploid 2707
A 785	<i>riboA1 pabaA1 yA2;AcrA1;galA1 ActA1;pyroA4 nicA2;sbA3;choA1;chaA1</i>	none	M 3252	dipl. 28 (A743/A592)
A 786	<i>SulA1 anA1 biA1;AcrA1;galA1 ActA1;methG1;nicA2;sbA3;choA1;fwA2</i>	none	M 3258	diploid 28
A 787	<i>SulA1 anA1 biA1;wA2 cnxE16;galA1 ActA1;pyroA4;nicA2;sbA3;choA1;fwA2</i>	none	M 3262	diploid 28
A 788	<i>SulA1 anA1 biA1;wA2 cnxE16;galA1 ActA1;methG1;lysB5;sbA3;OliC2 malA1;chaA1</i>	none	M 3264	diploid 28
A 789	<i>riboA1 proA2 pabaA1;sC12 galA1 phenA2 SuB4pro</i>	none	M 3462	C 2202
A 790	<i>proA2 yA2 adE20;wA3;sC12 galA1 phenA2 SuB4pro</i>	none	M 3464	C 2202
A 791	<i>riboA1 proA2;galE9 sC12 dilA1 SuB4pro</i>	none	M 3482	C 2202
A 792	<i>proA2 pabaA1;galE9 sC12 dilA1 phenA2 SuB4pro</i>	none	M 3483	C 2201
A 793	<i>proA2</i>	none	M 3390	C 2718
A 794	<i>riboA1 biA1;AcrA1;lacA1 BwA1 sB3 sbA3</i>	none	M 3305	C 2715
A 795	<i>yA2;lacA1 BwA1 lysA1(AbVI) sB3 sbA3</i>	AbVI	M 3347	C 2719
A 796	<i>phenB6 pantoB100 sF211 malA1 nicB8;riboB2</i>	none	M 3393	C 2712
A 797-A 807 Section IX, <i>A. niger</i> mutants				
A 808-A 812 Section VII, <i>A. awamori</i> mutants				
A 813	<i>pyrN25</i>		1744 (HNA)	
A 814	<i>yA2;pyrN25</i>		1744 (HNA)	
A 817	<i>pabaA1 biA1;wA3 thiA4 cnxE16;actA1</i>	none	M 3433	diploid 27
A 818	<i>suA1adE20 yA2 adE20;acrA1;galA1 actA1;pyroA4 facA303;sbA3;choA1 fwA2</i>	none	M 3613	diploid 31
A 819	<i>sulA1 anA1 biA1;wA2 cnxE16;methG1;nicA2;sbA3;malA1;riboB2 chaA1</i>	none	M 3608	diploid 31
A 820	<i>yA2;benA33</i>		BRO2 (BRO)	UV of <i>pabaA1 yA2</i>
A 821	<i>proA1 pabaA1 adE20 yA2;wA3;pyroA4;tubA4</i>		LO196 (BRO)	
A 822	<i>pabaA1;pyroA4;tamA200</i>			UV of <i>biA1</i>
A 823	<i>biA1 pabaA1;pyroA4;tamA200</i>			
A 824	<i>proA1 pabaA6 adE20 biA1;acrA1;wB1;riboB2</i>		728	
A 825	<i>suA1adE20 adE20 biA1;uvsI501;ssbA1;sbA3;choA1;chaA1</i>		B 1 (HSK)	NG of A168
A 826	<i>suA1adE20 adE20 biA1;uvsB505 ssbA1;sbA3;choA1;chaA1</i>		B 5 (HSK)	4-NQO of A168
A 827	<i>suA1adE20 adE20 biA1;uvsB504 ssbA1;cotA1;sbA3;choA1;chaA1</i>		B 4 (HSK)	UV of A168
A 828	<i>biA1;T2(I;III);AcrA1;nicA2;musM225</i>		EK 2755	
A 829	<i>pabaA1;AcrA1;chaA1</i>	none	EK 2389	
A 830	<i>pabaA1;AcrA1;ActA1;choA1;riboB2 chaA1</i>	none	EK 2892	
A 831	<i>uvsA101;pyroA4;choA1;chaA1</i>	none	EK 3935	
A 832	<i>pabaA1;uvsB110;nicA2;chaA1</i>	none	EK 3930	
A 833	<i>pabaA1;choA1;uvsC114 chaA1</i>	none	EK 3571	
A 834	<i>pabaA1;pyroA4;uvsD153;choA1;chaA1</i>	none	EK 3811	
A 835	<i>pabaA1;ActA1;uvsE182;choA1;chaA1</i>	none	EK 3733	
A 836	<i>uvsF201 pabaA1;ActA1;nicA2;sbA3;riboB2 chaA1</i>	none	EK 3813	
A 837	<i>pabaA1;uvsH77 pyroA4;choA1;chaA1</i>	none	EK 3961	
A 838	<i>pabaA1;AcrA1;uvsI501;choA1;riboB2 chaA1</i>	none	EK 3547	
A 839	<i>pabaA1;pyroA4;uvsJ1;choA1;chaA1</i>	none	EK 3938	
A 840	<i>pabaA6;AcrA1;musK228</i>	none	EK 3764	
A 841	<i>riboA1 adE20 biA1 musL222</i>	none	EK 3776	
A 842	<i>riboA1;AcrA1;dilA1;musN227</i>	none	EK 3005	
A 843	<i>pabaA6;sbA3;musO226 T2(III;VII) choA1</i>		EK 3753	
A 844	<i>musP234 T2(VII-II) oliC2 pantoB100 nicB8</i>		EK 3844	
A 845	<i>riboA1 yA2;musQ230;choA1</i>	none	EK 3707	
A 846	<i>SulA1 pabaA1 yA2;musR223</i>	none	EK 3647	
A 847	<i>musS224 T3(III;VII) pantoB100</i>	none	EK 3758	
A 848	<i>biA1;wA3;niiA4 gatA312</i>		MH1055 (MJH)	

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A 849	<i>pabaA1 yA2; ΔargB::trpCΔB ΔrodA::argB;veA1 trpC801</i>		TM S015(MAS)	D of A 851
A 850	<i>biA1;ΔargB::trpCΔB;methG1;veA1 trpC801</i>		RMS010 (MAS)	
A 851	<i>pabaA1 yA2; ΔargB::trpCΔB;veA1 trpC801</i>		RMS011 (MAS)	
A 852	<u><i>diploid:biA1;ΔargB::trpCΔB;methG1;veA1 trpC801</i></u> <i>pabaA1 yA2; ΔargB::trpCΔB;veA1 trpC801</i>		RMS010 (MAS)	
A 853	<i>yA2 pabaA1;suA1veA1;veA1</i>		TU 31	
A 854	<i>pabaA1;suA1veA1;veA1</i>		TU 32	
A 855	<i>pabaA1;suD1veA1;veA1</i>		TU 44	
A 856	<i>yA2 pabaA1;suD1veA1;veA1</i>		TU 47	
A 857	<i>pabaA1;suC3veA1;veA1</i>		TU 48	
A 858	<i>yA2 pabaA1;suC3veA1;veA1</i>		TU 49	
A 859	<i>pabaA1;suB1veA1;veA1</i>		TU 50	
A 860	<i>pabaA1;suC1veA1;veA1</i>		TU 52	
A 861	<i>yA2 pabaA1;suC1veA1;veA1</i>		TU 53	
A 862	<i>pabaA1;suC2veA1;veA1</i>		TU 54	
A 863	<i>yA2 pabaA1;suC2veA1;veA1</i>		TU 55	
A 864	<i>riboA1;AcrA1 wA3 thiA4 cnxE16;choA1</i>	none	3620	
A 865	<i>biA1;AcrA1;phenA2;nicA2 pA2 facA303 hxA1 riboD5</i>	none	2926	
A 866	<i>SulA1 anA1 biA1;wA2 cnxE16;galA1; methG1;facA303; sbA3;choA1;fwA2</i>	none	3615	
A 867	<i>suA1adE20 yA2 adE20;wA2 cnxE16; galA1 ActA1;pyroA4; nicA2;sbA3;choA1;riboB2 chaA1</i>	none	3616	
A 868	<i>riboA1 yA2;puA1</i>	none	3941	
A 869	<i>yA2;acrB2;choA1</i>	none	3882	
A 870	<i>yA2;wA3 cnxE16</i>	none	3883	
A 871	<i>yA2;adC1;choA1</i>	none	3884	
A 872	<i>biA1;apl^C7</i>		CS51	UV of A26
A 873	<i>biA1;alX4</i>		CS764	UV of A26
A 874	<i>biA1;uaZ11</i>		CS1131	UV of A26
A 876-A 943 Section IX, <i>A. niger</i> mutants				
A 944	<i>pyrG89;chaA1;nudA1;snaD385</i>			UV
A 945	<i>pyrG89;chaA1;nudA1;snaA26</i>			UV
A 946	<i>pyrG89;chaA1;nudA1;snaB76</i>			
A 947	<i>pyrG89;chaA1;nudA1;snaC108</i>			
A 948	<i>pyrG89;chaA1;nudA1;snaE285</i>			
A 949	<i>sulA1 adE20;AcrA1;ActA1;ssbA1 pyroA4;facA303;lacA1 sB3;choA1;chaA1</i>		S513	
A 950	<i>pabaA1;alc delta 500;riboB2</i>			
A 951	<i>yA2;pabaA1;acuk248</i>			
A 952	<i>biAi alcR125</i>			
A 953	<i>acuM301;wA3;pyroA4</i>			
A 954 - A 985 Section IX, <i>A. niger</i> mutants				
A 986	<i>liA1, argB⁺::P_{alcA}: Aras^{G17V}, veA1</i>		AST27	
A 987	<i>liA1, argB⁺::P_{alcA}: Aras^{S22N}, veA1</i>		AST29	
A 988	<i>liA1, argB⁺::P_{alcA}: Aras, veA1</i>		AST30	
A 989	<i>yA2, pabaA1; sbrA1; pyroA4; trpC801, veA1</i>		rM13	
A 991	Edgebaston, Birmingham Wild Type		A 65	
A 992	Birmingham, 1954 Wild Type		B 1	
A 993	from Polyporus sporophore, 1962 Wild Type	diploid	C 31	
A 994	from Collybia sporophore, 1962 Wild Type	T(IV,II)	D 34	
A 995	Soil, Durham, 1962 Wild Type		E 43	
A 996	Soil, Kent, 1962 Wild Type		F 108	
A 997	Soil, Cornwall, 1963 Wild Type		G 143	
A 998	Soil, Kent 1962, Wild Type		H 109	
A 999	Nicotiana bed soil, Edgebaston, 1962 Wild Type		I 66	
A 1000	Compost, Birmingham, 1962 Wild Type	diploid	J 67	
A 1001	Compost, Birmingham, 1962 Wild Type		K 68	

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A1002	Soil, Pembroke, 1962 Wild Type		L80	
A1003	Soil, Pembroke, 1962 Wild Type	"B" chromosome T(VI,VIII)	M85	
A1004	Soil, Cambridgeshire, 1962 Wild Type		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	
A1011	<i>nudF6 pyrG89 snfC1524</i>		snf1524	UV of XX20(<i>nudF6 pyrG89</i>)
A1012	<i>nudF6; wA3; pyroA4; snf1524</i>		DW38	
A1013	<i>nudF6 pyrG89 snfE798</i>		snf798	
A1014	<i>nudF6 pyrG89; snfA890</i>		DW15	UV of XX20
A1015	<i>wA3; pyroA4; snfA890</i>		DW17	
A1016	<i>nudF6; wA3; pyroA4; snfA890</i>		DW16	
A1017	<i>nudF6 pyrG89 snf1267</i>		snf1267	
A1018	<i>nudF6 pyrG89 snfD860</i>		snf860	UV of XX20
A1019	<i>nudF6 pyrG89; snfC1232</i>		snf1232	UV of XX20
A1020	<i>nudF6; wA3; pyroA4; snfC1232</i>		DW35	
A1021	<i>nudF6 pyrG89 snfD1468</i>		snf1468	UV of XX20
A1022	<i>nudF6 pyrG89 snfD1292</i>		snf1292	UV of XX20
A1023	<i>yA2 riboA1; nicB8 snfD1292</i>		DW40	
A1024	<i>nudF6 pyrG89 snfD1555</i>		snf1555	UV of XX20
A1025	<i>wA3; pyroA4 snfD1555</i>		DW45	
A1026	<i>nudF6 pyrG89 snf1364</i>		snf1364	UV of XX20
A1027	<i>nudF6 pyrG89 snf1062</i>		snf1062	UV of XX20
A1028	<i>pyrG89; pyroA4 snf1364</i>		DW61	
A1029	<i>nudF6 pyrG89 snf1422</i>		snf1422	UV of XX20
A1030	<i>pabaA1; AcrA1; ActA1; choA1 musN227; riboB2 chaA1</i>		EK4048	
A1031	<i>pabaA1; AcrA1; ActA1; nicA2; choA1; riboB2 chaA1 musK228</i>		EK4069	
A1032	<i>pyrG89 yA2; wA2 cnxE16; ActA1; pyroA4; nicA2; sbA3; choA1; riboB2 chaA1</i>		EK4169	
A1033	<i>pyrG89 yA2; AcrA1; ActA1; pabaB22; nicA2; sbA3; malA1; fwA2</i>		EK4172	
A1034	<i>biA1; flbA</i>		MBN13	
A1035	<i>yA2; fadA^{G203R}</i>		RJY115.4	
A1036	<i>biA1; methG1; Δ-fadA::argB</i>		RJY918.5	
A1037	<i>biA1; fadA^{G42R}</i>		BDNM4	
A1038	<i>biA1; Δ-fasA::arg/ biA1; Δ fasB</i>		DDB57/51A	
A1039	<i>pabaA1, yA2; Δ-stcK::trpC</i>		TDB4	
A1040	<i>methG1, Δ-stcJ::argB; biA1</i>		TDB2	
A1041	<i>biA1; Δ-stcE::argB2, methG1 wA1</i>		TJH3.40	
A1042	<i>pabaA1, yA2; Δ-stcN::trpC</i>		TAHK45.44	
A1043	<i>Δ-stcP::argB2; methG1, biA1</i>		TAHK54.11	
A1044	<i>biA1; Δ-stcP::argB2</i>		TAHK64.42	
A1045	<i>Δ-stcQ::argB2, methG1; biA1</i>		TAHK67.11	
A1046	<i>Δ-stcL::argB2 methG1; biA1</i>		TAHK70.29	
A1047	<i>Δ-stcL::argB2, Δ-stcU::hph; methG1 biA1</i>		TAHK78.36	
A1048	<i>Δ-stcB::argB2, methG1, biA1</i>		TAHK87.29	
A1049	<i>Δ-stcF::argB2, methG1, biA1</i>		TAHK68.44	
A1050	<i>Δ-stcW::argB2, methG1, biA1</i>		TAHK79.4	
A1051	<i>Δ-stcI::argB2, methG1, biA1</i>		TAHK72.25	
A1052	<i>Δ-afIR::argB2, methG1, biA1</i>		TMF4.12	
A1053	<i>pabaA1, yA2; ΔargB::trpCΔB, catA::argB; trpC801</i>		TRN1	
A1054	<i>pabaA1, yA2; ΔargB::trpCΔB, catB::argB; trpC801</i>		TLK12	
A1055	<i>biA1; ΔcatA::argBΔA; metG1; ΔcatB::argB</i>		CLK20	
A1056	<i>yA2; ΔfadA::argB</i>		RJY918.10	
A1057	<i>yA2 pabaA1; pantoC3</i>		C1	
A1058	<i>biA1; argB2</i>		C3	
A1059	<i>biA1; argB::AraS:lacZ</i>		AST32	
A1060	<i>biA1</i>		AST33	
A1061	<i>pyrG89 pabaA; wA3; bimD6 pyroA4; chaA1</i>		EK4078	
A1062	<i>pyrG89; bimD6; riboB2 chaA1</i>		EK4247	
A1063	<i>riboA1; sC12; bimD6 pyroA4</i>		M3659 (GMay 6.9)	

FGSC #	Genotype	Trans- location	Depositor's Stock # or initials	Origin of strain or lesion
A1064	pabaA1; biA1; bimD6 pyroA4		M3692	
A1065	pabaA1 yA2; bimB3		3132	
A1066	aromA1248 riboA1 adG14 yA2		G1100	
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; delta-brlA; veA+		TU85	
A1080	yA2 pabaA1; biA1; pyroA4; delta-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; delta-argB::trpC+; pyroA4; trpC801(?); ve+		TU130	
A1096	pabaA1		WIM243	
A1097	wild type		12S	
A1098	niaD1		RAWMI	
A1099	Lemore (<i>A. niger</i>)		DL	
A1100	<i>A. fumigatus</i>		AF293	

VII. *Aspergillus awamori* mutants.

All were obtained from Dr. Renato Bonatelli, Jr.

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

VIII. *Aspergillus oryzae*

FGSC #	Genotype or characteristics	Obtained from
A815	wild type	T. Uozumi
A816	<i>ade</i> (requires adenine)	T. Uozumi

IX. *Aspergillus niger* mutants

FGSC #	Genotype	Other Number	Deposited by
A730	<i>cspA1 hisD4 lysA7 leuA1 nicA1 pabA1</i>	N612	CJB
A731	<i>cspA1 fwnA1 hisD4 lysA7 leuA1 nicA1 pabA1</i>	N616	CJB
A732	wild type	N400	CJB
A733	<i>cspA1</i>	N402	CJB
A734	<i>cspA1 metB10</i>	N500	CJB
A735	<i>cspA1 nicA1 pabA1</i>	N494	CJB
A736	<i>cspA1 fwnA1</i>	N410	CJB
A737	<i>cspA1 nicA1 bioA1</i>	N493	CJB
A738	<i>cspA1 nicA1</i>	N423	CJB
A739	<i>cspA1 fwnA1 lysA7</i>	N436	CJB
A740	<i>cspA1 hisD4</i>	N434	CJB
A741	<i>cspA1 leuA1</i>	N414	CJB
A742	<i>cspA1 pyrA5</i>	N592	CJB
A797	<i>cspA1 cysA2</i>	N406	CJB
A798	<i>cspA1 argL2</i>	N409	CJB
A799	<i>cspA1 argA1</i>	N408	CJB
A801	<i>cspA1 trpA1</i>	N469	CJB
A800	<i>cspA1 nicA1 pdxA2</i>	N630	CJB
A802	<i>cspA1 olvA1 argF8</i>	N474	CJB
A803	<i>cspA1 fwnA1 trpA1 lysA7 bioA1 leuA1 nicA1 pabA1</i>	N620	CJB
A804	<i>cspA1 fwnA1 hisD4 lysA7 bioA1 leuA1 metB1 pabA1</i>	N655	CJB
A805	<i>cspA1 fwnA1 trpA1 argB2 leuA1 nicA1 pabA1</i>	N661	CJB
A806	<i>cspA1 fwnA1 hisD4 lysA7 bioA1 leuA1 nicA1 pdxA2</i>	N690	CJB
A807	<i>cspA1 olvA1 hisD4 lysA7 bioA1 argF8 nicA1 pabA1</i>	N669	CJB
A875	<i>cspA1;olvA1;proC9</i>	N476	KS
A876	<i>cspA1;cysB3</i>	N403	KS
A877	<i>cspA1;proC3</i>	N404	KS
A878	<i>cspA1;lysB2</i>	N425	KS
A879	<i>cspA1;lysC5</i>	N428	KS
A880	<i>cspA1;argD6</i>	N430	KS
A881	<i>cspA1 hisA1</i>	N431	KS
A882	<i>cspA1;metC3</i>	N441	KS
A883	<i>cspA1;gryA1;leuB3;argE5</i>	N458	KS
A884	<i>cspA1;argE5</i>	N459	KS
A885	<i>cspA1;cysA2;leuA1;argA1</i>	N462	KS
A886	<i>cspA1;olvA1;adeA1</i>	N478	KS
A887	<i>cspA1;olvA1;argG11</i>	N479	KS

FGSC #	Genotype	Other Number	Deposited by
A888	<i>cspA1;argB13 nicA1</i>	N492	KS
A889	<i>cspA1;adeB2;nicA1</i>	N495	KS
A890	<i>cspA1 adeC3</i>	N499	KS
A891	<i>cspA1 hisE5;nicA3</i>	N508	KS
A892	<i>cspA1;fwnA1;adeD5</i>	N518	KS
A893	<i>cspA1;fwnA1;adeE6</i>	N519	KS
A894	<i>cspA1;fwnA1 metD12</i>	N523	KS
A895	<i>cspA1;ntrA2 fwnA1</i>	N525	KS
A896	<i>cspA1;fwnA3;pabB2 trpA1</i>	N531	KS
A897	<i>cspA1;brnA2;metB2</i>	N639	KS
A898	<i>cspA1;nicA1;proA4</i>	N681	KS
A900	<i>cspA1;olvA1;bioB2;niaD2</i>	N694	KS
A901	<i>cspA1;olvA1;bioB2;cnxB3</i>	N699	KS
A902	<i>cspA1;olvA1;bioB2;cnxC5</i>	N701	KS
A903	<i>cspA1;cnxD6;metB10</i>	N702	KS
A904	<i>cspA1;olvA1;bioB2;cnxE8</i>	N704	KS
A905	<i>cspA1;olvA1;bioB2;nirA3</i>	N707	KS
A906	<i>cspA1;proB5;metB10</i>	N714	KS
A907	<i>cspA1;bioA1;leuA1;nicA1;pabA1; oliC2;nirA1</i>	N716	KS
A908	<i>cspA1;nicA1;adeF12</i>	N717	KS
A909	<i>cspA1;acrA1 brnA2;nicA1</i>	N724	KS
A910	<i>cspA1;cnxG13 fwnA1 metD12;pabA1</i>	N725	KS
A911	<i>cspA1 hisD4;adeG13</i>	N753	KS
A912	<i>cspA1 hisF6;nicA1</i>	N734	KS
A913	<i>cspA1;cysC5;nicA1</i>	N747	KS
A914	<i>cspA1;nicA1;argK16</i>	N748	KS
A915	<i>cspA1;thiA1;metB10</i>	N749	KS
A916	<i>cspA1;fwnA1;pabA1 cnxA1 pyrB4</i>	N761	KS
A917	<i>cspA1 pyrC7;metB10</i>	N766	KS
A918	<i>cspA1;fwnA1;leuD8 lysC27</i>	N779	KS
A919	<i>cspA1 hisG7;metB10</i>	N786	KS
A920	<i>cspA1;fwnA1;pyrG5;nicB5</i>	N814	KS
A921	<i>cspA1;cnxF12;nicA1</i>	N819	KS
A922	<i>cspA1;olvA1;bioB2;crnA11</i>	N829	KS
A923	<i>cspA1;bioA1;serA1</i>	N833	KS
A924	<i>cspA1;fwnA1;argH12;lysA7;hisC3; pheA1;pdxA2;nicB5;trpB2</i>	N835	KS
A925	<i>cspA1;fwnA1;argH12;lysA7; leuA1;hisB2;pdxA2;cnxC5;trpB2</i>	N837	KS
A926	<i>cspA1;fwnA1;trpA1;pyrG5;hisC3; pheA1;pdxA2;nicB5;crnB12</i>	N840	KS
A927	<i>cspA1;metB10;adeF12 cnxC5</i>	N850	KS
A928	<i>cspA1;pdxB3;nicA1</i>	N853	KS
A929	<i>cspA1;bioA1;pabC5</i>	N854	KS
A930	<i>cspA1;nicA1;pabD6</i>	N860	KS
A931	<i>cspA1;bioA1;pyrE9</i>	N872	KS
A932	<i>cspA1;bioA1;lysF29</i>	N873	KS
A933	<i>cspA1;bioA1 proD6</i>	N874	KS
A934	<i>cspA1;bioA1;trpE6</i>	N880	KS
A935	<i>cspA1;fwnA1;metB11;proE7</i>	N883	KS
A936	<i>cspA1;fwnA1;argH12;pyrG5; leuA1;pheA1;lysD25;oliC2;crnB12</i>	N890	KS
A937	<i>cspA1;fwnA1;bioA1 pyrG5 hisH8;pheA1</i>	N893	KS
A938	<i>cspA1;olvA1;leuC5;pyrD8</i>	N894	KS
A939	<i>cspA1 hisI9;bioA1</i>	N898	KS
A940	<i>cspA1;ntrC4;pheA1</i>	N899	KS
A941	<i>cspA1;bioA1;ntrD5</i>	N903	KS
A942	<i>cspA1;fwnA1;argH12;pyrG5;ntrB3; metB11;lysD25;oliC2;crnB12</i>	N907	KS

FGSC #	Genotype	Other Number	Deposited by
A943	<i>cspA1;fwnA1;trpA1;bioA1 lysE28;pdxA1;crnB12</i>	N912	KS
A954	<i>cspA1;acrA1 brnA2; choA101; nicA1</i>	EK053	EK
A955	<i>cspA1;acrA1 brnA2 ;cysA101;nicA1</i>	EK054	EK
A956	<i>cspA1; fwnA1;choA101;thiB101;pdxA2</i>	EK163	EK
A957	<i>cspA1;fwnA1;choA101;pdxA2;nicB101</i>	EK164	EK
A958	<i>cspA1;fwnA1;leuA1;pdxA2;sftC102</i>	EK211	EK
A959	<i>cspA1;acrA1 brnA2;choA101; pdxA2;sftB103</i>	EK217	EK
A960	<i>cspA1; fwnA1; pyrG5 choA101; nicB5</i>	EK189	EK
A961	<i>cspA1;acrA1 brnA2; fpaD19;</i> <i>choA101 lysA14; (+/- ntrB3); metB11; nicB101</i>	EK196	EK
A962	<i>cspA1;fwnA1;fpaD19;lysA14; ntrB3 thiB101;oliC2</i>	EK200	EK
A963	<i>cspA1;fwnA1;choA101;pdxA2; oliC2 sftC101;crnB12</i>	EK218	EK
A964	<i>cspA1;acrA1 brnA2;choA101;niaD2</i>	EK134	EK
A965	<i>cspA1; olvA1; bioB2; leu A1; niaD2</i>	EK140	EK
A966	<i>cspA1fwnA1;lysA7;pdxA2; niaD2</i>	EK141	EK
A967	<i>cspA1;adrA1 brnA2; pyrG5; metB11;cnxC5; crnB12</i>	EK157	EK
A968	<i>cspA1;acrA1 brnA2; pyrG5; pdxA2; nicB5</i>	EK185	EK
A969	<i>cspA1;fwnA1;pyrG5; metB10</i>	EK182	EK
A970	<i>cspA1;fwnA1;pyrG5 choA101; pdxA2; nicB5</i>	EK187	EK
A971	<i>cspA1; brnA2;pyrG5;metB10; nicB5</i>	EK184	EK
A972	<i>cspA1;acrA1 brnA2; pyrG5; niaD2</i>	EK191	EK
A973	<i>cspA1; fwnA1; fpaD19; lysA14; pdxA2; nicB101</i>	EK199	EK
A974	<i>cspA1;fwnA1;leuA1;pdxA2; sftC101</i>	EK210	EK
A975	<i>cspA1;acrA1 brnA2;fpaD19;</i> <i>choA101;pdxA2;sftC101;crnB12</i>	EK219	EK
A976	<i>cspA1;fwnA1;fpaD19;choA101;</i> <i>pdxA2;sftC101; crnB12</i>	EK221	EK
A977	<i>cspA1;fwnA1;leuA1;pdxA2;oliC2 sftC101; crnB12</i>	EK222	EK
A978	<i>cspA1;acrA1 brnA2;argH12;</i> <i>choA101;ntrB3;metB11;pdxA2;oliC2;crnB12</i>	EK138	EK
A979	<i>cspA1;fwnA1;fpaD19;lysA14;ntrB3;</i> <i>metB11;pdxA2;oliC2;crnB12</i>	EK192	EK
A980	<i>cspA1; fwnA1;fpaD19;choA101;</i> <i>ntrB3;metB11;pdxA2;oliC2;crnB12</i>	EK194	EK
A981	<i>cspA1;acrA1 brnA2;fpaD19;</i> <i>choA101;thiB101;metB11;pdxA2;oliC2</i>	EK201	EK
A982	<i>cspA1;fwnA1 fpaD19;choA101;</i> <i>thiB101;metB11pdxA2;oliC2;crnB12</i>	EK223	EK
A983	<i>cspA1;acrA1 brnA2;fpaD19;</i> <i>lysA14;ntrB3 thiB101; metB11;pdxA2;oliC2;crnB12</i>	EK224	EK
A984	<i>cspA1;fwnA1;fpaD19;lysA14;ntrB3;</i> <i>metB11;pdxA2;oliC2;crnB12</i>	EK225	EK
A985	<i>cspA1;acrA1 brnA2;fpaD19;choA101;</i> <i>thiB101;metB11;pdxA2;oliC2;crnB12</i>	EK226	EK

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	arginine requiring	A885	N462	070
argB13	V	arginine requiring	A888	N492	073
argD6	III	arginine requiring	A880	N430	065
argE5	VI	arginine requiring	A884	N459,458	069,068
argF8	IV	arginine requiring	A802	N474	018
argG11	VI	arginine requiring	A887	N479	072
argH12	II	arginine requiring	A925	N837,907	040,106
argK16	VI	arginine requiring	A914	N748	085
argL2 (was B2)	III	arginine 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 requiring	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
fwnA1,3I		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	
lysC5,27IV		lysine requiring	A879,918	N428,779	064
lysD25		lysine requiring	A942	N907	104
lysE28	IV	lysine requiring	A943	N912	107

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 (nitrate reductase)	A964 A900	N694	134 032
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* mutants

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

XI. *Aspergillus heterothallicus*

FGSC #	Genotype	Other Number	Origin
A 251	<i>A. heterothallicus</i>	WB 5096	Wild types of Raper
A 252	<i>A. heterothallicus</i>	WB 5097	

XI. *Aspergillus fumigatus*

FGSC #	Genotype	Other Number	Origin
A1100		AF293	MA

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

Section D. Plant Pathogenic fungi

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

Fusarium

Gibberella fujikuroi anamorphs:

Strains from J.F. Leslie.

FGSC#	JFL#	Mating type	VCG	Origin; other markers
<i>Fusarium moniliforme</i>				
7598*	A-102	A+	A1	sorghum, San Joaquin Co. California (<i>Sk^K</i>)
7599	A-148	A-	A2	corn, Visalia California
7600*	A-149	A-	A7	corn, Visalia California (<i>Sk^S</i>)
7601	A-171	A+	?	rice, Italy
7602	A-411	A-	?	corn; <i>hsi1</i> (heterokaryon self-incompatible)
7603*	A-999	A+	A17	corn, Knightstown Indiana (<i>Sk^K</i>)
7604	A-2903	A-	A48	corn, Red Spring North Carolina; <i>pall</i> (albino perithecia)
7605	A-2949	A-	A49	corn, Crowder Mississippi; <i>pall</i> (albino perithecia)
7606	A-4516	A+	?	corn, Kathmandu Nepal; <i>fum1</i> (no fumonisin mycotoxins) (<i>Sk^S</i>)
7607	A-5113	A-	?	cross 7600 x 7606; <i>fum1</i> (no fumonisin mycotoxins) (<i>Sk^S</i>)
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	<i>Fusarium fujikuroi</i>
8382	MP C MATC-1	HKM41	1997, Lalitpur Nepal	<i>Fusarium fujikuroi</i>
8383	MP D MATD-1	HKM28	1997, Lalitpur Nepal	<i>Fusarium proliferatum</i>

Fusarium moniliforme auxotrophs

Nitrate non-utilizing strains.

Klittich and Leslie 1988. Genetics **118**:417-423

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

Other mutants.

Puhalla & Spieth 1983. Exp. Mycol. **7**:328-335

and/or Puhalla and Spieth 1985. Exp. Mycol. **9**:39-47.

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

Other references:

Chairsisook 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 *Fusarium* spp.). Leslie et al. 1992. Phytopathology **82**:341-345 (Fumonisin 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
<i>Pda1</i>	8119	77-2-3	Maloney and VanEtten, Mol Gen Genet 243 :506-514
<i>Pda2</i>	8120	96-17	Miao <u>et al.</u> , Mol Gen Genet 226 : 214-223
<i>Pda3</i>	8121	62-22	Miao <u>et al.</u> , Mol Gen Genet 226 : 214-223
<i>Pda4</i>	8122	196-10-7	Miao <u>et al.</u> , Mol Gen Genet 226 : 214-223
<i>Pda5</i>	8123	55-5-1	Miao <u>et al.</u> , Mol Gen Genet 226 : 214-223
<i>Pda6.1</i>	8124	156-30-6	Miao <u>et al.</u> , Appl Environ Microbiol 58 :801-808
<i>Pda6.2</i>	8125	24-1-1	Miao <u>et al.</u> , Mol Gen Genet 226 : 214-223

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	Philippines
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 Fertile MAT-1	8913	KSU 10653

Fusarium graminearum

FGSC #	JFL #
8630	parent Z-3693
8631	parent Z-5047
8632	nit- Z-11570
8633	nit- Z-11572

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)

More *F. graminearum* (from M. Urban)

FGSC #	Other#	Designation
8733	16A	Wild Type
8734	CAM1	MAP1
8735	CAM2	MAP1
8736	CAM8	Hyg::MAP1 ^E

Magnaporthe grisea

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.

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).

<u>FGSC #</u>	<u>Other #</u>	<u>Depositor</u>	<u>FGSC #</u>	<u>Other #</u>	<u>Depositor</u>
8417	5982	MF	8464	6095	MF
8418	6000	MF	8465	6099	MF
8419	6003	MF	8466	6100	MF
8420	6604	MF	8467	6101	MF
8421	6005	MF	8468	6102	MF
8422	6007	MF	8469	6103	MF
8423	6008	MF	8470	6106	MF
8424	6022	MF	8471	6109	MF
8425	6023	MF	8472	6111	MF
8426	6024	MF	8473	6112	MF
8427	6025	MF	8474	6115	MF
8428	6026	MF	8475	10058	MF
8429	6027	MF	8476	10077	MF
8430	6028	MF	8477	4360-R-1	BV
8431	6029	MF	8478	4360-R-2	BV
8432	6039	MF	8479	4360-R-7	BV
8433	6047	MF	8480	4360-R-8	BV
8434	6050	MF	8481	4360-R-9	BV
8435	6051	MF	8482	4360-R-10	BV
8436	6052	MF	8483	4360-R-12	BV
8437	6054	MF	8484	4360-R-13	BV
8438	6055	MF	8485	4360-R-14	BV
8439	6058	MF	8486	4360-R-15	BV
8440	6059	MF	8487	4360-R-16	BV
8441	6061	MF	8488	4360-R-17	BV
8442	6062	MF	8489	4360-R-18	BV
8443	6063	MF	8490	4360-R-19	BV
8444	6066	MF	8491	4360-R-20	BV
8445	6068	MF	8492	4360-R-21	BV
8446	6069	MF	8493	4360-R-22	BV
8447	6071	MF	8494	4360-R-23	BV
8448	6072	MF	8495	4360-R-24	BV
8449	6075	MF	8496	4360-R-25	BV
8450	6076	MF	8497	4360-R-26	BV
8451	6077	MF	8498	4360-R-27	BV
8452	6079	MF	8499	4360-R-28	BV
8453	6080	MF	8500	4360-R-29	BV
8454	6081	MF	8501	4360-R-30	BV
8455	6082	MF	8502	4360-R-31	BV
8456	6085	MF	8503	4360-R-32	BV
8457	6086	MF	8504	4360-R-34	BV
8458	6087	MF	8505	4360-R-35	BV
8459	6089	MF	8506	4360-R-36	BV
8460	6090	MF	8507	4360-R-37	BV
8461	6092	MF	8508	4360-R-39	BV
8462	6093	MF	8509	4360-R-40	BV
8463	6094	MF	8510	4360-R-41	BV

Magnaporthe grisea, continued.

<u>FGSC #</u>	<u>Other #</u>	<u>Depositor</u>
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

Locus	Allele	FGSC number		Linkage	Genetic	Muta-	Obtained
		A	a				
AMINATION DEFICIENT , continued from previous page							
<i>am</i>	<i>am</i> ₁₇ -RN35	4388		VR	SL7	UV	JRF
<i>am</i>	<i>am</i> ₁₇ -RU4		4387	VR	SL7	UV	JRF
Ectopic integrations							
<i>am</i> ₁₃₂	<i>am</i> ⁺ T85 (204-5)		7115		SL		JRF
<i>am</i> ₁₃₂	<i>am</i> ⁺ T75 (214-1)		7116		SL		JRF
<i>am</i> ⁺	<i>am</i> ⁺ T75 (3)		7117		SL		JRF
<i>am</i> ⁺	<i>am</i> ⁺ T85 (2)	7118			SL		JRF
<i>am</i> ₁₃₂	<i>am</i> ⁺ T75 <i>am</i> ⁺ T85 (4)	7119			SL		JRF
Induced by RIP							
<i>am</i> ₃ *	(= <i>am</i> _{3SH})	7120			SL	RIP	JRF
<i>am</i> _S -1		7121			SL	RIP	JRF
<i>am</i> _S -6			7122		SL	RIP	JRF
<i>am</i> _H -2		7123			SL	RIP	JRF
<i>am</i> _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*

AMYCELIAL

<i>amyc</i>	K422	305	306	IL	SL3		DDP
-------------	------	-----	-----	----	-----	--	-----

ANAEROBIOSIS (FACULTATIVE)

<i>an</i> ⁺	2B-12-3		3442	--	SL	UV	KDM
<i>an</i> ⁺	2B-16-9	3443		--	SL	UV	KDM
<i>an</i> ⁺	5B-8-2		3445	--	SL	UV	KDM

ARGINASE see *aga*

ARGININE

<i>arg-1</i>	36703	1459		IL	M	UV	DDP
<i>arg-1</i>	46004	528	407	IL	M	UV	RWB
<i>arg-1</i>	B369	325	324	IL	SL5	G	DDP
<i>arg-1</i>	CD145	3585		IL	M	UV	RHD
<i>arg-1</i>	CR237(t)	2382		IL	M	NNG	WMT
<i>arg-1</i>	K166		747	IL	M	UV	DGC
<i>arg-1</i>	K209		748	IL	M	UV	DGC
<i>arg-1</i>	K287		774	IL	M	UV	DGC
<i>arg-1</i>	K337		749	IL	M	UV	DGC
<i>arg-1</i>	K351		750	IL	M	UV	DGC
<i>arg-1</i>	K401		751	IL	M	UV	DGC
<i>arg-1</i>	K406		1331	IL	M	UV	DGC
<i>arg-1</i>	SDS1		2381	IL	M	UV	WMT
<i>arg-2</i>	33442	4760	66	IVR	SL/M		RHD/DDP
<i>arg-2</i>	CD80	3586	4232	IVR	M	UV	RHD/DDP
<i>T(I;IV)MEP24 arg-2</i>	MEP24	3170	3171	IVR			DDP
<i>arg-3</i>	30300	1068	1069	IL	SL3	UV	DNP
<i>arg-3</i>	NM136	2663		IL	M	UV	DDP
<i>T(I;IV;IV→V)MEP35 arg-3</i>	MEP35	3844	3845	IL			DDP
<i>arg-3</i>	CD-37	8402		IL	SL		RHD
<i>arg-4</i>	21502		90	VR	M	X	DDP
<i>arg-4</i>	21502		778	VR	M	X	DGC
<i>arg-4</i>	34105	91	84	VR	M	UV	DDP
<i>arg-4</i>	34105		779	VR	M	UV	DGC

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ARGININE , continued from previous page							
<i>arg-5</i>	27947	4034	4035	IIR	SL6	X	EK
<i>arg-5</i>	CD6	3589	3590	IIR	M	UV	RHD
<i>arg-5</i>	K124		741	IIR	M	UV	DGC
<i>arg-5</i>	K128		752	IIR	M	UV	DGC
<i>arg-6</i>	29997	266		IR	M	UV	DDP
<i>arg-6</i>	29997		4015	IR	SL7	UV	EK
<i>arg-6</i>	C116	929		IR	M	S	MBM
<i>arg-6</i>	C122	549		IR	M	UV	DDP
<i>arg-6</i>	CD25	3591		IR	M	UV	RHD
<i>arg-6</i>	CD29	3592		IR	M	UV	RHD
<i>arg-6</i>	CD63	3593		IR	M	UV	RHD
<i>arg-6</i>	HY176(t)		1240	IR	M	UV	JH
<i>arg-6</i>	HY227(t)		1242	IR	M	UV	JH
<i>arg-6</i>	K131		773	IR	M	UV	DGC
<i>arg-6</i>	K142		693	IR	M	UV	DGC
<i>arg-6</i>	K169		753	IR	M	UV	DGC
<i>arg-6</i>	K190		754	IR	M	UV	DGC
<i>arg-6</i>	K374		755	IR	M	UV	DGC
<i>arg-6</i>	K395		742	IR	M	UV	DGC
<i>arg-6</i>	VP102	8259	8260	IR	M		DDP
<i>arg-7</i>	CD51		3594	VR	M	UV	RHD
<i>arg-8</i>	see <i>pro-3</i>						
<i>arg-9</i>	see <i>pro-4</i>						
<i>arg-10</i>	B317	4091	4092	VIIR	SL9	UV	EK
<i>arg-10</i>	HY93(t)		1241	VIIR	M	UV	JH
<i>arg-10</i>	K112		743	VIIR	M	UV	DGC
<i>arg-10</i>	K323		745	VIIR	M	UV	DGC
<i>arg-10</i>	K402		772	VIIR	M	UV	DGC
<i>arg-10</i>	K405		756	VIIR	M	UV	DGC
<i>arg-11</i>	30820	145	136	VIIR	SL3	X	DDP
<i>arg-11</i>	44601	1532	3616	VIIR	SL3/SL4	UV	DDP
<i>arg-12</i>	CD3	3595		IIR	M	UV	RHD
<i>arg-12</i>	UM3	978		IIR	M	UV	RHD
<i>arg-12</i>	UM107	979	1527	IIR	M/SL2	UV	RHD/DDP
<i>arg-12</i>	37301s	893		IIR	L	UV	RHD
<i>arg-13</i>	CD7	3596	3597	IR	M	UV	RHD
<i>arg-13</i>	RU3	3157		IR	SL2	UV	DDP
<i>arg-13</i>	RU12	4018	4019	IR	SL7	UV	EK
<i>arg-13</i>	RU20	1726		IR	M	UV	KJM
<i>arg-14</i>	CD197	3598	3599	IVR	M	UV	RHD
<i>T(IV-VII;I;II;IV)</i> <i>S1229 arg-14 pe</i>	S1229	2946	268	IVR			EGB/DDP

A variety of arg mutants from the collection of R.H. Davis are available from the FGSC.

AROMATIC AMINO ACIDS

<i>aro-1</i>	311-1027	6142		IIR	SL	UV	MEC
<i>aro-1</i>	311-1075	6143		IIR	SL	UV	MEC
<i>aro-1</i>	311-1134	6144		IIR	SL	NG	MEC
<i>aro-1</i>	311-1183		6145	IIR	SL	NG	MEC
<i>aro-1</i>	Y306M80	1742	3617	IIR	SL	EMS	MEC/DDP
<i>aro-1</i>	Y7655	3629	3630	IIR	M	M	DDP
<i>aro-1</i>	Y7655		1695	IIR	L	M	SRG
<i>aro-2</i>	311-1084	6146		IIR	SL	UV	MEC
<i>aro-2</i>	311-1234	6148		IIR	SL	NG	MEC
<i>aro-2</i>	311-1277	6147		IIR	SL	NG	MEC
<i>aro-2</i>	Y306M81	1743		IIR	SL	EMS	MEC
<i>aro-3</i>	306-47	6167	6168	IIR	SL	EMS	MEC

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
AROMATIC AMINO ACIDS, continued from previous page							
<i>aro-3</i>	C163	1293	53	IIR	M	UV	DDP
<i>aro-3;inl</i>	R2017;89601	1103		IIR;VR	M	UV	MEC
<i>aro-3;inl</i>	R2202;89601	1098		IIR;VR			MEC
<i>aro-3;inl</i>	R2203;89601	1099		IIR;VR			MEC
<i>aro-3;inl</i>	R2205;89601	1100		IIR;VR			MEC
<i>aro-3;inl</i>	R2209;89601	1101		IIR;VR	M	UV	MEC
<i>aro-3;inl</i>	R2212;89601	1102		IIR;VR	M	UV	MEC
<i>aro-3;inl</i>	R2333;89601	1104		IIR;VR	M	UV	MEC
<i>aro-3</i>	Y306M87	1744		IIR	SL	EMS	MEC
<i>aro-4</i>	311-1044	6149		IIR	SL	UV	MEC
<i>aro-4</i>	311-1050	6150		IIR	SL	UV	MEC
<i>aro-4</i>	311-1057	6151		IIR	SL	UV	MEC
<i>aro-4</i>	311-1201	6152		IIR	SL	UV	MEC
<i>aro-4</i>	R2204	162	171	IIR	M	UV	DDP
<i>aro-4;inl</i>	R2219;89601	1105		IIR;VR	M	UV	MEC
<i>aro-4</i>	Y306M49	1745		IIR	SL	NG	MEC
<i>aro-5</i>	Y306M56	1863		IIR	SL	EMS	MEC
<i>aro-5</i>	311-1146	6153		IIR	SL	NG	MEC
<i>aro-5</i>	311-1154	6154		IIR	SL	NG	MEC
<i>aro-5</i>	311-1185	6155		IIR	SL	NG	MEC
<i>aro-5</i>	311-1224	6156		IIR	SL	NG	MEC
<i>aro-6</i>	DH1	1712	1713	VI	SL	UV	DMH
<i>aro-7</i>	DH7	1714	1715	IC	SL	UV	DMH
<i>aro-8</i>	DH8	1716	1717	IR	SL	UV	DMH
<i>aro-9;inl;qa-2</i>	M6-11;89601;M246	3952		IIR;VR;VIIR			MEC
<i>aro-9</i>	Y325M6	3938	3939	IIR	M		DDP
<i>aro(p)</i>	Y306M54	1862	1854	IIR	SL	EMS	MEC
<i>aro(p)(A-C)</i>	311-1131	6157		IIR	SL	NG	MEC
<i>aro(p)(A-C)</i>	311-1163	6158		IIR	SL	NG	MEC
<i>aro(p)(A-C)</i>	311-63		6172	IIR	SL	UV	MEC
<i>aro(p)(A)</i>	311-58		6180	IIR	SL	UV	MEC
<i>aro(p)(A)</i>	311-1063	6182		IIR	SL	NG	MEC
<i>aro(p)(B)</i>	311-14	6163	6162	IIR	SL	UV	MEC
<i>aro(p)(B)</i>	311-1036	6176		IIR	SL	NG	MEC
<i>aro(p)(B)</i>	311-1136	6185		IIR	SL	NG	MEC
<i>aro(p)(C)</i>	311-1052	6175		IIR	SL	UV	MEC
<i>aro(p)(C)</i>	311-1148	6178		IIR	SL	UV?	MEC
<i>aro(p)(D)</i>	311-75	6169	6170	IIR	SL	UV	MEC
<i>aro(p)(D)</i>	311-1094	6177		IIR	SL	NG?	MEC
<i>aro(p)(D)</i>	311-1113	6183		IIR	SL	NG	MEC
<i>aro(p)(D)</i>	311-1116		6186	IIR	SL	UV	MEC
<i>aro(p)(D)</i>	311-1199	6159		IIR	SL	NG?	MEC
<i>aro(p)(E)</i>	311-34	6165	6166	IIR	SL	UV	MEC
<i>aro(p)(E)</i>	311-54	6171	6172	IIR	SL	UV	MEC
<i>aro(p)(E or F)</i>	311-1150	6184		IIR	SL	NG	MEC
<i>aro(p)(F)</i>	311-25	6164	6179	IIR	SL	UV	MEC
<i>T(II;III)C161 aro</i>	C161	2106	2107	IIR;III			DDP

ARYL SULFATASE DEFECTIVE

<i>ars</i>	101		1864	VIIR	SL	UV	RLM
<i>ars</i>	101-PR1		1871	VIIR	SL	UV-101	RLM
<i>ars</i>	103		1865	VIIR	SL	UV	RLM
<i>ars</i>	108		1866	VIIR	SL	UV	RLM
<i>ars</i>	111		1868	VIIR	SL	UV	RLM
<i>ars</i>	113		1869	VIIR	SL	UV	RLM
<i>ars</i>	301		1867	VIIR	SL	UV	RLM
<i>ars</i>	312		1870	VIIR	SL	UV	RLM
<i>ars*</i>	343		2052	VIIR			RLM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ARYL SULFATASE DEFECTIVE , continued from previous page							
<i>arys*</i>	UFC-220	1909		VIIR			RLM
* - originated in <i>N. tetrasperma</i>							
ABNORMAL ASCUS MORPHOLOGY							
<i>asc(JL155)</i>	JL155	7511	7512		M		NBR
<i>asc(JL164)</i>	JL164	7514	7515		M		NBR
<i>asc(JL174)</i>	JL174	2222	7516		M		NBR
<i>asc(JL179)</i>	JL179	7517	7518		M		NBR
<i>asc(JL209)</i>	JL209	2225	7519		M		NBR
<i>asc(JL219)</i>	JL219	7520	7521		M		NBR
<i>asc(JL223)</i>	JL223	7522	7523		M		NBR
<i>asc(JL235)</i>	JL235	7524	7525		M		NBR
<i>asc(JL239)</i>	JL239	7526	7527		M		NBR
<i>asc(JL266)</i>	JL266	430	7530		M		NBR
ASCOSPORE ABORTION (same locus as <i>lys-5</i>)							
<i>asco</i>	37402	4096	4095	VIL	SL6	UV	EK
ASCUS DEVELOPMENT							
<i>asd-1</i>	A1	7570	--		SL	RIP	MAN
<i>asd-1</i>	A2		7571	--	SL	RIP	MAN
<i>asd-2</i>	N7		7572	VIII	SL	TR	MAN
<i>asd-2</i>	N18	7573		VIII	SL	TR	MAN
ASCOSPORE MATURATION							
<i>mep his-3+::Asm-1; 10;Asm;SR62;Y153M96</i>		8298			OR		RLM
<i>mtr;pan-2;Asm::mtr+</i>							
<i>mep his-3+::Asm-1; 10;Asm;SR62;Y153M96</i>		8300	8299		OR		RLM
<i>mtr;pan-2;Asm::mtr+</i>							
<i>mep his-3+::Asm-1; 10;Asm;SR62;Y153M96</i>		8302	8301		OR		RLM
<i>mtr;pan-2;Asm::mtr+</i>							
<i>mep his-3+::Asm-1; 10;Asm;SR62;Y153M96</i>			8303		OR		RLM
<i>mtr;pan-2;Asm::mtr+</i>							
ASPARAGINE							
<i>asn</i>	C123	111	114	VR	M	UV	DDP
<i>asn</i>	S1007	3620	3621	VR	M	X	DDP
<i>asn</i>	<u>T</u> 51M147	2351		VR	M	X	DDP
<i>asn</i>	<u>T</u> 51M158(t)		3602	VR	SL	UV	DDP
ASPARTIC ACID							
<i>asp</i>	44303	3873	3874	V	M	UV	DDP
ATTENUATED							
<i>at</i>	D307	1666		VC	M	UV	DDP
<i>at</i>	D315	1667		VC	M	UV	DDP
<i>at</i>	M111	1664	1884	VC	M	S	DDP
<i>at</i>	NM221(t)	1665		VC	M	UV	DDP
AMINO TRIAZOLE RESISTANT							
<i>atr-1</i>	RC2	2296	2299	IL	SL	DS	DDP
AURESCENT see <i>al-1</i> , allele 34508							
AZAPURINE RESISTANT							
<i>aza-3;his-2 ad-3A</i>	006(r);C94 Y112M31	3182		III(?);IR R		UV	GRH
<i>ad-3B nic-2;ad-2;inl</i>	35203 43002;Y175M256;JH319			R R;IIIR;VR			

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
BALLOON							
<i>bal</i>	B56	105	337	IIL	SL3	UV	DDP
<i>bal</i>	C-1405	823		IIL	SL	P	DDP
<i>(bal arg-5 + a^{ml} ad-3B cyh-1)</i>	B56 27447		8251	IIL R	M		DDP
BANANA							
<i>Ban</i>	N452P63	2989		IL	M	S	DNP
<i>Ban mei-3;inl</i>	N452P63 N289;89601		2990	IL L;VR	M	S	DNP
BASIC AMINO ACID TRANSPORT							
<i>bas^a;his-3</i>	no#;K57	3271		II?;IR	E	UV	CWM
BAND							
<i>bd</i>	no#	1858	1859	IVR	SL3	S	MLS
BALD							
<i>bld</i>	NM213t	8252	1658	IVR	M		DDP
BENOMYL RESISTANT							
<i>Bml</i>	111(r)	2964		VIL	SL	UV	HDB
<i>Bml</i>	511(r)	2965	3460	VIL	SL	UV	HDB
BISCUIT see <i>pk</i>							
BUTTON							
<i>bn</i>	B40	3954		VIIC	SL4	UV	DDP
<i>(bn A + a^{ml} ad-3B cyh-1)</i>	B40 + 1 2-17-114 KH52(r)	4895		VII+I			DDP
<i>bn</i>	Y5296	4622	4577	VII	M	M	DDP
<i>(bn A + a^{ml} ad-3B cyh-1)</i>	Y5296 +12-17-114 KH52(r)	4446	4578	VII+I			DDP
BROWN ASCOSPORE							
<i>bs</i>	AR62	1780	1781	IR	SL	UV	DDP
CAFFEINE RESISTANT (see <i>cfs</i> for Caffeine sensitive)							
<i>caf-1</i>	KH101(r)	993	994	VL	SL	S	KSH
CALCIUM EXCHANGER							
<i>cax-RIP, his-3</i>	cax-10B-13		8629	VIL		RIP	BB
CANAVANINE see <i>cnr</i>							
CAPRYLATE RESISTANT							
<i>cap</i>	1005(r)	1057	--		M	UV	HBH
CARBOHYDRATE TRANSPORT							
<i>car</i>	I-20	2745		IVL	M	EMS	RH
CELLOBIOHYDROLASE							
<i>cbh-1</i>	FT3		7826	--	SL	RIP	AR
<i>cbh-1</i>	FT4	7823		--	SL	RIP	AR
<i>cbh-1</i>	FT7		7827	--	SL	RIP	AR
CLOCK CONTROLLED GENE (allelic with <i>grg-1</i>)							
<i>his-3;bd;ccg-1</i>	Y234M723;no#;Δccg-1	7487		IR;IVR;V	M	RIP	JCD
<i>bd;ccg-1</i>	no#;Δccg-1		7488	IVR;V	M	RIP	JCD
<i>ccg-2</i> (see <i>eas</i>)							

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
IMPAIRED CHAIN ELONGATION OF FATTY ACIDS							
<i>cel</i>	EB2853(t)	5411	5412	IVR	M	S	EGB
<i>cel</i>	R2366o	6783	819	IVR	M	UV	FGSC/DDP
<i>cel-2</i>	mb-5	8293		IVR	OR	RIP	MT
<i>cel-2</i>	mb-17	8294		IVR	OR	RIP	MT
<i>cel-2</i>	mb-27	8295		IVR	OR	RIP	MT
<i>cel-2</i>	mb-19		8296	IVR	OR	RIP	MT
<i>cel-2</i>	mb-26		8297	IVR	OR	RIP	MT
<i>cel-2</i>	mb-27		8321	IVR	OR		RLM
CELLOBIASE/CELLULASE							
<i>cell-1</i>	T11(2-1)	4335			SL	UV	BME
<i>cell-1</i>	T11(2-3)	4336			SL	UV	BME
CAULIFLOWER <i>cfl</i> see <i>ro-3</i>							
CAFFEINE SENSITIVE							
<i>cfs(OY305)</i>	OY305(s)	3526	3527	I	SL8	UV	OCY
<i>cfs(OY306)</i>	OY306(s)	3528		IR	SL8	UV	OCY
<i>cfs(OY306) al-2</i>	OY306(s) 15300	3529		IR R	SL8	UV	OCY
<i>cfs(OY307)</i>	OY307(s)	3530	3531	I	SL8	UV	OCY
CHEESE ?							
<i>che</i>	H453G1	646		--			MJM
CHLORAMPHENICOL SENSITIVE see <i>cpl</i>							
CHOLINE							
<i>chol-1</i>	34486	2982	485	IVR	M	UV	DDP/RWB
<i>chol-1</i>	Y3261	8131	1116	IVR	M	M	ELT
<i>chol-2</i>	47904(t)	4093	4094	VIL	SL6	UV	EK
<i>chol-2</i>	47904(t)	8261	8262	VIL	M		DDP
<i>chol-3</i>	S2586	4645	4646	VR	SL3	EF	DDP
<i>chol-4</i>	S1089	4647	4648	IVR	SL2	X	DDP
CHROMATE RESISTANT see <i>cys-13</i>							
CHRONO							
<i>bd;chr</i>	no#;no#	4908		IVR;V	SL	NG	JFF
CHITIN SYNTHETASE							
<i>chs-2</i>	no #	8319		IV		RIP	OY
<i>chs-4</i>	no #	8244				RIP	OY
CLOCK							
<i>cl</i>	CL11	1166		VR	M	UV	AS
CLOCK AFFECTING GENE							
<i>bd;cla-1</i>	no#;no#		7504	IVR;VIIR	M	S	SB
CYANIDE INSENSITIVE							
<i>cni-1;inl</i>	1;89601	3232		--;VR	M	UV	DLE
CANAVANINE RESISTANT							
<i>cnr^R</i>	no#(r)	Use Oak Ridge wild types					
<i>cnr^S</i>	no#(s)	19	635	IR	SL3/M	O	DDP/PT
<i>cnr^S al-2</i>	no#(s) 15300	99	263	IR R	SL2/-	X/-	DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
cog see RECOMBINATION AFFECTORS							
COIL							
<i>coil-1</i>	J131	3648	3649	IVR	SL5	S	REB
<i>coil-1?</i>	P4120	3650		IVR			REB
COLONIAL							
<i>col-1;pe;al-2</i>	Y8743c;Y8743m;15300	536		IVR;IIR;IR	M	MC→col	ELT
<i>col-1;pe</i>	Y8743c;Y8743m		535	IVR;IIR	M	MC→col	ELT
<i>col-1</i>	Y8743c	8135	7020	IVR	M	MC	FGSC
<i>col-2</i>	Y5331	4560	4561	VII	SL4	MC	DDP
<i>(col-2 + a^{ml} ad-3B cyh-1)</i>	Y5531 + 1 2-17-114 KH52(r)	4562	4563	VII+I			DDP
<i>col-3 (allelic bn)</i>							
<i>col-4</i>	70007c	1177	1178	IVR	SL3	UV	DDP
<i>col-4</i>	B148	943	1442	IVR	SL	UV	DDP
<i>col-4</i>	D316	1615		IVR	M	UV	DDP
<i>col-4</i>	NM164	1307		IVR	M	UV	DDP
<i>col-4</i>	P4874	7403		IVR	SL3	S	DDP
<i>col-5 (=col-1?)</i>	B28	1656	1378	IVR	SL3/SL	UV	DDP/ELT
<i>col-6 (see part VI)</i>	S1302		1400	IVC	L	X-pe	ELT
<i>col-7 (allelic rg-1)</i>							
<i>col-8</i>	R2356	8128	1401	IVR	M	UV	ELT
<i>col-9 inl</i>	R2417 89601	8211	1385	VR R	M	UV	FGSC/ELT
<i>col-10 (=pi?)</i>							
<i>col-12</i>	R2440	1376	8210	I	M	UV	ELT/FGSC
<i>col-13 (allelic vel)</i>							
<i>col-14 (allelic sc)</i>							
<i>col-15</i>	R2531	3847	3848	IIR	SL2	S	DDP
<i>col-16</i>	R2539	3461	3462	IIR	M	UV	DDP
<i>col-17</i>	B5	1373	8133	VII	SL	UV	ELT
<i>col-18</i>	P4494	8283	8284	VIR	M		DDP
<i>(col-18 A + a^{ml} ad-3B cyh-1)</i>	P4494	8280	8279	VIR	M		DDP
<i>col(B235r)</i>	B235r	1652		IIR	M	UV	DDP
<i>col(D5)</i>	D5		1633	IR	M	UV	DDP
<i>col(D302)</i>	D302		1653	IIC	M	UV	DDP
<i>col(P2615)</i>	P2615	1643		I	M	S	DDP
COMPACT							
<i>com</i>	B54	106	179	IIR	SL3	UV	DDP
COBALT AND NICKEL RESISTANT							
<i>cor</i>	Co ^R	7289	7290	IIR	SL	S	PMM
COLONIAL TEMPERATURE SENSITIVE							
<i>cot-1</i>	C102(t)	4065	4066	IVR	SL6	UV	EK
<i>(cot-1^{ir} *+ a^{Ml} ad-3B cyh-1)</i>	P4121+ helper	7658	7659	IVR	SL2	Spont	DDP
<i>cot-2</i>	R1006(t)	1513	2263	VR	SL2/M	UV	DDP
<i>cot-3</i>	R2006(t)	1517	1516	IVR	SL2	UV	DDP
<i>cot-4</i>	R2101(t)	3600	3601	VR	SL2	UV	DDP
<i>cot-5</i>	R2479(t)	3560	3561	IIL	M	UV	DDP
* ir = irreparable							
CROSS-PATHWAY CONTROL							
<i>cpc-1</i>	CD-15	4264		VIL	SL2	UV	RHD
<i>cpc-1;arg-12^S</i>	CD-15;37301s	4262	4263	VIL;IIR	SL	S	RHD
<i>cpc-1</i>	j-2	4431	4432	VIL	SL	UV	IB
<i>T(VI→I)IBj-5 cpc-1</i>	j-5	4433	4434	VIL	SL	UV	IB

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
CROSS-PATHWAY CONTROL , continued from previous page							
<i>cpc-1</i>	j-9	4435	4436	VIL	SL	UV	IB
<i>cpc-1</i>	MN1	4379	4380	VI	SL2	UV	DDP
<i>T(IV;VI)MN9 cpc-1</i>	MN9	6700	6699	VIL	SL2		IB
<i>cpc-2</i>	U142	6918	6919	VII	SL	UV	IB
<i>cpc-3::hph; cyh-2</i>	no #; KH53(r)	8405	8406	V	SL7	D	ES
CYCLIC AMP-DEPENDENT PROTEIN KINASE							
<i>cpk</i>	no#	5138	5139	IIR	SL	S	TM
CHLORAMPHENICOL SENSITIVE							
<i>cpl-1</i>	ANTAS6(s)	3739	2459	VIL	SL4/SL3	UV	DDP/JHC
CARPET							
<i>cpt</i>	P564	292	104	IIR	M	S	DDP
CRISP							
<i>cr-1</i>	B74	826	4345	IR	M	UV	DDP/ELT
<i>cr-1</i>	B122	804		IR	SL	UV	DDP
<i>cr-1</i>	B123	4008	4009	IR	SL9	UV	EK
<i>cr-1</i>	C-Ex-11-67		814	IR	M	P	DDP
<i>cr-1</i>	L	20		IR	SL3	S	DDP
<i>cr-1</i>	L151		5068	IR	SL		DDP
<i>cr-1</i>	R2360	4344	806	IR	M	UV	ELT/DDP
<i>cr-2</i>	AR5	1632		IR	M	UV	DDP
<i>cr-2</i>	R2445	3515	3516	IR	SL	UV	DDP
<i>cr-3</i>	R2509	3449	2329	IR	SL2/M	M	DDP
<i>cr-4</i>	RLP558	5858	5859	IV	SL		DDP
<i>cr(RLP805)</i>	RLP805	6652	6653	IR	SL2		FGSC
<i>cr(RLP808)</i>	RLP808	5971		IR	SL2		FGSC
<i>cr(RLP815)</i>	RLP815	6701	6702	IR	SL2		FGSC
<i>cr(RLP816)</i>	RLP816	6669	6670	IR	SL2		FGSC
<i>cr(RLP914)</i>	RLP914	6671	6672	IR	SL2		FGSC
<i>cr(RLP957)</i>	RLP957	6141		IR	SL2		FGSC
<i>cr?</i>	B180	825		IR	M	UV	DDP
CYTOPLASMIC RIBOSOME BIOSYNTHESIS							
<i>crib-1</i>	PJ30201(t)	3300		IVR	M	NG	PJR
<i>crib(PJ31562)</i>	PJ31562	4283		IVR	M	NG	PJR
CUSHION							
<i>csh</i>	STL8	4518	4519	IR	SL2	S	DDP
<i>(csh a + a^{m1} ad-3B cyh-1)</i>	STL8 + 1 2-17-114 KH52(r)		4575	IR+IL R R			DDP
CONIDIAL SEPARATION							
<i>csp-1</i>	UCLA37	2554		IL	SL4	EMS	CPS
<i>csp-2</i>	FS590	2521	2522	VII	SL4	UV	CPS
<i>csp-2</i>	FS591	2523	2524	VII	SL4	UV	CPS
<i>csp-2</i>	UCLA101	4085	4086	VII	SL6	S	EK
<i>csp-2;nic-2</i>	UCLA102;43002	3871		VII;IR	SL4	S	CPS
<i>csp-2 nic-3</i>	UCLA102 Y31881	3872		VII L	SL4	S	CPS
CYCLOSPORIN RESISTANCE							
<i>csr-1</i>	B12	6920	6921	IR	SL	UV	IB
<i>csr-1</i>	B32	6922	6923	IR	SL	UV	IB
<i>csr-1</i>	B60	6924	6925	IR	SL	S	IB

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
CUMULUS							
<i>cum</i>	P5241	3877	3878	IIIL			DDP
CUT							
<i>cut</i>	LLM1	2385	2386	IVL	M	S	DDP
<i>T(1;IV)HK53 cut</i>	HK53	2272	2068	IC;IVL			DAS/DDP
CROSSWALL							
<i>(cwl-1 + a^{ml} ad-3B cyh-1)</i>	R2441 + 1 2-17-114 KH52(r)	5951	5952	IIR			DDP
<i>(cwl-2 + a^{ml} ad-3B cyh-1)</i>	P1998 + 1 2-17-114 KH52(r)	6875	6876	IIR	SL2		DDP
CURLY							
<i>cy</i>	C170c	3859	3860	IL	M		DDP
CYTOCHROME a							
<i>cya-3;nic-1 al-2</i>	cya-3-16;3416 15300		7594	VIL;IR R	SL	NG	FEN
<i>cya-5</i>	cya-5-34		7596	IVR?	SL	NG	FEN
<i>cya-8</i>	P9178	4522	4523	VIII	S		DDP
<i>(cya-8 + a^{ml} ad-3B cyh-1)</i>	P9178 + 1 2-17-114 KH52(r)	4524	4525	VIII+IL R R		DDP	
<i>cya-9</i>	299-1(t)		3551	IVR			THP
CYTOCHROME b							
<i>cyb-1;nic-1 al-2;pan-2</i>	<i>cyb-1-1</i> ;3416 15300;B3		7593	VR;IR R;VIR	SL	NG	FEN
<i>cyb-3</i>	A10-301-8(t)	3651	3652	IIL	SL	UV	DDP
CYTOCHROME c							
<i>cyc-1 (= cyt-12)</i>	12	4505	4506	IIR	SL	UV	DDP
<i>cyc-1</i>	RK3-21		3558	IIR;VIL	SL	UV	THP
CYCLOHEXIMIDE RESISTANT							
<i>cyh-1</i>	54(r)	2576		IR	SL	UV	WK
<i>cyh-1</i>	1003(r)	1056		IR	SL	UV	HBH
<i>cyh-1</i>	KH52(r)	4012	4013	IR	SL8	S	EK
<i>cyh-2</i>	KH53(r)	4071	4072	VR	SL7	S	EK
CYSTEINE							
<i>cys-1 ylo-1</i>	84605 Y 30539y	1092	2086	VIL L	M	X	NEM/DDP
<i>cys-1</i>	84605		323	VIL	M	X	NHH
<i>cys-2</i>	38401	2109	2110	VIL	M	UV	DGC
<i>cys-2</i>	80702	125		VIL	M	N	DDP
<i>cys-2 ylo-1</i>	80702 Y 30539y		489	VIL L	M	N	BDM
<i>cys-3;intl</i>	29T(t);89601		3761	IIL;VR	M	UV	DRS
<i>cys-3</i>	NM27(t)	2292	1272	IIL	M/E	UV	DDP/NEM
<i>cys-3</i>	P22	1089	1090	IIL	E	UV	NEM
<i>cys-3</i>	P22	4028	4029	IIL	SL7	UV	EK
<i>cys-4</i>	K7	4067	4068	IVR	SL6	UV	EK
<i>cys-4</i>	NM252(t)		1273	IVR	M	UV	NEM
<i>cys-4</i>	P1		193	IVR	M	UV	NEM
<i>cys-5</i>	35001	977		IL	M	UV	NEM
<i>cys-5</i>	NM44		1274	IL	E	UV	NEM
<i>cys-9</i>	T156	1094	2160	IR	E2/M		NEM/DDP
<i>cys-10</i>	39816	4053	4054	IVL	SL6	UV	EK
<i>cys-11</i>	85518	887	2373	IL	M/SL5	M	NNH/RLM
<i>cys-11</i>	NM86		1276	IL	M	UV	NEM
<i>cys-12</i>	NM268(t)	1275	2383	IR	E/M	UV	NEM/DDP
<i>cys-13</i>	w4	2075	2076	IR	SL	UV	GAM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
CYSTEINE , continued from previous page							
<i>cys-13;cys-14</i>	p1;p2		1839	IR;IV	SL	UV	GAM
<i>cys-14</i>	p2		2077	IV	O		GAM
<i>cys-15 (oxD)</i>	1	1872	888	IVR	M	UV	NHH/DDP
<i>cys(71310)</i>	71310	1091	972	VI	M	UV	NEM
CYTOCHROME							
<i>cyt-1</i>	C115	4292	3488	IL	SL2	S	DDP
<i>cyt-1 al-2</i>	C115 15300	7938	7939	IL IR	M		HB
<i>cyt-2</i>	C117	339	1981	VIL			MBM
<i>cyt-2 pan-2</i>	<i>cyt-2-1</i> Y153M66		7364	VIL VIR			FEN
<i>cyt-4</i>	7	3919	3920	IR	SL		DDP
<i>cyt-7</i>	20	7578	7579	VIII	SL	UV	DDP
<i>cyt-9</i>	17		3925	V	M		DDP
<i>cyt-12</i> see <i>cyc-1</i>							
<i>cyt-18 al-2</i>	299-9 no#		5062	IR R	SL	UV	AL
<i>cyt-19;pan-2</i>	1701;B3		5063	IVR;VIR	SL	NG?	AL
<i>cyt-20(289-56)</i>	1	4278	3541	IL	SL		AL/THP
<i>cyt-21</i>	297-24(t)		4279	--			AL
<i>cyt-22</i>	289-4(t)		3539	IIIL	SL2	UV	THP
D-AMINO ACID OXIDASE DEFICIENT see <i>oxD</i>							
<i>het-d, het-D</i> see Part VII							
DAPPLE							
<i>da</i>	R2375	1077	1078	IIL	M	UV	DDP
<i>da</i> (formerly <i>ro-9</i>)	R2526	2167	2168	IIL	SL2	S	DDP
DEFECTIVE IN METHYLATION-2							
<i>dim-2, arg-10</i>	HMF1, B3A	8593	8592	VIIR,VIIR	OR		EUS
<i>his-3; dim-2::hph</i>	1-234-723; EK1		8594	IR, VIIR	M		EUS
DELICATE							
<i>del</i>	B137	7425	2069	VIR	SL2	UV	DDP
DEOXYGLUCOSE RESISTANT							
<i>dgr-1</i>	BE52	4326	4325	VL	SL	UV	BME
<i>dgr-1</i>	BEX5		4332	VL	SL	UV	BME
<i>dgr-1</i>	BEX5		4331	VL	SL	UV	BME
<i>dgr-1</i>	KHY15		8285	VL			SF
<i>dgr-2</i>	L1	4327	4328	IL	SL	UV	BME
<i>dgr-3</i> (allelic <i>sor-4</i>)							
<i>dgr-4</i>	KHY7		8287	IR			SF
DINGY							
<i>dn</i>	38502d	64	3308	IVR	SL3	UV	DDP
DOILY							
<i>do</i>	DS5-51	2261	2262	VIII	SL2	UV	DDP
DOT							
<i>dot</i>	P789	1211	1218	IR	SL3	S	DNP
DOWNY							
<i>dow</i>	D308	1654		IIIR	M	UV	DDP
<i>dow</i>	P616	4051	4052	IIIR	SL8	S	EK
<i>dow</i>	P3053d	8263	8264	IIIR	M	DDP	
DRIFT							
<i>dr</i>	P1163	1673	3869	VIIR	M	S	DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
het-e, het-E see part VII							
EASILY WETTABLE (allelic with <i>ccg-2</i>)							
<i>eas</i>	UCLA191	2960	2961	IIR	SL4	EMS	CPS
<i>eas;bd</i>	<i>ccg-2</i> ;no#	7489		IIR;IVR	M	RIP	JCD
<i>eas</i>	JD105	7582	7583	IIR	SL2	RIP	DDP
<i>T(IL;IIR)KH5-9 eas</i>	KH5-9	7143	7144	IIR	M		DDP
See also section K,part VII (special teaching strains)							
EDEINE RESISTANT							
<i>edr-1</i>	18(r)	2578		VI	SL	NG	WK
<i>edr-2</i>	29(r)	2579	2580	VI	SL	NG	WK
ENHANCER OF <i>am</i>							
<i>en(am)-1</i>	no#	3961	3962	VR	SL2		JRF
<i>en(am)-1</i>	no#		3963	VR	SL2		JRF
<i>en(am)-2</i>	ABT367-24		3930	IIR	M	UV	RHG
<i>en(am)-2;am</i>	C24;32213	1624		IIR;VR	M	UV	MS
<i>en(am)-2 pe;am</i>	C24 Y8743m;32213		1625	IIR R;VR	M	UV	MS
ENHANCER OF <i>pdx</i> PIGMENT							
<i>En(pdx) al(G2)</i>	K30 G2		649	IL R			MJM
ERGOSTEROL DEFICIENT							
<i>erg-1</i>	UV1		2721	VR	SL	UV	MG
<i>erg-1;pan-2</i>	UV1;Y153M66	2722		VR;VIR	M	UV	MG
<i>erg-2</i>	NAN25		2723	VR	SL	NA	MG
<i>erg-2;pan-2</i>	NAN25;Y153M66	2724		VR;VIR	M	NA	MG
<i>erg-3</i>	UV41	3439	2725	IIIR	M	UV	DDP/MG
63,277,322,366, 367							
<i>erg-4</i>	UVC53(t)	3653	3654	IR	SL	NA	DDP
<i>erg(RES208) al-3</i>	RES208(r) RP100		3155	VR R	SL	UV	RES
ENHANCER OF SPERMIDINE REQUIREMENT							
<i>esr-1;aga</i>	BMH566;UM906	7923		VR;VIIR		UV	RHD
<i>esr-2;aga</i>	BMH422;UM906	7922		I;VIIR		UV	RHD
<i>esr-3;aga</i>	BMH36;UM906	7921		--;VIIR		UV	RHD
<i>esr(BMH8);aga</i>	BMH8;UM906	7920		I;VIIR		UV	RHD
ETHIONINE RESISTANT							
<i>eth-1</i>	no#(r)(t)	1212	1220	IL	SL3	UV	DNP
EXOAMYLASE							
<i>exo-1</i>	SF26		2256	I	SL		HGG
EXTRANUCLEAR [<i>exn</i>] see Part IV							
FAST-MODIFIER OF [<i>poky</i>]							
f see <i>su([mi-1])-f</i>							
FLUORODEOXYURIDINE RESISTANT							
<i>fdu-2;</i>	GH14-6(r);	2542		IVR;	M	S	GRH
<i>his-2 ad-3A ad-3B</i>	C94 Y112M13 35203			IR R R			
<i>nic-2;ad-2;inl</i>	43002;Y175M256;JH319			R;IIR;VR			
FEMALE FERTILITY							
<i>ff-1 (glp-3)</i>	JC744	3831	3832	IIR	SL5	S	DDP
<i>ff-1 fl</i>	JC744 P	7545	7546	IIR R	SL		SC

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
FEMALE FERTILITY , continued from previous page							
<i>ff-1 (glp-3)</i>	T30		2318	IIR	M	S	HCC
<i>ff-1;his-3;hlp-1</i>	T30;K458;B538	2320		IIR;IR;VIIR	M	UV	HCC
<i>ff-3;ty-3(T22)</i>	no#;135-333(T22)	2962		IR;IIIR	M	UV	JFF
<i>ff(AB-I4);ad-2</i>	STL2;AB-I4	3094		--;IIIR	M	UV	TEJ
<i>ff(AB-J7);ad-2</i>	STL2;AB-J7	3095		--;IIIR	M	UV	TEJ
<i>ff(AB-K1);ad-2</i>	STL2;AB-K	3096		--;IIIR	M	UV	TEJ
<i>ff(AB-P5);ad-2</i>	STL2;AB-P5	3097		--;IIIR	M	UV	TEJ
<i>ff(AB-P6);ad-2</i>	STL2;AB-P6	3098		--;IIIR	M	UV	TEJ
<i>ff(AB-P11);ad-</i>	AB-P11;STL2	3099		--;IIIR	M	UV	TEJ
<i>ff(AB-R3);ad-2</i>	STL2;AB-R3	3100		--;IIIR	M	UV	TEJ
<i>ff(AB-R7);ad-2</i>	STL2;AB-R7	3101		--;IIIR	M	UV	TEJ
<i>ff(AB-R8);ad-2</i>	STL2;AB-R8	3102		--;IIIR	M	UV	TEJ
<i>ff(AB-T1);ad-2</i>	STL2;AB-T1	3103		--;IIIR	M	UV	TEJ
<i>ff(AB-T5);ad-2</i>	STL2;AB-T5	3104		--;IIIR	M	UV	TEJ
<i>ff(AB-T9);ad-2</i>	STL2;AB-T9	3105		--;IIIR	M	UV	TEJ
<i>ff(AB-T10);ad-2</i>	AB-T10;STL2	3106		--;IIIR	M	UV	TEJ
<i>ff(PB-I8);pyr-3</i>	PB-I8;KS43	3074		--;IVR	SL	UV	TEJ
<i>ff(PB-J3);pyr-3</i>	PB-J3;KS43	3075		--;IVR	SL	UV	TEJ
<i>ff(PB-J4);pyr-3</i>	PB-J4;KS43	3076		--;IVR	SL	UV	TEJ
<i>ff(PB-M4);pyr-3</i>	PB-M4;KS43	3077		--;IVR	SL	UV	TEJ
<i>ff(PB-M7);pyr-3</i>	PB-M7;KS43	3078		--;IVR	SL	UV	TEJ
<i>ff(PB-M8);pyr-3</i>	PB-M8;KS43	3079		--;IVR	SL	UV	TEJ
<i>ff(PB-N1);pyr-3</i>	PB-N1;KS43	3080		--;IVR	SL	UV	TEJ
<i>ff(PB-N4);pyr-3</i>	PB-N4;KS43	3081		--;IVR	SL	UV	TEJ
<i>ff(PB-R3);pyr-3</i>	PB-R3;KS43	3082		--;IVR	SL	UV	TEJ
<i>ff(PB-S1);pyr-3</i>	PB-S1;KS43	3083		--;IVR	SL	UV	TEJ
<i>ff(PB-S4);pyr-3</i>	PB-S4;KS43	3084		--;IVR	SL	UV	TEJ
<i>ff(PB-S7);pyr-3</i>	PB-S7;KS43	3085		--;IVR	SL	UV	TEJ
<i>ff(PB-S8);pyr-3</i>	PB-S8;KS43	3086		--;IVR	SL	UV	TEJ
<i>ff(PB-S9);pyr-3</i>	PB-S9;KS43	3087		--;IVR	SL	UV	TEJ
<i>ff(PB-T1);pyr-3</i>	PB-T1;KS43	3088		--;IVR	SL	UV	TEJ
<i>ff(PB-T2);pyr-3</i>	PB-T2;KS43	3089		--;IVR	SL	UV	TEJ
<i>ff(PB-T3);pyr-3</i>	PB-T3;KS43	3090		--;IVR	SL	UV	TEJ
FISSURE							
<i>fi</i>	M155-2	1303	1304	IVL	M	S	DDP
FLAME see <i>os-1, os-4</i>							
FLUFFY							
<i>fl</i>	blo	4960	4961	IIR	SL	S	HGK
<i>fl</i>	C-1835		818	IIR	O	S?	DDP
<i>fl</i>	L	7430	7431	IIR	M	S	DDP
<i>fl</i>	M155-5		807	IIR	M	S	DDP
	P4499		2033	IIR	M	S	DDP
<i>fl</i>	P961	1616		IIR	M	S	DDP
<i>fl(OR)</i>	P	4317	4347	IIR	SL5	S	DDP
<i>fl(RL);scot</i>	P	6682	6683	IIR	RL4	S	DDP
<i>fl(WE)</i>	P	6962	6963	IIR	M		DDP
<i>fl^y</i>	Y234M474	4240	4241	II	SL	UV	DDP
FLUFFYOID							
<i>fld</i>	P628	7022	7023	IVR	M	S	FGSC
FLUFFYISH							
<i>fls</i>	STL6	255		IR	M	UV	DDP
<i>fls al-1</i>	STL6 34508		60	IR R	M	UV	DDP

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
FEMALE AND MALE FERTILITY							
<i>fmf-1;pyr-3</i>	PB-J6;KS43	3108		IL;IVR	SL	UV	TEJ
<i>fmf-1;tol pan-1</i>	PB-J6;N83 5531	3109	3110	IL;IVR R	M	UV	TEJ
FEMALE STERILE see <i>fs</i>							
FORMATE							
<i>for</i>	C24	9	3850	VIIR	M	UV	DDP
<i>for</i>		8611		VIIR			DDP
FOUR-SPORED ASCUS see <i>Fsp</i>							
p-FLUOROPHENYLALANINE RESISTANT							
<i>fpr-1</i>	R2-69(r)	8134	1696	VR	M	S	JAK
<i>fpr-3</i>	no#	3875	3876	IIIR	SL3	UV	DDP
<i>fpr-4;su(mtr)</i>	no#;17-2	3000		VR;IC	M	UV	JAK
<i>fpr-5;pan-1;al-2</i>	no#(r);5531;15300	3001	3002	IR;IVR;IR	M	UV	JAK
<i>fpr-6</i>	UM-300	4275	4276	VIR	SL	S	RHD
FROST							
<i>fr</i>	B110	103	102	IL	M	UV	DDP
<i>fr;acr-2</i>	P4445,KH5	8107	8108	IL;III	M		DDP
<i>(fr nit-2 A + a^{ml} ad-3B cyh-1)</i>	B110, nr7	7868		IL, L ILRR			DDP
FREQUENCY							
<i>frq¹;bd</i>	1; no#	2670	2671	VIIR;IVR	M	NG	JFF
<i>frq²;bd</i>	2;no#	2672	2673	VIIR;IVR	M	NG	JFF
<i>frq³;bd</i>	3;no#	2674	2675	VIIR;IVR	M	NG	JFF
<i>frq⁴;bd</i>	4;no#	2958	2959	VIIR;IVR	M	NG	JFF
<i>frq⁵</i> see <i>prd-1</i>							
<i>frq⁶;bd</i>	6;no#	4897		VIIR;IVR	SL	NG	JFF
<i>frq⁷;bd</i>	7;no#	4898	4899	VIIR;IVR	SL	NG	JFF
<i>frq⁸;bd</i>	8;no#	4900	4901	VIIR;IVR	SL	NG	JFF
<i>frq⁹;bd</i>	9;no#	7779	7780	VIIR;IVR	SL	UV	JJL
<i>frq¹⁰;bd</i>	10;no#	7490		VIIR;IVR		D/D	JCD
FEMALE STERILE							
<i>fs-1;nic-3</i>	19-2;Y31881	3235	3236	I or II;VIIL	M	S	OMM
<i>fs-2;pan-2</i>	10-4(t);Y153M96		3237	II?;VIR	M	S	OMM
<i>fs-2;pan-2;nic-3</i>	10-4(t);Y153M96;Y31881	3238		II(?);VIR;VIIL M	M	S	OMM
<i>fs-3;nic-3</i>	52-2;Y31881	3239		IL;VIIL	M	S	OMM
<i>fs-3;pan-2</i>	52-2;Y1531796	3240		IL;VIR	M	S	OMM
<i>fs-4;nic-3</i>	2326;Y31881		3241	I;VIIL	M	S	OMM
<i>fs-4;pan-2</i>	2326;Y153M96	3242		I;VIR	M	S	OMM
<i>fs-5;nic-3</i>	5-5;Y31881		3243	I or II;VIIL	M	S	OMM
<i>fs-6;pan-2</i>	2351;Y153M96	3244		I or II;VIR	M	S	OMM
<i>fs-n</i>	44-1		3245	I	M	S	OMM
<i>fs-n</i>	44-3	3246		I	M	S	OMM
<i>fs-n</i>	44-4		3247	I	M	S	OMM
<i>fs-n</i>	44-8	3248		I	M	S	OMM
FOUR-SPORED ASCUS							
<i>Fsp-1</i>	ALS141	2991	2992	IIR	M	UV	DDP
<i>Fsp-2</i>	DL709	4534	4535	IR	SL3	NG	NBR
<i>Fsp-1;Fsp-2</i>	ALS141;DL709	5069	5070	IIR;IR	SL		NBR
GIANT SPORE see <i>gsp</i>							

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
GINGER (from <i>N. sitophila</i> : possible <i>os-1</i> allele)							
<i>gin</i>	637/3.4		647	I		S	MJM
GLUCOAMYLASE [also see <i>sor(T9)</i>]							
<i>gla-1</i>	N15-3		7824	--	SL	RIP	AR
<i>gla-1</i>	N17-2		7825	--	SL	RIP	AR
GLUCOSEPHOSPHATE ISOMERASE DEFECTIVE see <i>gpi</i>							
GOLDEN ?							
<i>gld</i>	70007g		557		M	S?	ELT
GLUTAMINE							
<i>gln-1</i>	R1015		1449	VR	M		ER
<i>gln-1 inl</i>	R1015;89601	1450		VR R	M	M	ER
<i>gln-1b</i>	no#	4536		VR	SL	NG	RHG
GLUTAMINE REGULATION							
<i>gln^r</i>	no#		4615			NG	RMD
GLYCEROL NON-UTILIZER							
<i>glp-1 wc-2</i>	234 234(w)	2742	2743	IR R	M	UV	HGK
<i>glp-2; ylo-1</i>	JC17;Y30539y	2968*		IIR;VIL	M	UV	JBC
<i>glp-2; inl</i>	JC1444;83201(t)	2969*		IIR;VR	M	UV	JBC
<i>glp-3</i> see <i>ff-1</i>							
<i>ad-1 glp-4</i>	3254 G660		7216	VIL C	M	NG	DDP
* Heterokaryon compatibility type C d e							
OLIGOPEPTIDE TRANSPORT DEFECTIVE							
<i>glt; tys(LW101)</i>	<u>D</u> 240(r);LW101(s)	2736		--;IL	M	UV→2735	GAM
<i>glt; leu-2</i>	<u>D</u> 240(R);37501		2737	--;IVR	M	UV	GAM
β-GLUCOSIDASE DEFECTIVE							
<i>gluc-1; cot-1</i>	CM26(3-8);C102(t)		1224	--;IVR	M	UV	BME
<i>gluc-2</i>	CM62	1227		--	M	UV	BME
GLYCINE RESISTANT							
<i>am; gly^r</i>	am ₁₃₂ ;gly ^r		6717	VR;--	SL	UV	JM
GLUCOSEPHOSPHATE ISOMERASE DEFECTIVE							
<i>gpi; sor(T9)</i>	<u>T</u> 21M3; <u>T</u> 9M150(r)	3431		IV;IL	M	UV	TI
<i>gpi; pp</i>	<u>T</u> 66M37g; <u>T</u> 66M37p	3432		IV;--	M	NG	TI
GLYCOHYDROLASE DEFECTIVE see <i>nada</i>							
GRANULAR							
<i>gran</i>	B42	794	793	VR	SL	UV	DDP
GREY							
<i>grey; cr-1; cot-1</i>	KH165;L;C102(t)	2327		IVR;IR;IVR	M	G	KSH
<i>grey; cr-1; cot-1; ylo-1</i>	KH165;L;C102(t);Y30539y	2328		IVR;IR;	M	G	KSH
GIANT SPORE							
<i>gsp</i>	26-125	3425	3426	IL	SL	NNG	AMS
GUANINE							
<i>gua-1</i>	OY301	3524	3525	IL	SL	UV→3448	OCY
<i>gua-2</i>	UW0525		3830	VR	M	EMS→3448	WLG

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
GULLIVER (modifier of <i>cot-1</i>)							
<i>gul-1;cot-1</i>	CA1;C102(t)	1962	1963	VR;IVR	E2		DS
<i>gul-1</i>	G		803	VR	SL2		DDP
<i>gul-1;cot-1</i>	G;C102(t)	817		VR;IVR	M		DDP
<i>gul-2;pe fl;cot-1;inl</i>	264;Y8743m L;C102(t);37401		1173	--;IIR R IVR;VR		UV	HFT
<i>gul-3;pe fl;pt cot-1</i>	845;Y8743m L;NS1(t) C102(t)		1174	IV;IIR R; IVR R		UV	HFT
<i>gul-4;pe fl;cot-1;inl</i>	42;Y8743m L;C102(t);37401 1605			VII;IIR R;IVR;VR		UV	JLR
<i>gul-5;cot-1</i>	BAT26-2;C102(t)		2956	VI;IVR	UV		JLR
<i>gul-6;cot-1</i>	BAT-26-21;C102(t)		3559	--;IVR			JLR
HAIRY							
<i>hair</i>	8615		648			X	MJM
HETEROKARYON COMPATIBILITY <i>het</i> see Part VII							
HEXAGONAL							
<i>hex-1</i>	KT73		8612	IL		RIP	BB
HISTIDYLGLYCINE UPTAKE							
<i>hgu</i>	4		2734	V	SL	UV	GAM
HISTIDINE							
<i>his-1</i>	C84	3435	3436	VR	M	UV	DDP
<i>his-1</i>	C85	403		VR	M	UV	MBM
<i>his-1</i>	C91	401	402	VR	M	UV	MBM
<i>his-1</i>	K85		729	VR	E	UV	DGC
<i>his-1</i>	K90		728	VR	E	UV	DGC
<i>his-1</i>	K93		703	VR	E	UV	DGC
<i>his-1</i>	K141		704	VR	E	UV	DGC
<i>his-1</i>	K624		727	VR	E	UV	DGC
<i>his-1</i>	K626		730	VR	E	UV	DGC
<i>his-1</i>	K744		919	VR	E	UV	DGC
<i>his-1</i>	K745		705	VR	E	UV	DGC
<i>his-1</i>	Y155M302	681		VR	SL	X	MEC
<i>his-1</i>	Y175M650		680	VR	SL	X	MEC
<i>his-2</i>	C94	950		IR	SL2	UV	DDP
<i>his-2</i>	FS1150(t)	3741	3742	IR	SL5	UV	SW
<i>his-2</i>	K74		706	IR	E	UV	DGC
<i>his-2</i>	K80		707	IR	E	UV	DGC
<i>his-2</i>	K153		708	IR	E	UV	DGC
<i>his-2</i>	K154		731	IR	E	UV	DGC
<i>his-2</i>	K246		709	IR	E	UV	DGC
<i>his-2</i>	K267		710	IR	E	UV	DGC
<i>his-2</i>	K545		711	IR	E	UV	DGC
<i>his-2</i>	K567		738	IR	E	UV	DGC
<i>his-2</i>	K571		732	IR	E	UV	DGC
<i>his-2</i>	K595		713	IR	E	UV	DGC
<i>his-2</i>	K605		733	IR	E	UV	DGC
<i>his-2</i>	K614		714	IR	E	UV	DGC
<i>his-2</i>	T51M152(t)	4624	4625	IR	SL	X	DDP
<i>his-2</i>	Y152M14	22	21	IR	SL	X	DDP
<i>his-2</i>	Y152M43	668		IR	SL	X	MEC
<i>his-2;mtr col-4</i>	Y152M43;10(r) 70007c		1720	IR;IVR R			DRS
<i>his-2</i>	Y175M611		667	IR	SL	X	MEC
<i>his-2;neu^f</i>	no#;HS-24	3273		IR;IVR?	E	UV	CEM
SEE PART VI FOR A FULL LIST OF YALE <i>his-3</i> ALLELES							
<i>his-3</i>	C140	2278	2277	IR	M	UV	FGSC
<i>his-3;pt</i>	C1710;S4342		206	IR;VR			DDP
<i>his-3</i>	K26 see <i>rec</i>						

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
HISTIDINE , continued from previous page							
<i>his-3</i>	K57		1682	IR	E	UV	DGC
<i>his-3</i>	K70		1154	IR	E	UV	DGC
<i>his-3</i>	K232		734	IR	E	UV	DGC
<i>his-3</i>	K433		720	IR	E	UV	DGC
<i>his-3</i>	K446		719	IR	E	UV	DGC
<i>his-3</i>	K458		1157	IR	E	UV	DGC
<i>his-3</i>	K469		718	IR	E	UV	DGC
<i>his-3</i>	K477		1155	IR	E	UV	DGC
<i>his-3</i>	K480		717	IR	E	UV	DGC
<i>his-3</i>	K504 see <i>rec</i>						
<i>his-3</i>	K727		716	IR	E	UV	DGC
<i>his-3</i>	K874 see <i>rec</i>						
<i>his-3</i>	K959		1153	IR	E	UV	DGC
<i>his-3</i>	K1164		1158	IR	E	UV	DGC
<i>his-3</i>	K1314		1156	IR	E	UV	DGC
<i>his-3</i>	TM42		4438	IR	SL		DDP
<i>his-3</i>	TM429 see <i>rec</i>						
<i>T(1;V9 his-3</i>	TM429	2530	2531	IR;VIIC			DDP
<i>his-3</i>	Y152M111	455		IR	SL	X	MEC
<i>his-3</i>	Y155M261	462	7088	IR	SL	X	MEC/FGSC
<i>his-3</i>	Y175M614	4495	4496	IR	SL	S	DDP
<i>his-3 nic-2</i>	Y269M5 43002	1855		IR R	M	EMS	MEC
<i>his-4</i>	C141	2161	2162	IVR	M	UV	DDP
<i>his-4</i>	P143h(t)	989		IVR	M	UV	NEM
<i>his-5</i>	K50		721	IVR	E	UV	DGC
<i>his-5</i>	K52		722	IVR	E	UV	DGC
<i>his-5</i>	K71		776	IVR	E	UV	DGC
<i>his-5</i>	K265		723	IVR	E	UV	DGC
<i>his-5</i>	K512		735	IVR	E	UV	DGC
<i>his-5</i>	K513		736	IVR	E	UV	DGC
<i>his-5</i>	K516		724	IVR	E	UV	DGC
<i>his-5</i>	K529		725	IVR	E	UV	DGC
<i>his-5</i>	K746		737	IVR	E	UV	DGC
<i>his-5</i>	Y152M108	456	8191	IVR	SL	X	MEC
<i>his-5</i>	K52	8208		IVR	M		FGSC
<i>his-5</i>	K71	8209		IVR	M		FGSC
<i>his-6</i>	K34	4342	775	VR	?/E	UV	ELT/DGC
<i>his-6</i>	Y152M105	4078	4079	VR	SL8	X	EK
<i>his-6</i>	Y175M616		459	VR	SL	X	MEC
<i>his-7</i>	K577		726	IIIR	E	UV	DGC
<i>his-7</i>	Y152M31	7499	7500	IIIR	SL	X	DDP

HISTIDINOL PERMEABILITY

<i>hlp-1;ff-1;his-3</i>	BS38;no#;K458	2320		VIIR;IIR;IR	M	UV	HCC
<i>hlp-2;his-3</i>	HC114;K458		2319	VIIR;IR	M	UV	HCC

HOMOSERINE

<i>hom</i>	35709	946	8194	IR	M	UV	DDP
<i>hom</i>	51504	3234	282	IR	M/SL2	UV	GWC/DDP

HISTIDINE SENSITIVE

<i>hss-1</i>	MN332	5785	5786	IVR	M	S	DDP
--------------	-------	------	------	-----	---	---	-----

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

IMPAIRED CHAIN ELONGATION OF FATTY ACIDS see *cel*

INDOLE see *trp-1, -2, -4*

Locus	Allele	FGSC number		Linkage	Genetic	Muta-	Obtained
		mating type	A				
INDURATED ASCUS							
<i>lasc</i>	29-405		3424	VR	SL	S	AMS
ISOLEUCINE							
<i>ile-1</i>	46003	123	124	VII	M	UV	DDP
<i>ile-1</i>	N596	2766	2767	VII		S	DDP
<i>ile-1</i>	OY338	3750	3751	VII	M	UV	DDP
<i>ile-1</i>	UK71-26	5885		VII	M	S	JAK
ISOLEUCINE + VALINE							
<i>ilv-1</i>	16117	3955	3956	VR	SL3	X	DDP
<i>ilv-1</i>	T304		1038	VR	E	UV	RPW
<i>ilv-1</i>	T311		1039	VR	E	UV	RPW
<i>ilv-1</i>	T318		1041	VR	E	UV	RPW
<i>ilv-1</i>	T321		1043	VR	E	UV	RPW
<i>ilv-1</i>	T323		1044	VR	E	UV	RPW
<i>ilv-1</i>	T326		1046	VR	M	UV	RPW
<i>ilv-1</i>	T327		1047	VR	M	UV	RPW
<i>ilv-1</i>	T328		1048	VR	M	UV	RPW
<i>ilv-1</i>	T329		1049	VR	M	UV	RPW
<i>ilv-1</i>	T330		1050	VR	M	UV	RPW
<i>ilv-1</i>	T331		1051	VR	M	UV	RPW
<i>ilv-1</i>	T332		1052	VR	M	UV	RPW
<i>ilv-2</i>	39709		1144	VR	L	UV	MEC
<i>ilv-2</i>	46807	501		VR	M	X	RWB
<i>ilv-2</i>	T313(t)		1040	VR	E	UV	RPW
<i>ilv-2</i>	T319	3744	3745	VR	E	UV	DDP
<i>ilv-2</i>	T320		1042	VR	E	UV	RPW
<i>ilv-2</i>	T322		1063	VR	E	UV	RPW
<i>ilv-2</i>	T324		1064	VR	E	UV	RPW
<i>ilv-2</i>	T325		1045	VR	E	UV	RPW
<i>ilv-2</i>	Y3786	574		VR	L	M	ELT
<i>ilv-3;lys-1</i>	T344;33933	1053		IVR;VL	M	UV	RPW
<i>ilv-3;lys-1</i>	T346;33933	1054		IVR;VL	M	UV	RPW
<i>ilv-3;lys-1</i>	T364;33933	1055		IVR;VL	M	UV	RPW
<i>ilv-3</i>	Y7110	575	1164	IVR	L/M	M	ELT/DDP
<i>ilv(47711)</i>	47711	395		VR	M	UV	MBM
<i>ilv(71103)</i>	71103	816	815	VR	M	UV	DDP
<i>ilv(?6201)</i>	(?6201)	169	69	VR	M	UV	DDP
<i>ilv(STL3)</i>	STL3	2431	2437	VR	M	S	DDP
INOSITOL							
<i>inl</i>	31719		4269	VR	L	X	ELT
<i>inl</i>	37102	669	2144	VR	M	UV	MEC/FGSC
<i>inl</i>	37401	4074	4075	VR	SL6	UV	EK
<i>inl</i>	46316		2321	VR	L	UV	ELT
<i>T(V;VI)46802 inl</i>	46802	670	1199	VR;VIL	L	UV	MEC/DDP
<i>inl</i>	64001	658	2146	VR	M	UV	MJM/FGSC
<i>inl</i>	83201(t)	2257	2258	VR	SL5	M	DDP
<i>inl</i>	89601	497	498	VR	M	M	RWB
<i>inl</i>	JH319	925	926	VR	M	UV+M	FJD
<i>inl</i>	JH2626	871	4360	VR	O?	M	ELT
<i>inl</i>	JH5652		671	VR	M	M	MEC
<i>inl</i>	P1882	1302		VR	M	S	DDP
<i>inl</i>	P4723	2066		VR			DDP
<i>inl acu-1</i>	R233 JI48	1731		VR R			RBF
INTENSE							
<i>int</i>	ALS8	1528	2462	IVR	SL	UV	DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
INVERTASE DEFICIENT							
<i>inv</i>	no#	1856	1857	VR	SL	S	MLS
ISOLEUCINE see <i>ile</i>							
ISOLEUCINE + VALINE see <i>ilv</i>							
IT POKES ALONG							
<i>ipa</i>	BVS7	3883	3884	IL	M	S	EGB
ISOPROPYLMALATE PERMEABILITY (+ = permeable; - = wild type)							
<i>ipm-1⁺;ipm-2⁺;leu-4</i>	no#;no#;R59	3365		--;--;IL	M	UV	SRG
<i>ipm-1⁺;ipm-2⁺;leu-4</i>	no#;no#;R59		7024	--;--;IL			SRG
<i>ipm-1⁺;ipm-2⁺;leu-4</i>	no#;no#;R59		3366	--;--;IL	M	UV	SRG
<i>ipm-1⁻;ipm-2⁻;leu-4</i>	no#;no#;R59		3369	--;--;IL	M		SRG
<i>ipm-1⁺ ipm-2⁺ leu-4 leu-1</i>	R59 D221		7025				SRG
<i>ipm-1⁺;ipm-2⁺</i>	no#;no#	3368		--;--	M	UV	SRG
<i>ipm-1⁻;ipm-2⁻</i>	no#;no#	3367		--;--	M		SRG
KYNURENINASE DEFECTIVE							
<i>kyn-1;leu</i>	RC71-3;no#		2512	VII;--	SL	NG	PJR
LACCASE							
<i>lacc, nic-3</i>	HR6; Y31881		8379	VII; L			HI
LACCASE HALO							
<i>lah-1</i>	H12-1	8372		IL			HI
LETHAL ASCOSPORE							
<i>le-1</i>	C-M3	746		IVR	M	P	JCM
<i>le-1;pe fl</i>	S4355;Y8743m L		1402	IVR;IIR R L		UV→pe	ELT
<i>le-2;inl</i>	R2411;89601	1395		VIIR;VR	M	UV	ELT
LEUCINE							
<i>leu-1</i>	33757	4047	4048	IIIR	SL6	UV	EK
<i>leu-1</i>	D221		4270	IIIR			ELT
<i>leu-1;leu-2</i>	D221;R86	7007	7008	IIIR;IVR	E	UV	SRG
<i>leu-1;leu-4</i>	D221;FLR92	1501		IIIR;IL	M	UV	SRG
<i>leu-2</i>	37501	4816	4817	IVR	M	UV	RMD
<i>leu-2</i>	D6		6964	IVR	E	UV	SRG
<i>leu-2</i>	D22	6970	6969	IVR	E	UV	SRG
Many more <i>leu-2</i> alleles from S.R. Gross are available. See part VI							
<i>leu-3</i>	47313	3740	539	IL	M	UV	SW/RWB
<i>leu-3</i>	66108		341	IL	M	UV	MBM
<i>leu-3</i>	R14		1321	IL	M	UV	SRG
<i>leu-3</i>	R120		1322	IL	M	UV	SRG
<i>leu-3</i>	R156	4002	4003	IL	SL8	UV	EK
<i>leu-3</i>	R203		1323	IL	M	UV	SRG
<i>leu-3</i>	R229		1324	IL	M	UV	SRG
<i>leu-3 cyt-1</i>	R156, C115	8109		IL	M		DDP
<i>leu-3 cyt-1 a^{m33}</i>	R156, C115, ^{m33}		8110	IL	M		DDP
<i>leu-4</i>	D133		4235	IL	SL2		DDP
<i>leu-4;leu-1</i>	FLR92;D221	1501		IL;IIIR	M	UV	SRG
<i>leu-4</i>	R59		3369	IL	M		SRG
<i>leu-4</i>	R108		175	IL	M	UV	DDP
<i>leu-4</i>	R142		7010	IL	E	UV	SRG
<i>leu-4</i>	R163		7011	IL	E	UV	SRG
<i>leu-4</i>	R173		7012	IL	E	UV	SRG
<i>leu-4</i>	R359	4233	4234	IL	SL3		DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
LEUCINE , continued from previous page							
<i>leu-4;inl</i>	D47		7013	IL	E	UV	SRG
<i>leu-4</i>	D63		7014	IL	E	UV	SRG
<i>leu-4</i>	D133		7015	IL	E	UV	SRG
<i>leu-4;inl</i>	D179;89601	7016		IL	E	UV	SRG
<i>leu-4</i>	D185		7017	IL	E	UV	SRG
<i>leu-4;inl</i>	D210;89601	7018		IL	E	UV	SRG
<i>leu-5</i>	45208(t)	939	340	VR	M	UV	DDP/MBM
LIGHT INSENSITIVE							
<i>lis-1;bd</i>	JP50;no#	7540		IR;IVR	SL	UV	JP
<i>bd;lis-2</i>	no# ;JP45	7541		IVR;VI	SL	NA	JP
<i>bd;lis-3</i>	no# ;JP52		7542	IVR;VR	SL	UV	JP
L-AMINO ACID OXIDASE							
<i>lox;pmn pmb;pmg</i>	rd9;no# no#;no#	4246	4247	IIIR;IVR R;IIL			RMD
LUMP							
<i>lp</i>	P736	421	555	II	M	S	DDP
LYSINE							
<i>lys-1</i>	33933	4069	4070	VL	SL6	UV	EK
<i>lys-1</i>	66202	400		VL	M	UV	MBM
<i>lys-2</i>	37101	2163	2164	VR	SL2	UV	DDP
<i>lys-2</i>	39302		1127	VR	M	UV	MBM
<i>lys-3</i>	28815		974	IR	M	UV	DDP
<i>lys-3</i>	4545	4302	540	IR	M	X	DDP
<i>lys-4</i>	15069	144	108	IR	M	X	DDP
<i>lys-4</i>	ST39	5436	5437	IR	SL		FJD
<i>lys-4</i>	STL4	3183	941	IR	M	S	DDP
<i>lys-5</i>	37402	4096	4095	VIL	SL6	UV	EK
<i>lys-5</i>	DS6-85	4097	4098	VIL	SL7	UV	EK
<i>lys-5</i>	STL7	139		VIL	SL	UV	DDP
<i>lys(60C)</i>	60C(t)	7576	7577	I	M	UV	FGSC
MICROCONIDIAL (m) see pe							
MALIC DEHYDROGENASE DEFECTIVE							
<i>ma-1</i>	M20	1108			M	UV	KDM
<i>ma-2</i>	M24	1109			M	UV	KDM
METHIONINE, ADENINE, CYSTEINE							
<i>mac</i>	65108	3609	3610	IR	SL3	UV	DDP
MAT A/a MATING TYPE							
<i>mat a^{m1} ad-3B cyh-1</i>	1 2-17-114 KH52(r)	4564		IL R R	M	UV	AJG
<i>mat a^{m2} ad-3B cyh-1</i>	2 2-17-114 KH52(r)	4565		IL R R	M	UV	AJG
<i>mat a^{m5} ad-3B cyh-1</i>	5 2-17-114 KH52(r)	4566		IL R R	M	UV	AJG
<i>mat a^{m7} ad-3B cyh-1</i>	7 2-17-114 KH52(r)	6840		IL R R	M	UV	DDP
<i>mat a^{m10} ad-3B cyh-1</i>	10 2-17-114 KH52(r)	6841		IL R R	M	UV	DDP
<i>mat a^{m12} ad-3B cyh-1</i>	12 2-17-114 KH52(r)	6842		IL R R	M	UV	DDP
<i>mat a^{m24} ad-3B cyh-1</i>	24 2-17-114 KH52(r)	6843		IL R R	M	UV	DDP
<i>mat a^{m26} ad-3B cyh-1</i>	26 2-17-114 KH52(r)	4567		IL R R	M	UV	AJG
<i>mat a^{m30}</i>	30	7450		IL	M	UV	RLM
<i>mat a^{m30} ad-3B</i>	30 2-17-114	6844		IL R R	M	UV	DDP
<i>mat a^{m33}</i>	33	5382		IL	M	UV	AJG
<i>mat a^{m33} ad-3B cyh-1</i>	33 2-17-114 KH52(r)	4568		IL R R	M	UV	AJG
<i>mat A^{m42} un-3 ad-3A</i>	42 55701(t) 2-17-814	4569		IL L R	M	UV	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R			

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
MAT A/a MATING TYPE , continued from previous page							
<i>mat A^{m44} un-3 ad-3A</i>	44 55701(t) 2-17-814	4570		IL L R	M	UV	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R			
<i>mat A^{m54} un-3 ad-3A</i>	54 55701(t) 2-17-814	4571		IL L R	M	UV	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R			
<i>mat A^{m56} un-3 ad-3A</i>	56 55701(t) 2-17-814	4572		IL L R	M	UV	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R			
<i>mat A^{m64} un-3 ad-3A</i>	64 55701(t) 2-17-814	4573		IL L R	M	UV	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R			
<i>lys-1; thi-4 ad-2</i>		8292		VL; III III			RLM
<i>mat A^{del}::ADE5^{SC}</i>				I -			
<i>mat ΔA::ADE5;inl</i>		8322			OR		RLM
<i>mat ΔA::ADE5;inl;ad-2</i>		8323			OR		RLM
<i>mat ΔA::ADE5 his-3; inl</i>		8324			OR		RLM
<i>mat ΔA::ADE5 his-3; thi-4 ad-2</i>		8325			OR		RLM
<i>mat ΔA::ADE5 his-3</i>		8326			OR		RLM
<i>mat ΔA::ADE5; Δam::mat-A</i>		8327			OR		RLM
<i>mat ΔA::ADE5; Δam::mat-A inl</i>		8328			OR		RLM
<i>mat ΔA::ADE5 his-3; Δam::mat-A</i>		8329			OR		RLM
MAT (see <i>rug</i>)							
MALE BARREN							
<i>mb-1</i>	V8455	3562	3563	VII	M	UV	DDP
<i>mb-2</i>	V8553	3564	3565	I	M	UV	DDP
<i>mb-3</i>	V5538	3566	3567	IR	M	UV	DDP
MICROCYCLE CONIDIATION							
<i>mcb</i>	no#		7094	VR	SL5	S	RM
<i>mcb</i>	no#		7453	VR	SL7		RM
<i>mcb</i>	no#		7454	VR	SL7		RM
<i>mcm</i>	no#	7089	7090	IIL	SL5	S	RM
<i>mcm</i>	no#	7455		IIL	SL9		RM
<i>mcm</i>	no#		7456	IIL	SL9		RM
MAD							
<i>md</i>	MW84		1296	VR	M		AS
MATERNAL INHERITANCE [<i>mi</i>] see Part IV							
METHYLAMMONIUM RESISTANT							
<i>mea-1</i>	no#	4537		IL	SL	UV	RHG
MEDUSA							
<i>med</i>	R2401	4341	1403	IV	M	S	ELT
MEIOTIC							
<i>mei-1</i>	no#	2919	2920	IVR	M	M	DDP
<i>Mei-2</i>	ALS181	2621		VR	M	UV	DAS
<i>Mei-2</i>	ALS181	6944	6945	VR	SL4	UV	ALS
<i>Mei-2;rg-1 cr-1</i>	ALS181;B53 B123		2622	VR;IC R	M	UV	DAS
<i>Mei-2;nic-3</i>	ALS181;Y31881		5889	VR;VIII			EK
<i>mei-3</i>	CF-3	6187	6188	IL	SL3	S	DDP
<i>mei-3</i>	JL102		6189	I	M	UV	NBR
<i>mei-3</i>	N289	2764		IL	SL3	S	DNP
<i>mei-3 sn cr-1 al-2;</i>	SC25 C136 B123 15300;	3908		I IC R R;	M	NG	NCM
<i>pan-1;al-3 inl</i>	5531;RP100 83201(t)			IVR;VR R			
<i>mei-3;sn (cr-1?)</i>	SC29;C136 (B123?)	3909		--;IR;	M	NG	NCM
<i>al-2;pan-1;al-3 inl*</i>	15300;5531;RP100 83201(t)			IVR;VR			

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
MEIOTIC , continued from previous page							
<i>mei-3;tol</i>	N289;N83		2765	IL;IVR	SL3	S	DNP
<i>mei-3^{pr1}</i>	N289(pr)		2936	I	M	S	DNP
<i>mei-4</i>	N395		2762	IIIR	M	S	DNP
<i>mei-4;arg-3</i>	N395;30300	2763		IIIR;IL	M	S	DNP
* Abnormal <i>sn cr-1</i> phenotype; possibly changed by secondary mutation							
MELON allelic with <i>do(?)</i>							
<i>mel-1</i>	C-L2B	185		VIII	SL	P	DDP
<i>mel-2</i>	see <i>bal</i>						
6-METHYLPURINE RESISTANT							
<i>mep</i>	LP10(r)	6012	6013	IL	M	UV	DDP
<i>mep(3)</i>	3(r)	3568	7468	IL	M	UV	AMW/RLM
METHIONINE							
<i>met-1</i>	35599	317	922	IVR	M	UV	NHH
<i>met-1</i>	35599		3281	IVR	SL		NEM
<i>met-1</i> het Cde	38706	3049	3050	IVR	M	UV	EGB
<i>met-1</i>	38706		559	IVR	M	UV	RWB
<i>met-1</i>	K59		3274	IVR	E	UV	NEM
<i>met-1</i>	NM65(t)		1277	IVR	E	UV	NEM
<i>met-1</i>	NM66(t)		1278	IVR	E	UV	NEM
<i>met-1</i>	NM298		3276	IVR	E	UV	NEM
<i>met-2</i>	48004	316		IVR	M	UV	NHH
<i>met-2</i>	H98	283	201	IVR	E3	X	NEM
<i>met-2</i> het Cde	K5		3282	IVR	SL	UV	NEM
<i>met-2</i>	K23		200	IVR	E3	UV	NEM
<i>met-2</i>	K43	4061		IVR	SL5		EK
<i>met-2</i>	K44		199	IVR	M	UV	NEM
<i>met-2</i>	NM301(t)		1279	IVR	M	UV	NEM
<i>met-2</i>	P81		198	IVR	M	UV	NEM
<i>met-2</i>	P99		197	IVR	M	UV	NEM
<i>met-2</i>	P133		196	IVR	M	UV	NEM
<i>met-2</i>	P140		195	IVR	M	UV	NEM
<i>met-2</i>	P159	4062		IVR	SL5		EK
<i>met-2</i>	P169		194	IVR	M	UV	NEM
<i>met-3</i>	36104	112	502	VR	M	UV	DDP/NEM
<i>met-3 inl</i>	92935 37401	2159		VR R	M	UV	GAM
<i>met-4</i>	see <i>cys-10</i>						
<i>met-5</i>	9666	3861	3862	IVR	M	X	DDP
<i>met-5</i>	86304	319		IVR	M	M	NHH
<i>met-5</i>	K22	3277	3283	IVR	E/SL	UV	DDP
<i>met-5</i>	K55		3278	IVR	E	UV	NEM
<i>met-5</i>	K62		3279	IVR	E	UV	NEM
<i>met-5</i>	NM307(t)		1280	IVR	M	UV	NEM
<i>met-6</i>	35809	1330	301	IR	M/E3	UV	DNP/NEM
<i>met-6</i>	S2706	4248	4249	IR	SL		DNP
<i>met-7</i>	4894	4087	4088	VIIC	SL7	X	EK
<i>met-7</i>	39103	777	4340	VIIR	M	UV	DGC/ELT
<i>T(I;VII)K79 met-7</i>	K79	2297	2298	I;VIIR			DDP
<i>met-7 wc-1</i>	NM56 P829		3928	VIIR R	E	UV	DDP
<i>met-7 thi-3</i>	NM251 18558		3915	VIIR R	E	UV	DDP
<i>met-7 wc-1</i>	NM251 P829	3914		VIIR R	E	UV	DDP
<i>met-7</i>	NM297(t)	1281		VIIR	E	UV	NEM
<i>met-7 met-9 wc-1</i>	NM331 NM43(t) P829	3607		VIIR R R			AR
<i>met-8</i>	P53	5090	98	IIIR	SL/E2	UV	DDP
<i>met-9</i>	C124	552	3280	VIIR	M	UV	DDP
<i>met-9</i>	NM43(t)		1282	VIIR	M	UV	NEM

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
METHIONINE , continued from previous page							
<i>met-10</i>	PD1(t)	2937	2938	IR	SL2	UV?	DNP
<i>met(26U);inl</i>	26U(t);89601		3762	IVR;VR	M	UV	DRS
<i>met(105W);inl</i>	105W(t);89601		3764	IVR;VR	M	UV	DRS
<i>met(119W);inl</i>	119W(t);89601		3765	--;VR	M	UV	DRS
<i>met(152C) inl</i>	152C(t) 89601		3759	V(?) VR	M	UV	DRS
<i>met(T27)</i>	T27		969	--	E	UV	FJL
<i>met(T70)</i>	T70	970		I or II	E	UV	FJL
<i>met(T112)</i>	T112	971		--	E	UV	FJL

MIGRATION OF TREHALASE see *tre*

6-METHYLPURINE RESISTANT see *mep*

4-METHYLTRYPTOPHAN RESISTANT see *mtr*

5-METHYLTRYPTOPHAN SENSITIVE see *cpc*

MORPHOLOGICAL

<i>mo-1</i>	R2436	4361	4439	I	M	UV	ELT/DDP
<i>mo-2</i>	R2464	1394		VII	M	UV	ELT
<i>mo-4</i>	R2467	3912	3913	IIIR	SL3	UV	DDP
<i>mo-5</i>	R2487	4251	4252	IL	SL		DDP
<i>mo(36703-4-20)</i>	36703-4-20		1671	VI	M	UV	DDP
<i>mo(AR501)</i>	AR501	5932		II	SL2	A	DDP
<i>mo(B8)</i>	B8	1648		IIIR	SL	UV	DDP
<i>mo(B107)</i>	B107	1663		VR	SL3	UV	DDP
<i>mo(D301)</i>	D301		1640	IR			DDP
<i>mo(D306)</i>	D306		1659	IVR	M	UV	DDP
<i>mo(D309)</i>	D309	1647		II	M	UV	DDP
<i>mo(D314)</i>	D314		1660	IVR	M	UV	DDP
<i>mo(D318)</i>	D318	1668		V	M	UV	DDP
<i>mo(KH161);acr-5</i>	KH161;KH27(r)	2323	2324	--;IIR	M	G	KSH
<i>mo(M126)</i>	M126	1649		IIIR	M	S	DDP
<i>mo(M184)</i>	M184	4367	1634	IC	M/SL3	S	ELT/DDP
<i>mo(M193-1)</i>	M193-1	1635		IC	SL3	S?	DDP
<i>mo(NM119)</i>	NM119		1657	IVR	M	UV	DDP
<i>mo(NM201f)</i>	NM201f	1676		II	M	UV	DDP
<i>mo(NM203)</i>	NM203		1636	I	E	UV	DDP
<i>mo(NM211)</i>	NM211	1650		IIIR	E	UV	DDP
<i>mo(NM216s)</i>	NM216s		1639	I	E	UV	DDP
<i>mo(NM218)</i>	NM218		1645	II	E	UV	DDP
<i>mo(NM219)</i>	NM219		1651	III	M	UV	DDP
<i>mo(NM220)</i>	NM220		1646	II	M	UV	DDP
<i>mo(NM226)</i>	NM226	1672		VIIC	M	UV	DDP
<i>mo(NM359)</i>	NM359	1661		IVR	M	UV	DDP
<i>mo(P1135)</i>	P1135	1670		VIL	S		DDP
<i>mo(P1417)</i>	P1417	1641		IR	M	S	DDP
<i>mo(P1718)</i>	see <i>sk</i> allele P1718						
<i>mo(P1898)</i>	P1898		1662	VR	M	S	DDP
<i>mo(P3816)</i>	P3816	7340	7341	IVR	SL	S	DDP
<i>mo(R2374s)</i>	R2374s	7026	7027	IIIR	M		DDP
<i>mo(R2374)</i>	R2374	7311	7312	IIIR			DDP
(<i>mo(R2374) A +</i>							
<i>a^{ml} ad-3B cyh-1</i>)	R2374(3828-3)	7309	7310				DDP
<i>mo(VP103)</i>	VP103	8309	8310	IR	OR		DDP

MODIFIER OF PERMEABILITY

<i>mod-5</i>	no#		1603	VI	SL	UV	PSL
--------------	-----	--	------	----	----	----	-----

MODIFIER OF SCUMBO

<i>mod(sc) pan-1</i>	KH251 5531	1162	1163	IVR R	M	S	KSH
----------------------	------------	------	------	-------	---	---	-----

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
MORPHOLOGICAL-ENVIRONMENT SENSITIVE							
<i>moe-1</i>	Y6821	4272		VIIR	L	MC	ELT
<i>moe-2;inl</i>	R2532;89601	1386		VIC;VR	M	UV	ELT
4-METHYLTRYPTOPHAN RESISTANT							
<i>mtr</i>	6(r)	3043	3288	IVR	M	UV	DDP
<i>mtr col-4;su(mtr)</i>	10(r) 70007c;21-2	1719		IVR R;IC	M		DRS
<i>mtr col-4;his-2</i>	10(r) 70007c;Y152M43		1720	IVR R;IR			DRS
<i>mtr col-4;his-2</i>	14(r) 70007;Y152M43		3016	IVR R;IR			DRS
<i>mtr</i>	15(r)	4057	4058		SL8		EK
<i>mtr;su(mtr)</i>	21(r);21-0	1718		IVR;IR	M		DRS
<i>mtr;pdx-1;his-2</i>	26(r);37803;Y142M43		2728	IVR R;IR			NGB
<i>mtr;pdx-1;his-2</i>	26-R1364*(s);37803;Y142M43		2731	IVR R;IR			NGB
<i>mtr;pdx-1;his-2</i>	26-R1373*(s);37803;Y142M43		2729	IVR R;IR			NGB
<i>mtr;pdx-1;his-2</i>	26-R2435*(s);Y142M43;37803		2730	IVR R;IR			NGB
<i>mtr col-4;his-2</i>	30(r) 70007;Y152M43		3017	IVR R;IR	M	UV	DRS
<i>mtr;pdx-1;his-2</i>	112(r);37803;Y152M43	3018		IVR R;IR	M	UV	DRS
<i>mtr;pdx-1;his-2</i>	119(r);37803;Y152M43	3020		IVR R;IR	M	UV	DRS
<i>mtr;pdx-1;his-2</i>	120(r);37803;Y152M43	3021		IVR R;IR	M	UV	DRS
<i>mtr;pdx-1;his-2</i>	121(r);37803;Y152M43	3022		IVR R;IR	M	UV	DRS
<i>mtr(t-1)[†]</i>	1560(r)/(t;r)	3023		IVR;IR;IVRM		UV	DRS
<i>mtr(t-2)[†]</i>	1561(r)/(t;r)	3024		IVR;IR;IVR M		UV	DRS
<i>mtr(t-3)[†]</i>	1562(r)/(t;r)	3025		IVR;IR;IVR M		UV	DRS
<i>mtr(t-4)[†]</i>	1563(r)/(t;r)	3026		IVR;IR;IVR M		UV	DRS
<i>mtr(t-5)[†]</i>	1564(r)/(t;r)		3027	IVR;IR;IVR M		UV	DRS
<i>mtr(t-6)[†]</i>	1565(r)/(t;r)	3028		IVR;IR;IVR M		UV	DRS
<i>mtr(t-7)[†]</i>	1566(r)/(t;r)	3029		IVR;IR;IVR M		UV	DRS
<i>mtr(t-8)[†]</i>	1567(r)/(t;r)	3030		IVR;IR;IVR M		UV	DRS
<i>mtr(t-9)[†]</i>	1568(r)/(t;r)	3031		IVR;IR;IVR M		UV	DRS
<i>mtr</i>	flr271(s) [‡]	1317		IVR		Co-60	SRG
<i>mtr</i>	flr354(s) [‡]	1318		IVR		UV	SRG
<i>mtr</i>	flr380(s) [‡]	1319		IVR		UV	SRG
<i>mtr(pmn)</i>	Pm-22(r)	2274		IVR	M	UV	LW
<i>mtr(pmn)</i>	Pm-22(r)	4812	4813	IVR	SL		RMD
<i>mtr pmb</i>	Pm-22(r) can-37(r)		2276	IVR R		Co-60	SRG
<i>mtr;pmg</i>	Pm-22(r);no#	4808	4809	IVR;IIL	SL		RMD
<i>mtr</i>	SR33	7539	7538	IVR		S	RLM
<i>mtr</i>	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

[‡] trifluoroisoleucine sensitive

5-METHYLTRYPTOPHAN SENSITIVE see *cpc-1*

MUTAGEN SENSITIVE

<i>mus-7</i>	FK107	5142	5143	IIR	SL7	NG	EK
<i>mus-7</i>	FK116	6401	6402	IIR	SL2	4-NQO	EK
<i>mus-8</i>	FK108	5144	5145	IVR	SL7	NG	EK
<i>mus-9</i>	FK104	5146	5147	IR	SL7	NG	EK
<i>mus-9</i>	FK129	6403	6404	IR	SL4	4-NQO	EK
<i>mus-10</i>	FK110	5148	5149	VIIR	SL7	NG	EK
<i>mus-11</i>	FK111	5150	5151	VR	SL7	NG	EK
<i>mus-11</i>	FK117	6409	6410	VR	SL4	4-NQO	EK
<i>mus-12 al-3 inl;</i> <i>pan-1</i>	SC15 RP100 83201(t);5531	3906		VR R R; IVR	M	NG	NCM
<i>mus-14;al-2;pan-1</i>	SC3;15300;5531		3903	VIL;IR;IVR	M	NG	NCM
<i>mus-15 al-2;cot-1;</i> <i>pan-2</i>	SA7 Y112M38;C102(t); Y387-15.7	7296	7297	IC IR; IVR;V	SL	UV	HI
<i>mus-16;al-2;pan-2</i>	JMB15.2;Y112M38;Y387-15.7	6820	6821	V;IR;IVR	SL3	M	HI

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
MUTAGEN SENSITIVE , continued from previous page							
<i>mus-17</i>	SA17	7298	7299	IVR	SL	UV	HI
<i>mus-18;al-2;cot-1;pan-2</i>	SA8B;Y112M38;C102(t); Y387-15.7a	7137	7138	VL;IR; IVR;VIR	SL3	UV	HI
<i>mus-19 al-2;pan-2</i>	SA19 Y112M38;Y387-15.7	7300	7301	IR IR;VIR	SL	UV	HI
<i>mus-20;al-2;cot-1;pan-2</i>	SA2;Y112M38;C102(t); Y387-15.7	7302	7303	IIIR;IR; IVR;VIR	SL		HI
<i>mus-21</i>	FK120	6418	6419	IIIR	SL2	4-NQO	EK
<i>mus-21</i>	FK121	6414	6415	IIIR	SL6	4-NQO	EK
<i>mus-21</i>	FK127	6422	6423	IIIR	SL2	4-NQO	EK
<i>mus-21</i>	SC10	5890	5891	IIIR	M	NG	EK
may contain <i>T(II;III;VI)</i>							
<i>mus-21</i>	FK131	6459	6460	IIIR	SL2	UV	EK
<i>mus-21</i>	FK132	6463	6464	IIIR	SL2	UV	EK
<i>mus-22</i>	SA22	7304	7305	IR	SL		HI
<i>al-2; pan-2; mus-23</i>	Y112M38, Y387-15.7, SA23	8341	8342	IR; VI;II	OR		HI
<i>mus-24</i>	SA24	8344	8343	II			HI
<i>mus-25</i>	FK123	6424	6425	VIII	SL4	4-NQO	EK
<i>mus-26;al-2;cot-1 pan-2</i>	SA3B;Y112M38; Y387-15.7 C102(t)	6822	6823	IVR;IR; IVR;VIR	SL	S	HI
<i>mus-27</i>	FK124	6428	6429	IIR	SL4	4-NQO	EK
<i>mus-28</i>	FK118	6434	6435	IIIR	SL4	4-NQO	EK
<i>mus-29</i>	FK119	6438	6439	VIR	SL4	4-NQO	EK
<i>mus-30</i>	FK115	6444	6445	IVR	SL4	4-NQO	EK
<i>mus-38</i>	SA56	8352	8351	I	OR		HI
<i>mus-39</i>	FK133	6467	6468	VI	SL2	UV	EK
<i>mus(FK125)</i>	FK125	6450	6451	--	SL4	UV	EK
<i>mus(FK128)</i>	FK128	6456	6457	--	SL4	UV	EK
<i>mus(SC1);pan-1</i>	SC1;5531	3902		--;IVR	M	NG	NCM
<i>mus(SC13) al-2;pan-1</i>	SC13 15300;5531		3905	IR R;IVR	M	NG	NCM
<i>mus(SC17);al-3 inl;pan-1</i>	SC17;RP100 83201(t);5531		3907	V;IR; IVR;VR	M	NG	NCM
NAD(P) GLYCOHYDROLASE DEFECTIVE							
<i>nada</i>	61	2687	2688	IVC	SL3	EMS	REN
<i>nada</i>	62(t)	2689	2690	IVC	SL3	EMS	REN
<i>nada</i>	64	2691	2692	IVC	SL3	EMS	REN
<i>nada</i>	65	2693	2694	IVC	SL3	EMS	REN
<i>nada</i>	100	2695	2696	IVC	SL3	EMS	REN
NEUTRAL AND ACIDIC AMINO ACID PERMEABILITY							
<i>nap</i>	no#	1604		V	SL2	UV	ESJ
NATURAL DEATH							
<i>(nd al-2 a + lys-1 a)</i>			3572	IR	SL7	UV	KDM
<i>(nd al-2;lys-1 a + helper)</i>			3571	IR	SL7	UV	KDM
<i>(nd al-2;lys-1 a + helper)</i>			3570	IR	SL7	UV	KDM
<i>(nd al-2 nic-1 a + pan-2 a)</i>			6878	IR	SL	UV	BSR
NUCLEAR DIVISION CYCLE							
<i>ndc-1 inl</i>	1(t) 89601	7867	3441	VR R	M	UV	DDP/DRS
NEUTRAL AMINO ACID TRANSPORT							
<i>neu^a;his-3</i>	no#;K57	3272		--;IR	E	UV	CWM
<i>neu^a;his-2</i>	no#;HS-24	3273		IVR(?);IR	E	UV	CWM

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
NICOTINIC ACID							
<i>nic-1 os-1 al-1</i>	3416 B135 34508	3584		IR R R			DDP
<i>nic-1</i>	3416	8248	561	IR	M	X	RWB
<i>nic-1</i>	39113	765		IR	SL7	UV	PSL
<i>nic-1</i>	S1413	763	764	IR	SL7	X	PSL
<i>T(I-V)S1325 nic-2</i>	S1325	1558	1557	IR;VR		X	DDP
<i>T(I-III)4540 nic-2</i>	4540	766	767	IR;IIIR;IR			PSL
<i>nic-2</i>	39303		371	IR	M	UV	MBM
<i>nic-2</i>	43002	2527		IR	SL	UV	CPS
<i>nic-2</i>	43002	4006	4007	IR	SL9	UV	EK
<i>nic-2</i>	Y31455	770	771	IR	SL7	M	PSL
<i>nic-3</i>	Y31881	2528		VIIL	SL	M	CPS
<i>nic-3</i>	Y31881	4081	4082	VIIL	SL7	M	EK
NITRATE NONUTILIZATION							
<i>nit-1</i>	34547	54	32	IR	M	UV	DDP
<i>nit-2</i>	I7	2698		IL	SL	UV	GAM
<i>nit-2</i>	K31	33		IL			DDP
<i>nit-2 leu-3</i>	KGP0220 R156	6024		IL L	M	UV	GAM
<i>nit-2</i>	nr37	983	982	IL	SL	UV	GS
<i>nit-3</i>	KGP026	6028		IVR	M	UV	GAM
<i>nit-3</i>	KGP0213	6027		IVR	M	UV	GAM
<i>nit-3</i>	KGP1222	6026		IVR	M	UV	GAM
<i>nit-3</i>	KGP1211	6025		IVR	M	UV	GAM
<i>nit-3</i>	14789	3009	358	IVR	M	X	DDP
<i>nit-4</i>	no#	2993	2994	IVR	SL3		DDP
<i>nit-5=4</i>	nr15	985	984	IVR	SL	UV	GS
<i>nit-6</i>	OP4	3463	3464	VI	SL	NG	OCY
<i>nit-7</i>	V1M59	3933		IIIR	M	UV	RHG
<i>nit-8</i>	V1M44	4236	4237	IR	M	UV	DDP
<i>nit-9A</i>	V1M5	3935	8197	IVR	M	UV	RHG
<i>nit-9B</i>	V1M32	8196	3936	IVR	M	UV	RHG
<i>nit-9C</i>	V1M50	3937	8195	IVR	M	UV	RHG
<i>nit(25376)</i>	25376		653	IV	M	X	MJM
<i>nit(JH2003)</i>	JH2003	6011	2384	--	M		FGSC/DDP
NITROGEN METABOLITE REGULATION							
<i>nmr-1</i>	MS5	4609	4610	VR	SL	NG	RMD
<i>nmr-1</i>	V2M304	4611	4612	VR	SL	UV	RMD
NICOTINIC ACID OR TRYPTOPHAN							
<i>nt</i>	295	2438	2439	VIIR	M	NG	FHG
<i>nt</i>	39401	4348	563	VIIR	M	UV	ELT/RWB
<i>nt</i>	65001	4089	4090	VIIR	SL6	UV	EK
<i>nt</i>	A370	1736	1711	VIIR	M	UV	MA
<i>nt</i>	C86	4349	869	VIIR	M	UV	ELT
NUCLEASE DEFICIENT							
<i>nuc-1</i>	T28-M1 (Also A1)	1995	1994	IR	M	UV	TI
<i>nuc-1^C</i>	BC-152		3947	IR	UV		RLM
<i>nuc-2</i>	T28-M2 (Also B1)	1996	1997	IIR	M	UV	TI
<i>nuc-2 (pcon^C)</i>	UW6	2534		IIR	M	UV	RLM
<i>nuc-3</i>	701	4909		IIR	SL	NG	NCM
<i>nuc-3;pan-2</i>	701;1-153-96		4910	IIR;VIR	SL	NG	NCM
<i>nuc-4</i>	51		4911	IIR	SL	NG	NCM
<i>nuc-5;inl</i>	276;83201(t)		4912	IIR;VR	SL	NG	NCM
<i>nuc-6</i>	936	4913		IIR	SL	NG	NCM
<i>nuc-6;inl</i>	936;83201(t)		4914	IIR;VR	SL	NG	NCM
<i>nuc-7</i>	24	4915		IIR	SL	NG	NCM

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
NUCLEASE DEFICIENT , continued from previous page							
<i>nuc-7;pan-2</i>	24;1-153-96		4916	IIR;VR	SL	NG	NCM
NUCLEASE HALO							
<i>nuh-1</i>	FK001	4180	4181	IIIR	SL9	NG	EK
<i>nuh-2</i>	FK027	4182	4183	IIIR	SL7	NG	EK
<i>nuh-3</i>	FK003	4184	4185	VR	SL9	EMS	EK
<i>nuh-5</i>	FK005	4186	4187	IIR	SL9	EMS	EK
<i>nuh-6</i>	FK006	4188	4189	ICR	SL8	EMS	EK
<i>nuh-7</i>	FK017	4591	4592		SL6	NG	EK
<i>nuh-8</i>	FK018	4593	4594	IR	SL6	UV	EK
<i>nuh-9</i>	FK037	4595	4596	IIR	SL6	NG	EK
<i>nuh-10</i>	FK028	4597	4598	VIR	SL6	NG	EK
<i>nuh</i>	FK019	4599	4600		SL6	NG	EK
<i>nuh</i>	FK022	4601	4602		SL9	NG	EK
<i>nuh</i>	FK041	4603	4604		SL4	NG	EK
<i>nuh</i>	FK042	4605	4606		SL5	NG	EK
NYSTATIN RESISTANT see <i>erg</i>							
OAK							
<i>oak</i>	R2358		4579 4580	VR	M		DDP
OLIGOMYCIN RESISTANT							
<i>oli</i>	16-16	8739	8739	VIIR			RLM
<i>oli; csp-1; bd</i>	16-16; UCLA37; no#	3483		VIIR; IL; IVR	M		SB
<i>oli; csp-1; bd</i>	CD-5; UCLA37; no#	6706		VIIR; IL; IVR	M		SB
ORNITHINE see <i>arg-5, -6, -7</i>							
OSMOTIC							
<i>os-1</i>	AR2	1675		IR	M	S	DDP
<i>os-1</i>	B135	951	810	IR	SL4/SL2	UV	DDP
<i>os-1</i>	E11200	47	34	IR	M		DDP
<i>os-1</i>	171-1		3901	--	RL		NCM
<i>os-1</i>	M16	812	813	IR	SL3	UV	DDP
<i>os-1</i>	M155-1	824		IR	M	S	DDP
<i>os-1</i>	NM204(t)	1637	2273	IR	E/M	UV	DDP
<i>os-1</i>	NM233t	4493	4494	IR	SL6	UV	DDP
<i>os-1 al-2</i>	P641 15300		866	IR R	M	S/os	DDP
<i>os-1</i>	P668		973	IR	M	S	DDP
<i>os-1</i>	P3282		1508	IR	M	S	DDP
<i>os-1</i>	P5990	2432		IR	SL	S	DDP
<i>os-1</i>	P6549		2584	IR	M	S	DDP
<i>os-1 (=flm-1)</i>	Y256M209	3624	3625	IR	SL	UV	DDP
<i>os-2</i>	ALS10	1509	1510	IVR	M	S	DDP
<i>os-2</i>	UCLA80	2238	2239	IVR	SL	EMS	CPS
<i>os-4</i>	NM201o	2429	2430	IL	M	UV	DDP
<i>(os-4; pan-2 a + a^{ml} ad-3B cyh-1)</i>	NM201o + 1 2-17-114 KH52(r)		5894	IL; VIR	SL		DDP
<i>os-4 (=flm-2)</i>	Y256M223	6040	6041	IL	SL	UV	DDP
<i>(os-4 + a^{ml} ad-3B cyh-1)</i>	Y256M223 + 1 2-17-114 KH52(r)	6042	6043	IL	SL		DDP
<i>os-5</i>	NM216o	1638	4576	IR	M	UV	DDP/FGSC
<i>os-5</i>	P5341	2310		IR	M	S	DDP
<i>os-5</i>	UCLA84		2243	IR	SL4	EMS	CPS
<i>os-6</i>	14-3		3896	--	RL		NCM
<i>os-6</i>	56-4	3898		--	RL		NCM
<i>os-6</i>	171-7		3900	--	RL		NCM
<i>os(P3282)</i>	P3282		1644	IR	M	S	DDP

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ORNITHINE TRANSAMINASE DEFECTIVE							
<i>ota</i>	UM728	1700	1701	IIIR	SL3	UV	RHD
OVERACCUMULATOR OF CAROTENOIDS							
<i>ovc</i>	S20-16		4503	IVR	M	UV	RWH
D-AMINO ACID OXIDASE DEFICIENT							
<i>oxD (cys-15)</i>	1	1872	888	IVR	M	UV	DDP/NHH
<i>oxD</i>	8		889	IVR	M	UV	NHH
<i>oxD</i>	9	890		IVR	M	UV	NHH
<i>oxD</i>	11	891		IVR	M	UV	NHH
<i>oxD</i>	13		892	IVR	M	UV	NHH
p-AMINO BENZOIC ACID							
<i>pab-1</i>	830	496		VR	M	X	RWB
<i>pab-1</i>	1633	5953	3863	VR	M	X	DDP
<i>pab-1</i>	5359	564	4359	VR	M	UV	ELT
<i>pab-1</i>	21850	4358	8190	VR	L	X	ELT
<i>pab-1</i>	36111	363	8189	VR	M	UV	MBM
<i>pab-1</i>	38113	367	8249	VR	M	UV	MBM
<i>pab-2</i>	H193	4076	4077	VR	SL9	X	EK
PANTOTHENIC ACID							
<i>pan-1</i>	5531	4063	4064	IVR	SL7	X	EK
<i>pan-1</i>	S1246	5015	8192	IVR	SL		FGSC
<i>pan-2</i>	B2(Y153M66)	465	466	VIR	SL	X	MEC
<i>pan-2</i>	B3(Y153M96)	2248	2249	VIR	SL		OMM
<i>pan-2</i>	B5(Y154M64)	4103	4104	VIR	SL8	X	EK
<i>pan-2</i>	B36	4105	4106	VIR	SL8		EK
<i>pan-2;al-2;</i>	Y387-15.7;Y112M38;	2583		VIR;IR;	SL		FJD
<i>cot-1</i>	C102(t)			IVR			
Additional <i>pan-2</i> strains from Dr. M. Case are available. Please inquire if you are interested.							
PATCH							
<i>pat</i>	no#		981	IC	M		AS
PHOSPHATASE CONTROL see <i>nuc-2</i>							
PYRIDOXINE							
<i>pdx-1</i>	35405(t)	1408	1407	IVR	M	UV	AR
<i>pdx-1</i>	37803	4055	4056	IVR	SL7	UV	EK
<i>pdx-1</i>	39106(p)	1410	1409	IVR	M	UV	AR
<i>pdx-1</i>	39706(p)		1415	IVR	M	UV	AR
<i>pdx-1</i>	44204(p)	1413	1414	IVR	M	UV	AR
<i>pdx-1</i>	44602(p)	1412	1411	IVR	M	UV	AR
<i>pdx-1</i>	46904(p)	1417	1416	IVR	M	UV	AR
<i>pdx-1</i>	Y2329	1419	1418	IVR	M	UV	AR
<i>pdx-1</i>	Y30978	1313	3261	IVR	M	M	AR/ELT
<i>pdx-1</i>	Y31393	1314	1420	IVR	M	M	AR
<i>pdx(Y12274)</i>	Y12274	1312	1421	IVR	M	UV	AR
PEACH							
<i>pe</i>	L		567	IIR	L	S	ELT
<i>pe</i>	Y8743m	4036	4037	IIR	SL6	S?	EK
<i>pe</i>	no# (Sansome)		645	IIR	M		MJM
<i>pe arg-12</i>	Y874m, UM107	7656	7657	IIR,R			DDP
PERITHECIAL NECK							
<i>pen-1</i>	DL413	5830	5831	VII	SL	NG	DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
PERITHECIAL COLOR							
<u>Type I:</u>							
<i>per-1;ad-2</i>	ABI1;STL2	2547		VR;IIIR	M	UV	TEJ
<i>per-1;ad-2</i>	ABT8;STL2	2551		VR;IIIR	M	UV	TEJ
<i>per-1</i>	AR174	7035	4318	VR	SL	UV	HBH/DDP
<i>per-1</i>	P760*	6708	6709	VR	SL6	S	DDP
<i>per-1;pyr-3</i>	PBE1;KS43	2546		VR;IVR	M	UV	TEJ
<i>per-1</i>	PBJ1	3309	3310	VR	SL	UV	DDP
<i>per-1;csp-2</i>	PBJ1;UCLA101	6662	6663	VR;VIII	SL		DDP
<i>per-1;pyr-3</i>	PBP1;KS43	2550		VR;IVR	M	UV	TEJ
<i>per-1;pyr-3</i>	PBT4;KS43	2552		VR;IVR	M	UV	TEJ
<i>per-1;pyr-3</i>	PBT5;KS43	2553		VR;IVR	M	UV	TEJ
<i>per-1 al-3; csp-2</i>	AR174, RP100; UCLA 101	8412	8413	VR VR;VIII			DDP
* originated in <i>N. intermedia</i>							
<u>Type II:</u>							
<i>per-1</i>	29-278	2954		VR	SL	NG	HBH
<i>per-1</i>	29-281	2955		VR	SL	S	HBH
<i>per-1</i>	DL126	5787	5788	VR	SL	NG	DDP
<i>per-1</i>	UG1837	4558	4559	VR	SL2	S	DDP
PERMEASE GENERAL AMINO ACID see <i>pmg</i>							
PUFF							
<i>pf</i>	B141	419	420	IVR SL2		UV	DDP
POLYUNSATURATED FATTY ACIDS							
(<i>pfa-1</i> +							
<i>a^{ml} ad-3B cyh-1</i>)	no #	7942		VII	SL		MT
(<i>pfa-2</i> +							
<i>a^{ml} ad-3B cyh-1</i>)	no #		7943	-	SL		MT
(<i>pfa-3</i> +							
<i>a^{ml} ad-3B cyh-1</i>)	no #	7944		-	SL		MT
(<i>pfa-4</i> +							
<i>a^{ml} ad-3B cyh-1</i>)	no #	7945		VII	SL		MT
(<i>pfa-5</i> +							
<i>a^{ml} ad-3B cyh-1</i>)	no #		7946	-	SL		MT
PHOSPHORUS GOVERNANCE							
<i>pgov^C</i>	5		3479	IIIR	SL	UV	RLM
<i>pgov^C</i>	12		3478	IIIR	SL	UV	RLM
<i>pgov^C;nuc-1</i>	R42;T28-M1	3480		IIIR;IR	M	UV	RLM
PHENYLALANINE							
<i>phe-1</i>	H3791		504	IL	M	S35	RWB
<i>phe-1</i>	H6196	1096	492	IL	M	S35	DNP/RWB
<i>phe-1</i>	NM160	1294	1295	IL	SL2	UV	DDP
<i>phe-1</i>	UA119;89601	1167		IL;VR	M	NA	KKJ
<i>phe-2</i>	E5212	873		IIIR		AGD	
<i>phe-2 tyr-1;trp-2</i>	E5212 C167;75001		3255	IIIR R;VIR		RLM	
<i>phe-2(phe-3)</i>	Y16329	1332	1333	IIIR	SL3	X	DDP
PHENYLALANINE + TYROSINE see <i>pt</i>							
PHOSPHATASE-ACID							
<i>pho-3;al-2</i>	221(t);15300	3051	3052	IVR;IR	SL	UV	REN

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
PHOSPHATASE-ALKALINE							
<i>pho-2</i>	JFL134	3061	3062	VR	SL	UV	RLM
<i>pho-2</i>	JFL317		3063	VR	SL	UV	RLM
<i>pho-2</i>	JFL327	3064	3065	VR	SL	UV	RLM
<i>pho-2</i>	JFL341	3066	3067	VR	SL	UV	RLM
<i>pho-2</i>	JFL606	3068	3069	VR	SL	UV	RLM
<i>pho-2</i>	MKG-1	2535		VR	M	UV	RLM
<i>pho-2</i>	MKG-2	2536		VR	SL	UV	RLM
<i>pho-2</i>	RLM20	3057	3058	VR	SL	UV	RLM
<i>pho-2</i>	RLM72	3059	3060	VR	SL	UV	RLM
PHOSPHORUS CONTROL see <i>pcon</i> ^C							
PHOSPHORUS REGULATION see <i>preg</i> ^C							
PHOSPHATE PERMEASE							
<i>pho-4 (van)</i>	BRY1	4636	4637	VIII	L	UV	KEA
<i>pho-4 (van)</i>	BRY8		4638	VIII	L	UV	KEA
<i>pho-4 ; pyr-1</i>	RIP; tt263	8344		VII; IV		RIP	RLM
<i>pho-4; pho-5</i>	RIP; RIP	8347	8348	VII; IV		RIP	RLM
<i>pho-5</i>	RIP	8346		IV		RIP	RLM
<i>hkppsm; pho-4; pho-5</i>	su; RIP; RIP	8349	8350	?; VII; IV			HI
PILE							
<i>pi</i>	B101	4026	4027	IIL	SL9	UV	EK
<i>pi</i>	R2438	6845	6868	IIL	SL3	UV	FGSC
PEAK (=bis)							
<i>pk</i>	B6	277	278	VR	SL	UV	DDP
<i>pk</i>	B12	805		VR	SL	UV	DDP
<i>pk</i>	B30	811		VR	SL	UV	DDP
<i>pk</i>	B230r	1250		VR	SL4	X	DDP
<i>pk</i>	C-1810-1	1074		VR	SL	S	DDP
<i>pk</i>	C-1810-1		1075	VR	SL	S	DDP
<i>pk</i>	D12		822	VR	M	UV	DDP
<i>pk</i>	D312	923	924	VR	M	UV	DDP
<i>pk¹¹ pab-1</i>	17-575 1633?	3420	3421	VR R	SL	UV	AMS
<i>pk¹² pab-1</i>	19-773(peak) 1633?	3422	3423	VR R	SL	DS	AMS
<i>T(V;VII)17-088 pk^D</i>	17-088(dominant peak)	3672	3418	V;VII			DDP/AMS
<i>T(I;V)C-1670 pk</i>	C-1670	483	2761	IR;VR			DDP
PLUG							
<i>pl</i>	B118	96	97	VR	SL3	UV	DDP
PLUMOSE <i>plm</i> - see <i>T(VI;VII)NCRL91 plm</i> , Part VI							
PERMEASE BASIC AMINO ACID							
<i>pmb</i>	UM535 (57A)	1683		IVR	M	UV	WMT
<i>pmb</i>	can-37(r)	4814	4815	IVR	SL	RMD	
<i>pmb</i>	cnr-37(r)	2275		IVR	M	UV	LW
<i>pmb;pmg</i>	can-37(r);no#	4810	4811	IVR;IIL	SL		RMD
<i>pmb;aga</i>	DF101;UM906	7924	7925	IVR;VIIR		UV	RHD
PERMEASE GENERAL AMINO ACID							
<i>pmg</i>	FS667	4613	4614	IIL	M	UV	RMD
PERMEASE NEUTRAL AMINO ACID - see <i>mtr</i>							
POKY [<i>mi-1</i>] see Part IV							

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
PROTOPERITHECIA/ASCOSPORE GERMINATION see <i>gpi; pp</i>							
PARTIAL RESISTANCE TO SK-2 KILLING							
<i>pr(Sk-2) mod(pr)</i>	P2604		7398	IIIR			BCT
PERIOD							
<i>prd-1;bd</i>	no#;no#		4902	III;IVR	SL	NG	JFF
<i>prd-2;bd</i>	UVIV-2;no#	4903	4904	V;IVR	SL	UV	JFF
<i>prd-3;bd</i>	UVIV-4;no#	4905	4906	I;IVR	SL	UV	JFF
<i>prd-4;bd</i>	UVV-7;no#		4907	IR;IVR	SL	UV	JFF
PHOSPHORUS REGULATION							
<i>preg^C</i>	<i>preg^{C2}</i>	2532		IIR	M	UV	RLM
PERFORATED							
<i>(PrfA + Prf⁺a^{m33})</i>	DL1227	6190		VR	SL	NG	NBR
<i>(Prfa^{m33} + Prf⁺A)</i>	DL1227		6191	VR	SL	NG	NBR
PROLINE							
<i>pro-1</i>	21863	4516	4515	IIIR	SL	X	DDP
<i>pro-3</i>	44207	1310	1311	VR	SL2	UV	EGB
<i>pro-3</i>	51506	1308	1309	VR	SL2	UV	BVS
<i>pro-4</i>	35401	6	163	IIIR	SL3	UV	DDP
<i>pro(51505)</i>	51505	928	625	--	M	UV	MBM
<i>pro(K388)</i>	K388		1159	--	E	UV	DGC
PROTEIN SYNTHESIS INITIATION							
<i>psi-1</i>	34C(t)	3044	3289	IVR	M	UV	DDP
PHOSPHORYLATION OF SMALL PROTEIN							
<i>psp</i>	KO1	8307	8308	VR	M		KH
PHENYLALANINE + TYROSINE							
<i>pt</i>	NS1	4695	4696	IVR	M		DDP
<i>pt</i>	P4418	8265		IVR	M		DDP
<i>T(IV→III)S4342 pt</i>	S4342	109	92	IVR;IIR;IVR			DDP
PROTEASE							
<i>pts-1</i> (Groveland-1c) no#			1945	--			DDP
PUTRESCINE see SPERMIDINE							
PUTRESCINE UPTAKE							
<i>puu-1</i>	GB1	7044	7045	IVR	SL2	S	RHD
PYRIMIDINE							
<i>pyr-1</i>	H263	72	85	IVR	M	X	DDP
<i>pyr-1</i>	KS12p1	1301	8250	IVR	M		RHD
<i>pyr-1</i>	DFC33	8399		IVR	SL		RHD
<i>pyr-2</i>	37709		365	IVR	M	UV	MBM
<i>pyr-2</i>	38502	3465	3466	IVR	M	UV	DDP
<i>pyr-2</i>	DFC9	8398	8397	IVR	SL		RHD
<i>pyr-3</i>	1298(pyr-3e)		490	IVR	M	X	RWB
<i>pyr-3</i>	37301p	87	4356	IVR	M	UV	DDP/ELT
<i>pyr-3;arg-12</i>	37301p;37301s		894	IVR;IIR			RHD
<i>pyr-3 col-4</i>	37815(t) 70007c	392		IVR R	M	UV	MBM
<i>pyr-3</i>	37815(t)		366	IVR	M	UV	MBM
<i>pyr-3</i>	45502*	1900	937	IVR	M	UV	AR
<i>pyr-3</i>	49001	374		IVR	M	UV	MBM

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
PYRIMIDINE , continued from previous page							
<i>pyr-3</i>	67602	378		IVR	M	UV	MBM
<i>pyr-3;arg-3?</i>	43-101*;30300?	1890		IVR;IL	M	UV	AR
<i>pyr-3;arg-3?</i>	43-174*;30300?	1891		IVR;IL	M	UV	AR
<i>pyr-3;arg-3?</i>	43-180*;30300?	1892		IVR;IL	M	UV	AR
<i>pyr-3;arg-3?</i>	AR576*;30300?	1893		IVR;IL	M	A	AR
<i>pyr-3 arg-2?</i>	AR618* 33442?	1894		IVR R	M	A	AR
<i>pyr-3 arg-2?</i>	K0493-14* 33442?	1895		IVR R	M	NA	AR
<i>pyr-3 arg-2?</i>	K0493-54* 33442?	1896		IVR R	M	NA	AR
<i>pyr-3 arg-2?</i>	K0545-31* 33442?	1899		IVR R	M	NA	AR
<i>pyr-3 arg-2?</i>	K0545-122* 33442	1898		IVR R	M	NA	AR
<i>pyr-3 arg-2?</i>	K0556-185* 33442	1897		IVR R	M	NA	AR
<i>pyr-3</i>	KS1 [†]		839	IVR	SL	UV	VWW
<i>pyr-3</i>	KS1 [‡]	1964		IVR	M	UV	AR
<i>pyr-3</i>	KS3 [†]	835	838	IVR	M	UV	VWW
<i>pyr-3</i>	KS3 [‡]	1965		IVR	M	UV	AR
<i>pyr-3</i>	KS4 [†]	843	828	IVR	M	UV	VWW
<i>pyr-3</i>	KS6 [‡]	1980		IVR	M	UV	AR
<i>pyr-3</i>	KS7 [‡]	1966		IVR	M	UV	AR
<i>pyr-3</i>	KS8 [‡]	1967		IVR	M	UV	AR
<i>pyr-3</i>	KS11 [‡]	1968		IVR	M	UV	AR
<i>pyr-3</i>	KS12 [†]	832	836	IVR	M	UV	VWW
<i>pyr-3</i>	KS12p [†]	1298	1299	IVR			RHD
<i>pyr-3</i>	KS13 [†]	833	834	IVR	M	UV	VWW
<i>pyr-3</i>	KS15 [‡]	1969		IVR	M	UV	AR
<i>pyr-3</i>	KS16 [†]	829	831	IVR	M	UV	VWW
<i>pyr-3</i>	KS17 [‡]	1970		IVR	M	UV	AR
<i>pyr-3</i>	KS20 [†]	845	841	IVR	M	UV	VWW
<i>pyr-3</i>	KS23 [‡]	846	842	IVR	M	UV	VWW
<i>pyr-3</i>	KS23p [†]	840		IVR	M	UV/KS23	VWW
<i>pyr-3</i>	KS24 [‡]	1971		IVR	M	UV	AR
<i>pyr-3</i>	KS26 [‡]	1972		IVR	M	UV	AR
<i>pyr-3</i>	KS40 [‡]	1973		IVR	M	UV	AR
<i>pyr-3</i>	KS43*	844	837	IVR	M	UV	VWW
<i>pyr-3</i>	KS44 [‡]	1974		IVR	M	UV	AR
<i>pyr-3</i>	KS45 [‡]	1975		IVR	M	UV	AR
<i>pyr-3</i>	KS46 [‡]	1976		IVR	M	UV	AR
<i>pyr-3</i>	KS47 [‡]	1977		IVR	M	UV	AR
<i>pyr-3</i>	KS126 [‡]	1978		IVR	M	UV	AR
<i>pyr-3</i>	KS139 [‡]	1979		IVR	M	UV	AR
<i>pyr-3</i>	DFC3	8394	8396	IVR	SL		RHD
<i>pyr-4</i>	36601	4030	4031	IIL	SL6	UV	EK
<i>pyr-4</i>	DFC90	8395(nt)		IIL	SL		RHD
<i>pyr-6</i>	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

<i>qa-1F;aro-9</i>	A4-18A;Y325M6	1747		VIIR;IIR	SL	UV	MEC
<i>qa-1S qa-1F⁺;aro-9</i>	326-140;M6-11	5942		VIIR;IIR	SL	UV	MEC
<i>qa-1S qa-1F⁺;aro-9</i>	326-105(t);M6-11	5943		VIIR;IIR	SL	UV	MEC
<i>qa-1S qa-1F⁺;aro-9</i>	326-141;M6-11	6899		VIIR;IIR	SL	UV	MEC
<i>qa-1S qa-1F⁺;aro-9</i>	326-105(t);M6-11	6900		VIIR;IIR	SL	UV	MEC
<i>qa-1S qa-1F⁺;aro-9</i>	326-124;M6-11	6901		VIIR;IIR	SL	UV	MEC

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
QUINATE CATABOLISM , continued from previous page							
<i>qa-1S⁺ qa-1F;aro-9</i>	326-158;M6-11	5944		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-129;M6-11	6902		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-191(t);M6-11	6903		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-128;M6-11	6904		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-137;M6-11	6905		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-120;M6-11		6906	VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-181;M6-11	6907		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-189(t);M6-11	6908		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-108;M6-11	6909		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-177;M6-11	6910		VIIR;IIR	SL	UV	MEC
<i>qa-1S⁺ qa-1F;aro-9</i>	326-188(t);M6-11	6911		VIIR;IIR	SL	UV	MEC
<i>qa-1S^C qa-1F⁺;aro-9</i>	105R12-1.5	5945		VIIR;IIR	SL	UV	MEC
<i>qa-1S^C qa-1F⁺</i>	A1-1.4	5946		VIIR	SL	UV	MEC
<i>qa-1S^C qa-1F⁺</i>	E2-3	6896		VIIR	SL	UV	MEC
<i>qa-1S^C qa-1F⁺</i>	E1.1		6897	VIIR	SL	UV	MEC
<i>qa-1S^C qa-1F⁺</i>	E4-3	6898		VIIR	SL	UV	MEC
<i>qa-2;pan-2</i>	204;B23	3230		VIIR;VIR	SL		MEC
<i>qa-2;pan-2</i>	239;B36		3231	VIIR;VIR	SL		MEC
<i>qa-2;aro-9</i>	326M237;Y325M6	2718		VIIR;IIR	SL		MEC
<i>qa-2;aro-9</i>	M246;Y325M6	3957	3958	VIIR;IIR	SL		DDP
<i>qa-3</i>	Y330M16	2719		VIIR	M	UV	MEC
<i>qa-4</i>	Y330M18	2720		VIIR	M	UV	MEC

ROUND SPORE

<i>R</i>	35408	4022	4023	IR	SL7	UV	EK
----------	-------	------	------	----	-----	----	----

RESPIRATORY DEFECTIVE [*rsp*] see Part III.

RECOMBINATION AFFECTORS

<i>rec-1</i>	Dominant allele (<i>rec-1⁻</i>) reduces allelic recombination at <i>his-1</i> and <i>nit-2</i> . Also called <i>rec-z</i> .						
<i>rec-2</i>	Dominant allele (<i>rec-2⁺</i>) reduces crossover between <i>pyr-3 his-5;h-3</i> and <i>ad-3;arg-3</i> and <i>sn</i> ; also allelic recombination at <i>his-3</i> . Also called <i>rec-w, rec-4, rec-5</i> .						
<i>rec-3</i>	Dominant allele (<i>rec-3⁺</i>) reduces crossover between <i>sn</i> and <i>his-2</i> and allelic recombination at <i>am</i> and <i>his-2</i> . Allele <i>rec-3^L</i> differs from <i>rec-3⁺</i> by a reduced effect on allelic recombination at <i>am</i> . Also called <i>rec-x</i>						
<i>cog</i>	(recognition) allele <i>cog⁺</i> is a dominant promoter of recombination in the <i>his-3 - ad-3</i> region, with predominant conversion in the <i>cog⁺</i> strand.						
<i>rec-1;rec-3;</i>	no#;no#		1567	VR;IL;			DGC
<i>cot-1;am his-1</i>	C102(t);K314 K83			IVR;VR R			
<i>rec-1;rec-3⁺;</i>	no#;no#	1568		VR;IL;			DGC
<i>cot-1;his-1 inl</i>	C102(t);K651 37401			IVR;VR R			
<i>rec-1⁺;rec-3;cot-1;am</i>	no#;no#;C102(t);47305	1571		VR;IL;IVR;VR			DGC
<i>rec-1⁺;rec-3⁺;cot-1;am</i>	no#;no#;C102(t);47305	1570		VR;IL;IVR;VR			DGC
<i>rec-1⁺;rec-3⁺;</i>	no#;no#	1569		VR;IL;			DGC
<i>cot-1;his-1 inl</i>	C102(t);K651 37401			IVR;VR R			
<i>rec-2;cog;</i>	no#;no#;	2570	2571	VR;IR;			DGC
<i>cot-1;arg-1 his-3</i>	C102(t);K166 K504			IVR;IR R			
<i>rec-2;cog;</i>	no#;no#;	2569	2566	VR;IR;			DGC
<i>cot-1;his-3 ad-3</i>	C102(t);K504 K118			IVR;IR R			
<i>rec-2;cog;</i>	no#;no#;	2565		VR;IR;			DGC
<i>cot-1;his-3 ad-3</i>	C102(t);K874 K118			IVR;IR R			
<i>rec-2;cog⁺</i>	no#;Y8743cg;	2568		VR;IR			DGC
<i>cot-1;arg-1 his-3</i>	C102(t);K166 K26			IVR;IL R			
<i>rec-2;cog⁺</i>	no#;Y8743cg;	2573	2574	VR;IR			DGC
<i>cot-1;arg-1 his-3</i>	C102(t);K166 K874			IVR;IL R			
<i>rec-2;cog⁺;cot-1;arg-1</i>	no#;Y8743cg;C102(t);K166;	2563		VR;IR;IVR;IL			DGC
<i>T(I;VII)TM429 his-3</i>	TM429						
<i>rec-2;cog⁺</i>	no#;Y8743cg;	2567		VR;IR			DGC
<i>cot-1;his-3 ad-3</i>	C102(t);K26 K118			IVR;IR R			

Locus	Allele	FGSC number		Linkage	Genetic	Muta-	Obtained
		mating type					
		A	a	group	ground		
RECOMBINATION AFFECTORS , continued from previous page							
<i>rec-2;cog⁺;cot-1;his-3</i>	no#;Y8743cg;C102(t);K874		2564	VR;IR;IVR;IR R			DGC
<i>rec-2;cog⁺;cot-1;his-3;am</i>	no#;Y8743cg;C102(t);K874;K314		2572	VR;IR;IVR;IR;VR			DGC
RAGGED							
<i>rg-1</i>	B187		287	IR	SL3	UV	DDP
<i>rg-1</i>	B53	296	4517	IR	SL/SL6	UV	DDP
<i>rg-1</i>	R2357	101	1219	IR	M/SL2	S	DDP
<i>rg-2</i>	no# (from <i>N. sitophila</i>)	4238	4239	IR	SL3		DDP
RIBOFLAVIN							
<i>rib-1</i>	51602(t)	4101	4102	VIR	SL7	UV	EK
<i>rib-1;al</i>	C107;--		1225	VIR;IR			WSM
<i>rib-1</i>	K28(t)	659	4350	VIR	M	S	MJM/ELT
<i>rib-2</i>	Y30539r	1873	83	IVR	M	M	DDP
<i>rib(76R5)</i>	76R5		1226	VI	M	UV	WSM
RIBOSOME PRODUCTION DEFECTIVE							
<i>rip-1</i>	4M(t)	4041	4042	IIR	SL5		EK
ROPY							
<i>ro-1</i>	B15	4352	146	IVR			ELT/DDP
<i>ro-1</i>	B4	110	4351	IVR	SL3	UV	DDP/ELT
<i>ro-2</i>	B20	52	44	IIR	SL3	UV	DDP
<i>ro-3</i>	R2354	3	43	IIL	L	UV	DDP
<i>ro-3</i>	R2354	2372		IIL	M	UV	ELT
<i>ro-4</i>	B38	2980	2981	VR	SL	UV	DDP
<i>ro-4 (=ro-5)</i>	R2428		1529	VR	M	UV	DDP
<i>ro-4 inl</i>	R2428 89601	1356		VR VR	M	UV	ELT
<i>ro-4 (=ro-8)</i>	R2520	1511	1379	VR	M	UV	DDP
<i>ro-6</i>	R2431	3626	3627	IR	SL3	UV	DDP
<i>ro-7</i>	P997	3321	3322	IIL	SL	S	DDP
<i>ro-7</i>	R2470	4024	4025	IIL	SL5	UV	EK
<i>ro-9</i> see <i>da</i>							
<i>ro-10</i>	AR7	3618	3619	IL	M	UV	DDP
<i>ro-11</i>	P3053	7127	7128	IIR	SL	RIP	DDP
<i>ro(P904)</i>	P904	4355	1669	V			ELT/DDP
<i>ro(P1798)</i>	P1798	3910	3911	IR	M	S	DDP
ROPY-LIKE							
<i>rol-1</i>	B31	4353	1360	IVR	SL	UV	ELT
<i>rol-2</i>	R2459	3715	3716	VII	SL2	UV	DDP
<i>rol-3 inl</i>	R2498 89601	1354		VR R	M	UV	ELT
RUG							
<i>rug</i> (was <i>mat</i>)	B57	294	293	IVR	SL	UV	DDP
RESISTANT TO SPORE-KILLER							
<i>r(Sk-2)-1</i>	P527	7153		IIIL	M	S	DDP
<i>r(Sk-2)</i>	P112 (<i>N. intermedia</i>)	1832	1833		M	S	DDP
<i>r(Sk-3)</i>	P		7395	III			DDP
<i>r(Sk-3)</i>	P64 (<i>N. intermedia</i>)	1786			M	S	DDP
ROSY see <i>al-3^{ros}</i>							
SUPPRESSOR OF ASCUS-DOMINANT MUTANTS							
<i>sad-1^{uv}</i>			8737	I	OR	UV	RLM
<i>sad-1^Δ::hyg^f</i>		8740	8741	I	OR		RLM

Locus	Allele	FGSC number		Linkage	Genetic	Muta-	Obtained
		A	a				
SATELLITE-LESS							
<i>sat</i>	no#	944	945	VL			DDP
SCUMBO							
<i>sc</i>	5801	49	115	IIR	M	X	DDP
<i>sc</i>	R2386	1377		IIR	M	UV	ELT
<i>sc (=col-14)</i>	R2503	5075	5076	IIR	M	UV	ELT
SULFUR CONTROL							
<i>scon-1</i>	scon ^C		2142	VR	SL	UV	RLM
<i>scon-2</i>	PSD272	7452	7451	IIR	SL	UV	RLM
SPREADING COLONIAL-TEMPERATURE SENSITIVE							
<i>scot</i>	P7806(t)	3265	3266	VR	M	S	DDP
SCRUFFY							
<i>scr</i>	24-013(t)	2317	3864	IIR	M	DS	AMS/DDP
SERINE							
<i>ser-1</i>	C127	3305	3306	IIR	M	UV	DDP
<i>ser-1</i>	H605	116	118	IIR	M	X	DDP
<i>ser-2</i>	65004	2169	2170	VR	SL2	UV	DDP
<i>ser-3</i>	47903	1213	1221	IL	SL2	UV	DNP
<i>ser-3</i>	UK3-23	8106		IL	M		DDP
<i>ser-4</i>	DW110	1756		IVR	SL	UV	JBM
<i>ser-5</i>	JBM9		2686	IIR	M	UV	JBM
<i>ser-6</i>	DK42	3821	3822	VIL	O		DDP
<i>T(V;VI)OY325 ser-6</i>	OY325	3737	3738	VL;VIL	SL	UV	DDP
SLOW-FINE HYPHAE							
<i>sf</i>	C170sf	3732	1432	IL	SL2/M	S	DDP/MBM
SULFONAMIDE DEPENDENT							
<i>sfo</i>	E15172(d)	651	652	VIIC	M		MJM
<i>sfo nt</i>	E18829(d) 65001	576		VIIC	M		MJM
<i>sfo</i>	E18829(d)		506	VIIC	M		RWB
SHALLOW							
<i>sh</i>	R2371	88	13	VC	M/O	UV	DDP
SHAGGY							
<i>shg</i>	KH160	3923	3924	IIR	SL2	S	DDP
SIDEROPHORE TRANSPORT							
<i>sit-1</i>	GN140	4211	4212	--	M	UV	GWC
<i>sit-2</i>	GN328	4213	4214	--	M	UV	GWC
<i>sit-3</i>	GN235	4215	4216	--	M	UV	GWC
<i>sit-4</i>	GN435	4217		--	M	UV	GWC
<i>sit-5;ota</i>	GN218;UM78		4218	--;IIR	M	UV	GWC
SKIN							
<i>sk</i>	B106	6659	276	VIIR	SL3/SL	UV	DDP
<i>sk</i>	B234	7148	7149	VIIR	SL	X	DDP
<i>(nic-3 wc-1 sk a+ a^{ml} ad-3B cyh-1)</i>	Y31881 P829 B234 + m1 2-17-114 KH52		7220	VIIR			FGSC
<i>sk (mo(P1718))</i>	P1718		6679	VIIR	M	S?	DDP
<i>sk (mo-3)</i>	R2466	6703	3823	VIIR		UV?	DDP/ELT
<i>sk (moe-1)</i>	Y6821		1388	VIIR	M/L	MC	DDP/ELT

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
SLIME							
<i>fz;sg;os-1</i>	no#;no#;B135		1118	--;--;IR	M	UV	SE
<i>fz;sg;os-1</i>	no#;no#;B135		4761	--;--;IR	M	UV	GAS
<i>fz;sg;os-1*</i>	no#;no#;B135	(A/A)	1119	--;--;IR	M	UV	SE
<i>fz;sg;arg-1</i>	no#;no#;B369	(A/A)	327	--;--;IL	M	UV	SE
<i>cr-1 al-1 os-1[†]</i>	B123 34508 B135			R R R			
<i>fz;sg;arg-1</i>	no#;no#;B369	(A/a)	2713	--;--;IL	M	UV	REN
<i>cr-1 al-1 os-1[‡]</i>	B123 34508 B135			R R R			

* 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 ol*)

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

SLOW GROWTH

<i>slo-1</i>	B149		57	59	IR	SL2	UV	DDP
<i>slo-2</i>	P3007		3940	1533	VII	M	S	DDP
<i>slo-2</i>	no#		2312	1169	VIIC	M	S	ELT/LG

SEMICOLONIAL

<i>smco-1</i>	Y2330		1363		I	L	M	ELT
<i>smco-3;inl</i>	R2423;89601			1710	I;VR	M	UV	ELT
<i>smco-4</i>	R2435		8245	1367	IVR	M	UV	ELT
<i>smco-5</i>	R2442		8246	1361	I	M	UV	ELT
<i>smco-6</i>	R2477		4530	4531	VR	SL4	UV	DDP
<i>smco-7</i>	R2497		4253	4254	VR	SL	UV	DDP
<i>smco-7, qa-2, aro-9 inl</i>			8340					TM
<i>smco-8</i>	R2505		8247	1404	IVR	M	UV	ELT
<i>smco-9</i>	R2508		7365	7366	IVR			FGSC
<i>smco-9;inl</i>	R2508;89601			1405	IVR;VR	M	UV	ELT

SNOWFLAKE

<i>sn</i>	C136		507	947	IC	M	S	RWB
<i>sn</i>	JL301			4338	IC	SL	UV	DDP
<i>sn al-1</i>	JL301 34508		4337		IC IR	SL	UV	DDP

SOFT

<i>so</i>	B230		508	542	IR	SL3	X	RWB
<i>so</i>	P1490		1507	1506	IR	M	S	DDP

SUPEROXIDE DISMUTASE

<i>sod-1</i>	3C		7437	7438	IL	SL	RIP	DON
--------------	----	--	------	------	----	----	-----	-----

SORBOSE RESISTANT

<i>sor-1 (sor-A)</i>	1(r)		2374		VIL	M	NA	WK
<i>sor-3 (sor-C)</i>	17(r)		2575		IIR	SL	NA	WK
<i>sor-4 (dgr-3)</i>	BEX6		4334	4333	IL	SL	UV	BME
<i>sor-4 (sor-DS)</i>	DS(r)		1741		IL	SL2		DNP
<i>sor-4 (dgr-3)</i>	L5		4329	4330	IL	SL	UV	BME
<i>sor-4 (dgr-3)</i>	KHY19			8286	IL			SF
<i>sor-4 (sor(T9))</i>	T9M150(r)		3428	3429	IL	SL		TI
<i>sor-5</i>	14(r)		2376		V	SL	NA	WK
<i>sor-6</i>	6(r)		2380	3583	IIR?	SL	NA	WK/DDP
<i>sor(15)</i>	15(r)		2378		I	SL	NA	WK

SPORE KILLER see Part VI

Locus	Allele	FGSC number mating type		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
SPRAY							
<i>sp</i>	1405		1175	VR	M	UV	RRB
<i>sp</i>	B132	68	70	VR	SL3	UV	DDP
SPREADING COLONIAL							
<i>spco-2</i> (allelic with <i>wa</i>)							
<i>spco-3</i> (allelic with <i>spco-7</i>)							
<i>spco-4</i>	R2367	2233	1372	VIII L	M	UV	DDP/ELT
<i>spco-5;inl</i>	R2450;89601		1374*	VII;VR	M	UV	ELT
<i>spco-6</i>	R2456	4381	4382	VIII L	SL2	UV	DDP
<i>spco-6</i>	R2456	7766	7767	VIII L	SL3	UV	FGSC
<i>spco-7</i>	R2365	3195	3196	VIC	L	UV	DDP
<i>spco-7</i>	R2457		1392*	VIC	M	UV	ELT
<i>spco-8;inl</i>	R2462;89601		1383	IV;VR	M	UV	ELT
<i>spco-9</i>	R2480		1382*	VR	M	UV	ELT
<i>spco-9 inl</i>	R2480 89601	4366		VR R	M	UV	ELT
<i>spco-10</i>	R2488		1384	VR	M	UV	ELT
<i>spco-11</i>	R2502s	4383	4384	IL	SL2		DDP
<i>spco-12</i>	R2510	6946	6947	IL	SL2	UV	FGSC
<i>spco-13;inl</i>	R2530s;89601		1351	VI;VR	M	UV	ELT
<i>spco(R2537)</i>	R2537	2389		--	M	S	DDP
* Heterokaryon compatibility type C D E							
SPERMIDINE							
<i>spe-1</i>	462JM	3323	3324	VR	SL	UV	KJM
<i>spe-1 inl</i>	462JM 89601	4265	4266	VR R	M		RHD
<i>spe-1</i>	521KW	3325	3326	VR	M	UV	KJM
<i>spe-1</i>	TP-138	4268	4277	VR	SL	UV	RHD
<i>spe-1; aga</i>	LV10; UM906		8386	VR; VIIR	SL		RHD
<i>his-3; aga; spe-1::hph</i>	Y155M261; UM906; spe-1::hph	8388		I; VII; V	SL	D	RHD
<i>spe-2;aga</i>	JP100;UM906	7040	7041	VR;VIIR	M	UV	RHD
<i>spe-3;aga</i>	LV105;UM906	7042	7043	VR;VIIR	M	UV	RHD
A variety of strains carrying <i>spe-1</i> constructs described in Hoyt <i>et al.</i> , Mol Cell Biol. 20:2760-2773 are available from the FGSC, as are a selection of <i>spe</i> mutants.							
SPONGE							
<i>spg</i>	no#	6016	6017	III	SL3	S	DDP
SUPERSUPPRESSOR							
<i>ssu-1;am</i>	WRN33;am ₇	1687	1688	VIIR;VR		NA	TWS
<i>ssu-1;nit-2;inl</i>	WRN33;KGP0220;37401	6029		VIIR;IL;VR		UV	GAM
<i>ssu-1;nit-3;inl</i>	WRN33;KGP1211;37401		6023	VIIR;IVR;VR		UV	GAM
<i>ssu-1;nit-3;inl</i>	WRN33;KGP1222;37401	6030		VIIR;IVR;VR		UV	GAM
<i>ssu-1(?)</i>	Y319-44		1750	VIIR	SL	UV	MEC
<i>ssu-2;am;al</i>	WRU35;am ₁₇ ;no#	1689		IR;VR;--		UV	TWS
<i>ssu-3 am</i>	WRU118 am ₁₇		1851	IL;VR	M	UV	TWS
<i>ssu-4 am</i>	WRU18 am ₁₇	1852		VIIC;VR	M	UV	TWS
<i>ssu-5</i>	Y319-45		1751	(III or IV)	SL	UV	MEC
<i>ssu-5*</i>	Y319-45		2481	--			AJG
<i>ad-3B*</i>	2-17-34		2485	IR			AJG
+ (wild type)*		2479					AJG
<i>ssu-5;ad-3B*</i>	Y319-45;2-17-34	2483		--;IR			AJG
* Related stocks from the same tetrad							
<i>ssu-6</i>	Y319-26	1748		VR	SL	UV	MEC
<i>ssu-8</i>	Y319-37		1749	IR	SL	UV	MEC
<i>ssu-8;ad-3B al-2;</i>	Y319-37;12-21-22 Y112M38;	2487		IR;R R;VIR M		HA	AJG
<i>pan-2</i>	Y153M96						

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
SUPERSUPPRESSOR , continued from previous page							
<i>ssu-8;ad-3B al-2;</i> <i>pan-2</i>	Y319-37;12-21-76 Y112M38; Y153M96	2488		IR;R R;VIR M		HA	AJG
<i>ssu-9;am</i>	WRU98;am ₁₇		7584	--;VR	M	UV	MEC
<i>ssu-10;am</i>	WRU121(?);am ₁₇		7574	--;VR	M		MEC
STICKY							
<i>st</i>	B128	50	35	IR	M	UV	DDP
STOPPER [<i>stp</i>] see Part IV							
SUPPRESSOR OF arg-6							
<i>arg-1, al-2, sup-6</i>	CD145, 15300, CAL-8	8918	8917	IR,L,L			RHD
SUPPRESSOR OF bal							
<i>su(bal)</i>	B	3486		I	M	S	SB
SUPPRESSOR OF COLONIAL-2							
<i>su(col-2)</i>	C	3482		IL	M	S	SB
SUPPRESSOR OF ISOLEUCINE							
<i>su(ile-1);ile-1</i>	no#;UK71-26	5886		V;VII	M	UV	JAK
SUPPRESSOR OF METHIONINE							
<i>su(met-2)</i>	no#		690	--	M	S	BSS
<i>su(met-2);met-2</i>	no#;H98		689	--;IVR	M	S	BSS
<i>su(met-7) al-2</i>	S1 15300		39	IR R	M		DDP
SUPPRESSOR OF [mi-1]							
<i>su([mi-1])-f;[poky]</i>	no#	385	386	VR;--	M	S	MBM
SUPPRESSOR OF [mi-3]							
<i>su([mi-3])-1;[mi-3]</i>		2472		IR;--	M	S	HB
SUPPRESSOR OF mtr							
<i>su(mtr);fpr-3</i>	18;no#	2999		IC;IIR			JAK
<i>su(mtr);mtr</i>	21-2;21(r)	1718		IR;IVR	M	UV	DRS
<i>su(mtr);mtr col-4</i>	21-2;10(r) 70007c	1719		IC;IVR R	M	UV	DRS
<i>su(mtr₂₆);mtr;</i> <i>his-2;pdx-1</i>	26-R5035;26(r); Y152M43;37803	2732		VI;IVR; IR;IVR	M	NA	NGB
<i>su(mtr₂₆);mtr;</i> <i>his-2;pdx-1</i>	26-R5037;26(r); Y152M43;37803	2733		VI;IVR; IR;IVR	M	NA	NGB
SUPPRESSOR OF suc							
<i>su(suc)-1, suc, inl</i>	su(163R2),KG163,89601	7783		-,IL,VR		UV	HK
<i>su(suc)(R1), suc, inl</i>	su(163R1),KG163,89601	7782		-,IL,VR		UV	HK
<i>su(suc)(R4), suc, inl</i>	su(163R4),KG163,89601	7784		IL,IL,VR		UV	HK
<i>su(suc)(R6), suc, inl</i>	su(163R6),KG163,89601	7785		IL,IL,VR		UV	HK
<i>su(suc)-1</i>	su(163R2)	7786				UV	HK
SUPPRESSOR OF trp-3							
<i>su(trp-3^{td1})-1;trp-3</i>	su ₁₋₁ ;td1	5444		--;IIR			FJD
<i>su(trp-3^{td2})-2;trp-3</i>	su ₂ ;S1952(td2)	6136		III;IIR			ELT
<i>su(trp-3^{td201})-1;trp-3</i>	su ₂₀₁₋₁ ;td201		1618	VIIR;IIR	M	UV	SRS
<i>su(trp-3^{td201})-1;trp-3</i>	su ₂₀₁₋₄ ;td201	1619		VIIR;IIR	M	UV	SRS
<i>su(trp-3^{td201})-1;trp-3</i>	su ₂₀₁₋₆ ;td201	1620		VIIR;IIR	M	UV	SRS
<i>su(trp-3^{td201})-1;trp-3</i>	su ₂₀₁₋₇ ;td201	1621		VIIR;IIR	M	UV	SRS
SUPPRESSOR OF trp-5							
<i>su(trp-5);trp-5</i>	77;A420		7575	VIL;VR	M	UV	JAK

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
SUPPRESSOR OF <i>ure-1</i>							
<i>su(ure-1);ure-1 his-1</i>	no#9;9 C91	4300		--;VR R			HGK
<i>su(ure-1);ure-2 am</i>	no#9;47 32213(am1)	4301		--;VR R			HGK
SUCCINATE							
<i>suc</i>	35402		655	IL	M	UV	MJM
<i>suc</i>	37807		759	IL	M	UV	DGC
<i>suc</i>	39311	1248	1249	IL	SL5	UV	DDP
<i>suc</i>	46005	1110	1111	IL	SL2	UV	KDM
<i>suc</i>	47807		656	IL	M	UV	MJM
<i>suc</i>	55901		762	IL	M	UV	DGC
<i>suc</i>	66702	1214	377	IL	SL2/M	UV	DNP/MBM
<i>suc</i>	KG163	3004		IL	M	NG	HK
<i>suc</i>	NM121		2441	IL	M	UV	DDP
SULFUR METABOLISM CONTROL see <i>scon</i>							
SUPERSUPPRESSOR see <i>ssu</i>							
TYROSINASE STRUCTURAL GENE							
<i>T^L</i>	4-137		320	IR	M	S	NHH
<i>T^S</i>	4-121	321		IR	M	S	NHH
<i>T^S</i>	69-1113		2963	IR	M		JFF
<i>T</i>	T ^{PR}	1326		IR	M	S	NHH
TUFTED AERIAL							
<i>ta</i>	D317	1524	1525	IL	SL3	UV	DDP
TAD							
Tad Hyg ^r			8609				JAK
TRYPTOPHAN SYNTHASE DEFECTIVE <i>td</i> see <i>trp-3</i>							
THIAMINE							
<i>thi-1</i>	56501	4010	4011	IR	SL9	X	EK
<i>T(I;VII)17084 thi-1</i>	17084	216	215	IR;VIIL			DDP
<i>thi-2</i>	9185	5906	5907	IIIR	SL	X	DDP
<i>thi-2</i>	9185	1222	1223	IIIR	M	X	DGC
<i>thi-3</i>	18558	4083	4084	VIIC	SL7	X	EK
<i>thi-3</i>	UT305	3824	3825	VIIL	M	UV	DDP
<i>thi-4</i>	85902	55	3941	IIIC	M	M	DDP
<i>thi-5</i>	50005	2171	375	IVR	M	UV	DDP
<i>thi-1o;thi-1</i>	no#;56501	934		IIIC;IR	M	S	BME
THREONINE							
<i>thr-2</i>	35423	2	40	IIL	L/M	UV	DDP
<i>thr-3</i>	44104(t)	24	12	IIL	SL/M	UV	DDP
<i>thr-3</i>	T42M59(t)	2294	2291	IIL	M	UV	DDP
<i>thr(4V);inl</i>	4V(t);89601		3763	--;VR	M	UV	DRS
<i>thr(38E);inl</i>	38E(t);89601		3760	II;VR	M	UV	DRS
<i>thr(72C);inl</i>	72C(t);89601		3758	II;VR	M	UV	DRS
TINY							
<i>ti</i>	B233(t)	309	310	IC	SL3	X	DDP
TANGERINE							
<i>tng</i>	P4474	3921	3922	IIL	SL2	S	DDP

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
TENUOUS							
<i>tns</i>	P4394	8281	8282	VIIR	M		DDP
TOLERANT							
<i>tol</i>	CZ30.7	3453		IVR	M	S	DDP
<i>tol</i>	N43	3452		IVR	M	S	DDP
<i>tol</i>	N83	2338	1946	IVR	S		DDP/DNP
TRANSPORT SYSTEMS see <i>bas, can, car, fpr, hlp, hgu, mod-5, mtr, nap, pm, pmg, pmn, uc, ud, trk</i>							
TREHALASE							
<i>tre^{int}; inl</i>	19-31;89601	4507		--;VR	M	NG	MLS
<i>tre^{int}; inl</i>	31-601;89601	4508		--;VR	M	NG	MLS
<i>tre; inl</i>	39-10;89601	4510		IR;VR	M	NG	MLS
<i>tre; inl</i>	39-21;89601	4511		IR;VR	M	NG	MLS
<i>tre; inl</i>	39-25;89601	4512		IR;VR	M	NG	MLS
<i>tre; inl</i>	39-30;89601	4513		IR;VR	M	NG	MLS
<i>tre; inl</i>	39-3;89601	4509		IR;VR	M	NG	MLS
<i>tre; inl (mig^f)</i>	no#;89601	497	498	IR;VR	M	M	RWB
<i>tre (mig^s)</i>	--	4514		IR			MLS
TRANSPORT OF POTASSIUM							
<i>trk</i>	R2449	1953	1954	IIIR	M	UV	CWS
TRYPTOPHAN							
<i>trp-1</i>	8	2038	2039	IIIR	M		JAD
<i>trp-1</i>	15	1848		IIIR	SL	UV	JHC
<i>trp-1; am</i>	15;am ₁₇		1847	IIIR;VR	SL	UV	JHC
<i>trp-1</i>	20	2040	2041	IIIR	M	UV	JAD
<i>trp-1</i>	25	2042	2043	IIIR	M	NA	JAD
<i>trp-1</i>	28	2044	2045	IIIR	M	NA	JAD
<i>trp-1</i>	30	2046	2047	IIIR	M	NA	JAD
<i>trp-1</i>	10575	4049	4050	IIIR	SL ₆	X	EK
<i>trp-1</i>	A9		1146	IIIR	M	UV	DGC
<i>trp-1</i>	A10		694	IIIR	M	UV	DGC
<i>trp-1</i>	A28		695	IIIR	M	UV	DGC
<i>trp-1</i>	A38		1148	IIIR	M	UV	DGC
<i>trp-1</i>	A50		1149	IIIR	M	UV	DGC
<i>trp-1</i>	A62		1150	IIIR	M	UV	DGC
<i>trp-1</i>	A63		1457	IIIR	E	UV	DGC
<i>trp-1</i>	A94		696	IIIR	M	UV	DGC
<i>trp-1</i>	C1	2048	2049	IIIR	M	UV	JAD
<i>trp-1</i>	C2	2050	2051	IIIR	M	UV	JAD
<i>trp-1</i>	K1032		1456	IIIR	M	UV	DGC
<i>trp-1</i>	K1442		1152	IIIR	M	UV	DGC
<i>trp-2</i>	10	1850		VIR	SL	UV	JHC
<i>trp-2</i>	41	4109	4110	VIR	SL ₆	NA	EK
<i>trp-2</i>	40008	758		VIR	M	UV	DGC
<i>trp-2</i>	45302	135	134	VIR	M	UV	DDP
<i>trp-2</i>	66110		4362	VIR	O	UV	ELT
<i>trp-2</i>	75001	4107	4108	VIR	SL ₆	N	EK
<i>trp-2</i>	S4266	990	4364	VIR	M	UV	LG
<i>trp-2</i>	TB31	1846		VIR	M	UV	JHC
<i>trp-3</i>	A16		697	IIR	M	UV	DGC
<i>trp-3</i>	A18		698	IIR	M	UV	DGC
<i>trp-3</i>	A20		1147	IIR	E	UV	DGC
<i>trp-3</i>	A42		699	IIR	M	UV	DGC
<i>trp-3</i>	A72		700	IIR	M	UV	DGC

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
TRYPTOPHAN , continued from previous page							
<i>trp-3</i>	A73		701	IIR	M	UV	DGC
<i>trp-3</i>	A78		702	IIR	M	UV	DGC
<i>trp-3</i>	A78(tdA78 or td201)	860		IIR	M	UV	AML
<i>trp-3</i>	A78-101*	1026	1027	IIR	SL	UV	DMB
<i>trp-3</i>	A78-109*	1028	1029	IIR	SL	UV	DMB
<i>trp-3</i>	A78-110*	1030	1031	IIR	SL	UV	DMB
<i>trp-3</i>	A78-137*	1033	1032	IIR	SL	UV	DMB
<i>trp-3</i>	A78-149*	1035	1034	IIR	SL	UV	DMB
<i>trp-3</i>	A78-174*		1036	IIR	SL	UV	DMB
<i>trp-3</i>	C83	73	862	IIR	M/SL2	UV	DDP/AML
<i>trp-3</i>	S1952(td2)	861		IIR	SL2	MDAB	AML
<i>trp-3</i>	td3	854		IIR	SL3	UV	AML
<i>trp-3</i>	td6	858		IIR	SL3	UV	AML
<i>trp-3</i>	td7	857		IIR	SL2	UV	AML
<i>trp-3</i>	td16	855		IIR	SL	UV	AML
<i>trp-3</i>	td24	856	2070	IIR	SL2	UV	AML/DDP
<i>trp-3</i>	td37	4038	4039	IIR	SL7	X	EK
<i>trp-3</i>	td38	3535		IIR	SL	X	DDP
<i>trp-3</i>	td48 [†]	1002		IIR	SL	UV	DMB
<i>trp-3</i>	td7	859		IIR	SL	X	AML
<i>trp-3</i>	td96		1003	IIR	SL	UV	DMB
<i>trp-3</i>	td97	1005	1004	IIR	SL	UV	DMB
<i>trp-3</i>	td100	1009	1008	IIR	SL	UV	DMB
<i>trp-3</i>	td101	1010 [‡]		IIR	SL	UV	DMB
<i>trp-3</i>	td102	1013	1012	IIR	SL	UV	DMB
<i>trp-3</i>	td104	1014		IIR	SL	UV	DMB
<i>trp-3</i>	td120	1015	1016	IIR	SL	UV	DMB
<i>trp-3</i>	td128		1017	IIR	SL	UV	DMB
<i>trp-3</i>	td131		3536	IIR	SL		DDP
<i>trp-3</i>	td132 [†]	1020		IIR	SL	UV	DMB
<i>trp-3</i>	td133	3537		IIR	SL	UV	DDP
<i>trp-3</i>	td133		1021	IIR	SL	UV	DMB
<i>trp-3</i>	td138		1022	IIR	SL	UV	DMB
<i>trp-3</i>	td139	1023		IIR	SL	UV	DMB
<i>trp-3</i>	td140	3538		IIR	SL	UV	DDP
<i>trp-3</i>	td141		1025	IIR	SL	UV	DMB
<i>trp-4</i>	Y2198	4059	4060	IVR	SL6	M	EK
<i>trp-5</i>	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

<i>ts</i>	no#	821		VR	M	S	KN
-----------	-----	-----	--	----	---	---	----

TYROSINASE REGULATORY GENE

<i>ty-1</i>	913-83	322		IIR	M	S	NHH
<i>ty-2</i>	913-17		1194	IR			NHH
<i>ty-3</i>	T22	4878		IIR			HCC
<i>ty-3;ty-4;ff-3</i>	T22;no#;HC725	4877		IIR;--;IR	M		HCC

TYROSINE

<i>tyr-1(?)</i>	C167		3258	IIR			RLM
<i>tyr-1</i>	T145	874		IIR		UV	AGD
<i>tyr-1</i>	Y6994	2259	2260	IIR	SL2	M	DDP
<i>tyr-1</i>	acc ^{phe}		3045	IIR	SL	UV	AGD
<i>tyr-2</i>	STL1	36	25	IR	M	S	DDP

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
TYROSINE SENSITIVE							
<i>ty</i>	LW101(s)	2735		IL	M	UV	GAM
TYROSINASE STRUCTURAL GENE see <i>T</i>							
URACIL SALVAGE							
<i>uc-1 pyr-4;uc-2</i>	RW57 36601;RW135	2203		II L;I	M	UV	LGW
<i>uc-1 pyr-4;uc-3</i>	RW57 36601;RW203		2204	II L;--	M	UV	LGW
<i>uc-2</i>	RW135		2197	I	M	UV	LGW
<i>uc-3</i>	RW203		2198	--	M	UV	LGW
<i>uc-4</i>	RW341	2200	2199	VR	M	UV	LGW
PYRIMIDINE TRANSPORT							
<i>uc-5 pyr-1</i>	RW399 H263		2201	IVR R	SL	UV	LGW
PYRIMIDINE NUCLEOSIDE TRANSPORT							
<i>ud-1;pyr-1</i>	RW433;H263		2202	VIIR;IVR	SL	UV	LGW
URIDINE KINASE							
<i>udk uc-4</i>	FB-D425 RW341	4284	4285	VR R	SL	UV	FPB
UNSATURATED FATTY ACIDS							
<i>ufa(P73B118)</i>	P73B118	4440	4441	IVR	M	EMS	DDP
<i>(ufa(P73B118)A + a^{ml} ad-3B cyh-1)</i>	P73B118 + 1 2-17-114 KH52	4442	4443	IVR+IL R R		DDP	
<i>ufa-3</i>		7621		-	SL	γ	MT
<i>ufa-4</i>		7622		-	SL	γ	MT
ULTRAVIOLET PHOTOREACTIVATION see <i>upr</i>							
ULTRAVIOLET SENSITIVE see <i>uvs</i>							
UNKNOWN FUNCTION (Temperature sensitive lethal)							
<i>un-1</i>	44409(t)	6883	3942	IR	SL4	UV	DDP
<i>un-2</i>	46006(t)	1956	931	IC	SL3/M	UV	DDP/MBM
<i>un-2</i>	ALS9(t)	2129	2130	IC	M		DDP
<i>un-3</i>	55701(t)	636	4529	IL	SL3/SL4	X	DNP/DDP
<i>un-4</i>	66204(t)	131	2172	VIL	M	UV	DDP
<i>un-5</i>	b39(t)	4000	4001	IL	SL6	M	EK
<i>un-6</i>	83106(t)	1328	1329	IIIR	M	X	DDP
<i>un-7</i>	T53M50(t)	2175	2176	IR	SL	UV	DDP
<i>un-8</i>	T27M9(t)	2173	2174	IVR	SL	UV	DDP
<i>un-9</i>	T54M96(t)	2339	2340	VR	SL	UV	DDP
<i>un-10</i>	T42M45(t)	2341	2342	VIIR	SL	UV	DDP
<i>un-11</i>	T42M30(t)	2343	2344	VR	M	UV	DDP
<i>un-12</i>	T51M118(t)	2345	2921	IVR	M	X	DDP
<i>un-13</i>	T42M24(t)	2346	2347	VIL	M	UV	DDP
<i>un-14</i>	T54M55(t)	2348	2349	IIIR	SL	UV	DDP
<i>un-15</i>	T54M50(t)	4040	2391	IIR	SL5/M	UV	EK/DDP
<i>un-16</i>	T42M38(t)	4306		IL	SL	UV	DDP
<i>un-16</i>	T42M69(t)	2392		IL	M	UV	DDP
<i>un-16 acr-3</i>	T42M69(t) KH14(r)		4303	IL L	SL		DDP
<i>un-17</i>	T51M171(t)	2356	2357	IIIR	SL	X	DDP
<i>un-18</i>	T54M94(t)	4020	4021	IR	SL6	UV	EK
<i>un-19</i>	P73B 138(t)	2586	2587	VR	M	EMS	DDP
<i>un-20</i>	P2402(t)	3006	3007	IIR	M	S	DDP
<i>un-21</i>	T53M26(t)	3307	3320	IIIR	SL2		DDP
<i>un-22</i>	61C(t)	4323	4324	VII	SL	UV	DDP
<i>un-22; inl</i>	62C(t);89601		3786	VIIR;VR	M	UV	DRS
<i>un-23</i>	64D(t)	3926	3927	VIR	M	UV	DDP

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
UNKNOWN, continued from previous page							
<i>un-24 het-6OR</i>	DJ517 OR	7354		IIL L	SL	RIP	DJJ
<i>un(6B);inl</i>	6B(t);89601		3766	I;VR	M	UV	DRS
<i>un(6T);inl</i>	6T(t);89601		3781	IR;VR	M	UV	DRS
<i>un(16J) inl</i>	16J(t) 89601		3777	VR R	M	UV	DRS
<i>un(19D);inl</i>	19D(t);89601		3784	I;VR	M	UV	DRS
<i>un(20J) inl</i>	20J(t) 89601		3778	V VR	M	UV	DRS
<i>un(21T) inl</i>	21T(t) 89601		3782	V VR	M	UV	DRS
<i>un(23M);inl</i>	23M(t);89601		3779	--;VR	M	UV	DRS
<i>un(58E) inl</i>	58E(t) 89601		3775	V(?) VR	M	UV	DRS
<i>un(74E);inl</i>	74E(t);89601		3776	IV(?);VR	M	UV	DRS
<i>un(74M);inl</i>	74M(t);89601		3780	--;VR	M	UV	DRS
<i>un(120C);inl</i>	120C(t);89601		3768	IR;VR	M	UV	DRS
<i>un(121C) inl</i>	121C(t) 89601		3769	VR R	M	UV	DRS
<i>un(134C) inl</i>	134C(t) 89601		3770	VR R	M	UV	DRS
<i>un(145C);inl</i>	145C(t);89601		3783	I;VR	M	UV	DRS
<i>un(151C);inl</i>	151C(t);89601		3771	IL;VR	M	UV	DRS
<i>un(165C) inl</i>	165C(t) 89601		3772	VR R	M	UV	DRS
<i>un(181C) inl</i>	181C(t) 89601		3787	VR R	M	UV	DRS
<i>un(209C);inl</i>	209C(t);89601		3773	IL;VR	M	UV	DRS
<i>un(71103) see ilv(71103)</i>							
<i>un(OY351)</i>	OY351(t)	4316					DDP
<i>un(P73G14)</i>	P73G14(t)	4310		IR	SL	EMS	DDP
<i>un(P8319)</i>	P8319(t)	3849		IVR	M		DDP
<i>un(STL6) see fls</i>							
<i>un(T28M15)</i>	T28M15(t)	4304		I	SL	UV	DDP
<i>un(T33M8)</i>	T33M8(t)	4311			SL		DDP
<i>un(T42M34)</i>	T42M34(t)	4305			SL	UV	DDP
<i>un(T42M36)</i>	T42M36(t)	4312			SL		DDP
<i>un(T42M39)</i>	T42M39(t)		4307		SL	UV	DDP
<i>un(T42M46)</i>	T42M46(t)	4308			SL		DDP
<i>un(T42M54)</i>	T42M54(t)	4309			SL	UV	DDP
<i>un(T42M56)</i>	T42M56(t)	2352	2353	VI	M	UV	DDP
<i>un(T42M62)</i>	T42M62(t)		4293	--	M	UV	DDP
<i>un(T42M68)</i>	T42M68(t)		4294		M	UV	DDP
<i>un(T42M70)</i>	T42M70(t)	4295			M	UV	DDP
<i>un(T51M154)</i>	T51M154(t)	2354	2355	VIL	SL	X	DDP
<i>un(T51M166)</i>	T51M166(t)	4313		II	SL	X	DDP
<i>un(T52M23)</i>	T52M23(t)		4296		M	UV	DDP
<i>un(T54M57)</i>	T54M57(t)	4314			SL		DDP
<i>un(T54M58)</i>	T54M58(t)		4297		M	UV	DDP
<i>un(T54M68)</i>	T54M68(t)	4315			SL		DDP
UV PHOTOREACTIVATION							
<i>upr-1;</i>	no#	4171		IL	SL2	M	EK
<i>upr-1; cr-1 rg-1;</i>	no#	1705			M		RWT
<i>pe fl; met(331)</i>							
<i>upr-1; uvs-1; cr-1 rg-1; no#; no#</i>		1703					RWT
<i>pe fl; met(331)</i>							
UREASE DEFICIENT							
<i>ure-1</i>	9	1229	1230	VR	M	UV	HGK
<i>ure-1</i>	D1	3805		VR	SL	UV	HBH
<i>ure-1</i>	D2	3806		VR	SL	UV	HBH
<i>ure-1</i>	D3		3807	VR	SL	UV	HBH
<i>ure-1</i>	D23		3808	VR	SL	UV	HBH
<i>ure-2</i>	47	2056	2057	VR	M	UV	HGK
<i>ure-2 am</i>	47 32213		4299	VR R			HGK
<i>ure-2</i>	D74		3809	VR	SL	UV	HBH

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
UREASE DEFICIENT , continued from previous page							
<i>ure-2</i>	W2	3816		VR	SL	UV	HBH
<i>ure-3</i>	F29	3733	3734	IIR		UV	HBH
<i>ure-4</i>	601		3801	IR	SL	UV	HBH
<i>ure-4</i>	C21		3803	IR	SL	UV	HBH
<i>ure-4</i>	E12	3812		IR	SL	UV	HBH
<i>ure(A7)</i>	A7	3802		V	SL	UV	HBH
<i>ure(C5)</i>	C5		3804	--	SL	UV	HBH
<i>ure(E3)</i>	E3		3810	--	SL	UV	HBH
<i>ure(E7)</i>	E7	3811		--	SL	UV	HBH
<i>ure(K3)</i>	K3	3813		--	SL	UV	HBH
<i>ure(R2)</i>	R2		3814	--	SL	UV	HBH
<i>ure(S3)</i>	S3		3815	V	SL	UV	HBH
UV SENSITIVE							
<i>uvs-1;cr-1 rg-1; pe fl;met(331)</i>	no#	1630		--		UV	LTC
<i>uvs-2</i>	no#	4172	4173	IVR	SL6	UV	EK
<i>uvs-3</i>	ALS11	4174	4175	IVL	SL8	UV	EK
<i>uvs-3</i>	FK016	4589	4590	IVL	SL8	UV	EK
<i>uvs-4</i>	ALS12	4176	4177	IIC	SL6	UV	EK
<i>uvs-5</i>	ALS13	2970	2971	IIR	M	UV	DDP
<i>uvs-6</i>	ALS35	4178	4179	IR	SL6	UV	EK
VACUOLAR MEMBRANE ATPase							
(<i>vma-1-RIP am¹³² + mat a^{ml} ad-3B cyh-1</i>)	<i>pvn-1-121</i>	8628	8627	IR		RIP	BB
<i>vma-3</i>	<i>brf-21-E-1</i>	8613		V			BB
<i>vma-3</i>	<i>brf-21-E-2</i>		8614	V			BB
<i>vma-3</i>	<i>brf-33-A-1</i>	8615		V			BB
<i>vma-3</i>	<i>brf-33-A-9</i>		8616	V			BB
<i>vma-3</i>	<i>brf-65-A-7</i>	8617		V			BB
<i>vma-3</i>	<i>brf-65-A-10</i>		8618	V			BB
<i>vma-3</i>	<i>brf-89-A-2</i>		8619	V			BB
<i>vma-3</i>	<i>brf-89-A-3</i>	8620		V			BB
(<i>vma-13-RIP, his-3 +mat a^{ml} ad-3B cyh-1</i>)	10-5	8621		IR		RIP	BB
(<i>vma-5-RIP, +mat a^{ml} ad-3B cyh-1</i>)	2	8622				RIP	BB
(<i>vma-5-RIP, +mat a^{ml} ad-3B cyh-1</i>)	1	8623				RIP	BB
VACUOLAR PH-SENSITIVE ATPase							
(<i>vph-1-RIP, +mat a^{ml} ad-3B cyh-1</i>)	<i>rk-1-3</i>		8624			RIP	BB
(<i>vph-1-RIP, +mat a^{ml} ad-3B cyh-1</i>)	<i>rk-1-1</i>	8625				RIP	BB
VALINE							
<i>val</i>	33026	359	566	VC	M	UV	MBM
<i>val</i>	33050	3614	3615	VR	M	UV	DDP
VANADATE RESISTANT see <i>pho-4</i>							
VARIANT							
<i>var-1</i>	X10a		2474	--	M	S	HB

Locus	Allele	FGSC number mating type		Linkage group	Genetic back- ground	Muta- gen	Obtained from
		A	a				
VELVET							
<i>vel</i>	B18	2267	2268	IIIR	M	UV	DDP
<i>vel</i>	P1710		1655	IIIR	M	S	DDP
<i>vel;inl</i>	R2471;89601		1389	IIIR;VR	M	UV	ELT
VISIBLE							
<i>T(I;III)3317 vis</i>	3717	2682	2683	IR			DDP
VIVID							
<i>vvd</i>	SS-692	7852	7853	VIL	SL	UV	SNB
<i>vvd</i>	P4246	7854	7855	VIL	M		DDP
WASHED							
<i>wa</i>	R2359	6779	6780	VR	SL2	UV	DDP
WHITE COLLAR							
<i>wc-1</i>	ER45	4395	4396	VIIR	SL	UV	VEAR
<i>wc-1</i>	ER53	4397	4398	VIIR	SL	UV	VEAR
<i>wc-1</i>	ER57	4399	4400	VIIR	SL	UV	VEAR
<i>wc-1</i>	MK1	4401	4402	VIIR	SL	UV	VEAR
<i>wc-1</i>	MK2	4403	4404	VIIR	SL	UV	VEAR
<i>wc-1</i>	P4723	4444	4445	VIIR	SL3	S	DDP
<i>wc-1</i>	P829	128	143	VIIR	M	S	DDP
<i>wc-2</i>	234w	3817	3818	IR	M	O	DDP
<i>wc-2</i>	ER24(t)	4405	4406	IR	SL	UV	VEAR
<i>wc-2</i>	ER33	4407	4408	IR	SL	UV	VEAR
<i>wc-2</i>	ER44(t)	4409	4410	IR	SL	UV	VEAR
WHITE SPORE							
<i>ws-1</i>	RP99	1434	1435	VIR	SL	DS	RLP
<i>ws-2</i>	NM122		1617	VI	M	UV	DDP
XANTHINE DEHYDROGENASE							
<i>xdh-1</i>	NMR11	2702		II	SL	UV	GAM
<i>xdh-1</i>	NMR27	2703		II	SL	UV	GAM
YELLOW							
<i>ylo-1</i>	P1193	1514		VIL	SL2	S	DDP
<i>ylo-1</i>	Y30539y	4099	4100	VIL	SL7	M	EK
<i>ylo-2</i>	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 #		Linkage group	Obtained from
		A	a		
Linkage Group I					
<i>ro-10 un-5</i>	AR7 b39(t)	7222	7223	L L	DDP
<i>ro-10 nit-2 leu-3</i>	AR7 nr37 R156	7224	7225	L L L	DDP
<i>ro-10 In(IR;IL)OY323 al-2 arg-13</i>		7481	7482	L R R	DDP
<i>ro-10 al-2 un-18</i>	AR7 15300 <u>T</u> 54M94(t)	3789	3790	L R R	DDP
<i>ro-10 un-18</i>	AR7 <u>T</u> 54M94(t)	3754	3755	L R	DDP
<i>fr his-2 nic-2 al-2</i>	B110 C94 43002 1-112-38		5302	L R R R	FJD
<i>fr nic-2 al-2</i>	B110 43002 1-112-38		5303	L R R	FJD
<i>fr cr-1 al-1</i>	B110 L 34508	237		L R R	DDP
<i>fr al-1</i>	B110 34508	314	238	LR	DDP
<i>fr al-1 R</i>	B110 ALS4 35408R	2087	2088	L R R	DDP
<i>fr al-1 un-18</i>	B110 ALS4 <u>T</u> 54M94	2617	2618	L R R	DDP
<i>un-5 nit-2</i>	b39(t) nr37	7240		L L	DDP
<i>un-5 leu-3 sn cr-1</i>	b39(t) R156 C136 B123	5160		L L C R R R R	EK
<i>cyh-1 al-2 nic-1</i>	KH52(r) 15300 S1413				
<i>un-5 leu-3 nic-2 cyh-1</i>	39(t) R156 43002 KH52(r)	4111		L L R R	EK
<i>un-5 leu-3 cr-1 cyh-1</i>	b39(t) R156 B123 KH52(r)	5219		L L R R R R	EK
<i>al-2 nic-1</i>	15300 S1413				
<i>un-5 leu-3 cyh-1 al-2</i>	b39(t) R156 KH52(r) 15300	5162	5163	L L R R R	EK
<i>nic-1</i>	S1413				
<i>un-5 cyh-1 al-2 nic-1</i>	b39(t) KH52(r) 15300 S1413	5164	5165	L R R R	EK
<i>un-5 al-2 arg-13</i>	b39(t) 15300 RU3	2282	2283	L R R	DDP
<i>un-5 al-1 R</i>	b39(t) ALS4 35408R	2177	2178	L R R	DDP
<i>nit-2 leu-3</i>	KGP0220 R156	6024		L L	GAM
<i>nit-2 leu-3</i>	nr37 R156		7226	L L	DDP
<i>leu-3 arg-1</i>	R156 B369	1210	1216	L L	DNP
<i>leu-3 sn cr-1 cyh-1</i>	R156 C136 B123 KH52(r)	5161		L C R R R R	EK
<i>al-2 nic-1</i>	15300 S1413				
<i>leu-3 ad-3B cyh-1</i>	R156 2-17-34 KH52(r)	4147		L R R	EK
<i>leu-3 ad-3B thi-1 cyh-1</i>	R156 2-17-34 56501 KH52(r)	4146		L R R R	EK
<i>leu-3 cr-1</i>	47313 B122	257	247	L R	DDP
<i>leu-3 cyh-1 un-18</i>	R156 KH52(r) <u>T</u> 54M49(t)	5159		L R R	EK
<i>leu-3 mus-9</i>	R156 FK129	6405		L R	EK
<i>leu-3 al-2 nic-1 un-18</i>	R156 15300 S1413 <u>T</u> 54M49(t)		5158	L R R R	EK
<i>cyt-1 leu-4</i>	C115 R359		7227	L L	DDP
<i>cyt-1 al-2 nic-1</i>	C115 15300 3416		2473	L R R	HB
<i>en(pdx-1) al(G2)</i>	K30 G2		649	L R	MJM
<i>ser-3 un-16 acr-3</i>	47903 <u>T</u> 42M69 KH14(r)		5079	L L L	DDP
<i>mat a^{m1} ad-3B cyh-1</i>	1 2-17-114 KH52(r)		4564	L R R	AJG
<i>mat a^{m2} ad-3B cyh-1</i>	2 2-17-114 KH52(r)		4565	L R R	AJG
<i>mat a^{m5} ad-3B cyh-1</i>	5 2-17-114 KH52(r)		4566	L R R	AJG
<i>mat a^{m7} ad-3B cyh-1</i>	7 2-17-114 KH52(r)		6840	L R R	DDP
<i>mat a^{m10} ad-3B cyh-1</i>	10 2-17-114 KH52(r)		6841	L R R	DDP
<i>mat a^{m12} ad-3B cyh-1</i>	12 2-17-114 KH52(r)		6842	L R R	DDP
<i>mat a^{m24} ad-3B cyh-1</i>	24 2-17-114 KH52(r)		6843	L R R	DDP

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
Linkage Group I, continued					
<i>mat a^{m26} ad-3B cyh-1</i>	26 2-17-114 KH52(r)		4567	L R R	AJG
<i>mat a^{m30} ad-3B</i>	30 2-17-114		6844	L R R	DDP
<i>mat a^{m33} arg-3</i>	m33 30300		5383	L L	DDP
<i>mat a^{m33} ad-3B</i>	m33 2-17-128		4568	L R	AJG
<i>mat a^{m1} cyh-1</i>	1 KH52(r)		7448	IL R	RLM
<i>mat A^{m42} un-3 ad-3A</i>	42 55701(t) 2-17-814	4569		L L R	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R	
<i>mat A^{m44} un-3 ad-3A</i>	44 55701(t) 2-17-814	4570		L L R	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R	
<i>mat A^{m54} un-3 ad-3A</i>	54 55701(t) 2-17-814	4571		L L R	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R	
<i>mat A^{m56} un-3 ad-3A</i>	56 55701(t) 2-17-814	4572		L L R	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R	
<i>mat A^{m64} un-3 ad-3A</i>	64 55701(t) 2-17-814	4573		L L R	AJG
<i>nic-2 cyh-1</i>	43002 KH52(r)			R R	
<i>mat A^{m64} nic-2 cyh-1</i>	64 43002 KH52(r)		7449	IL R R	
<i>ta acr-3</i>	D317 KH14(r)	7228		L L	DDP
<i>un-16 acr-3</i>	T42M 69(t) KH14(r)		7558	L L	DDP
<i>un-16 acr-3</i>	T42M 69(t) KH14(r)		4303	L L	DDP
<i>cy sf</i>	C170c C170sf	1433		L L	MBM
<i>ad-5 his-2 cr-1</i>	Y152M40 Y152M14 B123		246	L R R	DDP
<i>ad-5 rg-1 cr-1</i>	71104 B53 B123	5435		L R R	FJD
<i>arg-1 mei-3</i>	B369 N289		7229	L L	DDP
<i>arg-1 arg-3</i>	UM-245, 30300	8400		L L	RHD
<i>arg-1 rg-1 cr-1 thi-1 al-2</i>	46004 B53 B123 56501 15300	4964		L R R R R	ELT
<i>arg-1 cr-1 al-1 os-1</i>	B369 B123 34508 B135	329		L R R R	DDP
<i>arg-1, arg-6</i>	CD-145, CD-29		8401	L R	RHD
<i>arg-1 al-1</i>	29997 34508	5091		L R	DDP
<i>arg-3 un-2</i>	30300 46006(t)	2704		L R	DDP
<i>arg-3 un-2 his-2</i>	30300 46006(t) Y152M14	2750		L R R	DDP
<i>arg-3 his-3 nic-2(?)</i>	30300 1-226-566 43002(?)	5526		L R	FJD
<i>arg-3 his-3 nic-2 al-1</i>	30300 1710 43002 1-234-471	5544		L R R R	FJD
<i>arg-3 nic-2 cr-1</i>	30300 43002 B123	211		L R R	DDP
<i>arg-3 ad-3B</i>	30300 2-17-158		5529	L R	FJD
<i>csp-1 nic-2</i>	UCLA37 43002	2513		L R	CPS
<i>sn his-2</i>	C136 C94	399		C R	MBM
<i>sn his-3</i>	C136 C140	387		C R	MBM
<i>sn cr-1</i>	C136 B123	4158	4159	C R	EK
<i>sn al-1</i>	JL301 34508	4337		C C	DDP
<i>un-2 his-2</i>	46006(t) Y152M14	2748	2749	R R	DDP
<i>his-2 ad-3A</i>	C94 1-112-13		5527	R R	FJD
<i>his-2 ad-3A nic-2</i>	C94 1-112-13 43002		5528	R R R	FJD
<i>his-2 his-3 nic-2 al-1</i>	C94 1710 43002 1-234-471	5550		R R R	FJD
<i>his-2 nic-2</i>	C94 43002	5058	5059	R R	FJD
<i>his-2 nic-2</i>	Y152M14 43002	3219		R R	DDP
<i>his-2 nic-2 al-2</i>	C94 43002 Y112M38	5509	4933	R R R	FJD
<i>his-2 al-2</i>	C94 1-112-38		5057	R R	FJD
<i>nuc-1 ad-3A</i>	T28-M1 no#	1999		R R	TI
<i>rg-1 his-3 nic-2</i>	B53 Y152M9 43002		4770	R R R	FJD
<i>rg-1 cr-1</i>	B53 B123	624	418	R R	DDP
<i>his-3 nic-2</i>	Y269M5 43002	1855		R R	MEC
<i>his-3 nic-2 al-1</i>	1710 43002 1-234-471		5545	R R R	FJD
<i>ad-3A nic-2</i>	Y112M13 43002	4769		R R	FJD
<i>ad-3A nic-2</i>	38701 43002	142		R R	DDP
<i>ad-3A al-2</i>	1-112-15 1-112-38		5850	R R	FJD
<i>ad-3B nic-2 al-2</i>	3-10-446 43002 1-112-38	5325		R R R	FJD

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
Linkage Group I, continued					
<i>ad-3B nic-2</i>	2-17-37 43002	5286		R R	FJD
<i>ad-3B al-2</i>	1-112-4 15300		5263	R R	FJD
<i>ad-3B thi-1 al-2</i>	35203 56501 15300		259	R R R	DDP
<i>cr-1 thi-1 nit-1 al-1 nic-1 os-1</i>	L 56501 34547 34508 3416 B135		245	R R R R R R	DDP
<i>cr-1 thi-1 al-2</i>	B123 56501 15300	6658		R R R	DDP
<i>cr-1 nit-1 al-1 os-1</i>	B122 34547 34508 B135	258	288	R R R R	DDP
<i>cr-1 al-1 os-1</i>	B123 34508 B135	250		R R R	DDP
<i>cr-1 os-1</i>	B122 B135	289	280	R R	DDP
<i>cys-9 un-1</i>	T156 44409		7241	R R	DDP
<i>thi-1 met-6</i>	56501 35809	7856	7857	R R	DDP
<i>thi-1 ad-9 nit-1 het-5^{PA}</i>	56501 Y154M37 34547 PA	7348	7349	R R R R	DDP
<i>cr-2 al-2</i>	R2445 15300		2209	R R	ELT
<i>fls al-1</i>	STL6 34508		60	R R	DDP
<i>we-2 glp-1</i>	234(w) 234	2742	2743	R R	HGK
<i>nit-1 al-1 nic-1 os-1</i>	34547 34508 3416 B135	228		R R R R	DDP
<i>cyh-1 al-2 arg-6</i>	KH52(r) 15300 29997	3450	3451	R R R	DDP
<i>cyh-1 al-2 al-1</i>	KH52(r) 15300 34508	4550	4551	R R R	DDP
<i>cyh-1 al-2 nic-1</i>	KH52(r) 15300 S1413		4148	R	EK
<i>cyh-1 al-2 nic-1 arg-13</i>	KH52(r) 15300 S1413 RU12		4112	R R R R	EK
<i>cyh-1 al-1</i>	KH52(r) 34508		4242	R R	DDP
<i>cyh-1 al-1</i>	KH52(r) JH216	6657		R R	DDP
<i>mus-9 nic-2</i>	FK129 43002	6407	6408	R R	EK
<i>al-2 arg-6</i>	15300 29997	313	272	R R	DDP
<i>al-2 nic-1 het-1</i>	15300 3416 no#	7343	7344	R R I or II	DDP
<i>het-5^{PA} arg-13</i>	PA RU3	7345		R R	DDP
<i>al-2 nic-1 arg-13 un-18</i>	15300 S1413 RU12 <u>T</u> 54M94(t)	4113	4114	R R R R	EK
<i>al-2 arg-13</i>	15300 RU3	1728		R R	KJM
<i>al-2 arg-13</i>	15300 RU12	1723		R R	KJM
<i>al-2 arg-13</i>	15300 RU20	1722		R R	KJM
<i>al-2 cnr^S</i>	15300 no#(s)	99	263	R R	DDP
<i>al-2 hom</i>	15300 51504	5093	5094	R R	DDP
<i>al-2 os-1</i>	15300 P641	866		R R	DDP
<i>al-2 su(met-7)</i>	15300 S1		39	R R	DDP
<i>al-2 cfs(OY306)</i>	15300 OY306(s)		3529	R R	OCY
<i>al-2 R un-18</i>	15300 35408 <u>T</u> 54M94(t)	7242		R R R	DDP
<i>hom al-1</i>	51504 34508		5092	R R	DDP
<i>al-1 lys-3</i>	JH612 4545	7231		R R	DDP
<i>al-1 nic-1 os-1</i>	34508 3416 B135	3603		R R R	DDP
<i>al-1 nic-1 arg-13</i>	34508 3416 RU3	3655	3656	R R R	DDP
<i>al-1 aro-8</i>	34508 DH8	1814	1815	R R	BCT
<i>R un-18</i>	35408 <u>T</u> 54M94(t)	7232		R R	DDP

Linkage Group II

<i>pi trp-3</i>	B101 td24	2071	2072	L R	DDP
<i>pi un-15</i>	B101 <u>T</u> 54M50(t)	2435	2436	L R	DDP
<i>ro-7 arg-5 rip-1</i>	R2470 27947 4M(t)	6563	6564	L R R	DDP
<i>ro-7 rip-1</i>	R2470 4M(t)	3467	3468	L R	DDP
<i>cys-3 arg-5</i>	P22 27947	1290	4149	L R	DDP
<i>cys-3 eas</i>	NM27(t) UCLA 191	4689	4690	L R	MLS
<i>cys-3 fl</i>	P22 P		1289	L R	DDP
<i>un-24 het-6^{OR}</i>	DJ517 OR	7354		L L	DDP
<i>het-6^{PA} arg-12</i>	PA UM107	7350	7351	L R	DDP
<i>cot-5 het-C pyr-4 thr-2</i>	R2479 C 36601 35423	7147		L L L L	DDP
<i>cot-5 het-C^{OR} pyr-4 thr-2</i>	R2479 C ^{OR} 36601 35423	7355	7356	L L L L	DDP
<i>cot-5 het-c</i>	R2479	7447		L L	DDP
<i>het-c pyr-4</i>	c ^{OR} 36601	7306	7307	L L	DDP

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
Linkage Group II, continued					
<i>het-c^{AD} pyr-4 thr-2</i>	c ^{AD} 36601 35423	7313		L L L	DDP
<i>pyr-4 arg-12</i>	36601 UM 107	2997	2998	L R	DDP
<i>ro-3 arg-5 pe</i>	R2354 27947 Y 8743m	2705	2705	L R R	DDP
<i>ro-3 pe</i>	R2354 Y 8743m	3008	159	L R	DDP
<i>thr-2 arg-5</i>	35423 27947	7192	7193	L R	DDP
<i>bal arg-5</i>	B56 27447		2751	L R	DDP
<i>arg-5 aro-3</i>	27947 C167	7194		R R	DDP
<i>arg-5 pe fl</i>	27947 Y8743m L	4150	2706	R R R	EK
<i>arg-5 fl</i>	27947 L	312	155	R R	DDP
<i>arg-5 pe fl trp-3</i>	27947 Y8743m L td37	4115	4116	R R R R	EK
<i>arg-5 arg-12^S</i>	27947 37301s		895	R R	RHD
<i>arg-5 mus-27</i>	27947 FK 124	6430	6431	R R	EK
<i>arg-5 eas</i>	CD6 UCLA 191	4681	4682	R R	MLS
<i>nuc-2 aro-1</i>	T28-M2 Y7655	2000		R R	TI
<i>pe aro-1 fl</i>	Y8743m Y7655 L	1681		R R R	RWB
<i>pe fl</i>	Y8743m L	3072	3073	R R	KDM
<i>pe fl</i>	Y8743m L	4169	4170	R R	EK
<i>pe fl</i>	L L	5512	5511	R R	FJD
<i>arg-12 ure-3</i>	UM107 F29		7195	R R	DDP
<i>arg-12 ure-3 un-20</i>	UM107 F29 P2402		7196	R R	DDP
<i>arg-12 ure-3 un-20</i>	UM107 F29 P2402t		7308	R R R	DDP
<i>arg-12 un-20</i>	UM107 P2402	7197		R R	DDP
<i>arg-12 fl rip-1</i>	UM107 P 4M	7198	7207	R R R	DDP
<i>mus-27 nuc-2</i>	FK 124 T28-M 2	6432	6433	R R	EK
<i>un-20 ace-1</i>	P2402 Y 2492	7199		R R	DDP
<i>ace-1 eas</i>	Y 2492, JD105	8111		R R	DDP
<i>fl trp-3</i>	P605 td24		7200	R R	DDP
<i>trp-3 un-15</i>	td24 T54M 50	7201	7202	R R	DDP

Linkage Group III

<i>cum cyt-22 r(Sk-2)-1</i>	P5241 289-4 P527	7154		L L L	DDP
<i>cum r(Sk-2)-1</i>	P5241 P527	7379	7380	L L	BCT
<i>cum r(Sk-2)-1 acr-7</i>	P5241 P527 P1676		7155	L L L	DDP
<i>cum r(Sk-2)-1 acr-7</i>	P5241 P527 P1676		7389	L L L	BCT
<i>cum Sk-2^K acr-7</i>	P5241 B P1676		7432	L L L	DDP
<i>cum Sk-2^K acr-2</i>	P5241 J KH5	7383	7384	L III C	BCT
<i>cum Sk-3</i>	P5241 P	7382	7381	L III	BCT
<i>cum Sk-3 his-7</i>	P5241 P Y 152M 31	7390	7391	L III R	BCT
<i>cum r(Sk-3)</i>	P5241 P		7396	L L	BCT
<i>cum r(Sk-3) leu-1</i>	P5241 P 33757		7394	L L R	BCT
<i>cum acr-7</i>	P5241 P1676	7156	7157	L L	DDP
<i>cum acr-7 dow</i>	P5241 P1676 P616	4540	4541	L L R	DDP
<i>cum acr-2 his-7</i>	P5241, KH5, Y 152M 31	8599	8600	L C R	DDP
<i>cum dow</i>	P5241 P616	4542	4543	L R	DDP
<i>acr-7 dow</i>	P1676 P616	7078	7079	L R	DDP
<i>Sk-2^K acr-7</i>	Borneo P1676	6930		L L	DDP
<i>Sk-2^K acr-7 leu-1 his-7</i>	Borneo P1676 33757 Y 152M 31		7373	III L R R	BCT
<i>Sk-2^K acr-2</i>	P KH5	7385	7386	III III	BCT
<i>Sk-2^K acr-2</i>	Borneo KH5	6928	6929	L L	DDP
<i>Sk-2^K acr-2 leu-1</i>	Borneo KH5 33757	7375	7374	III C R	BCT
<i>Sk-2^K acr-2 his-7</i>	Borneo KH5 Y 152M 31	7376		III C R	BCT
<i>Sk-2^K acr-2 leu-1 his-7</i>	Borneo KH5 33757 Y 152M 31	7387	7388	III C R R	BCT
<i>Sk-2^K leu-1</i>	Borneo 33757	7371		III R	BCT
<i>Sk-2^K his-7</i>	Borneo Y 152M 31	7378		III R	BCT
<i>Sk-2^K phe-2 dow</i>	Borneo Y 16329 P616	4538	4539	L R R	DDP
<i>Sk-2^K dow</i>	Borneo P616	4260	4261	L R	DDP

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
Linkage Group III, continued					
<i>Sk-3^K acr-7</i>	-- P1676	6931	6932	L L	DDP
<i>r(Sk-3) acr-7 ser-1</i>	P P1676 C127	7397		L L R	BCT
<i>acr-2 spg</i>	KH5(r) no#	7158	7159	C C	DDP
<i>acr-2 uvs-4 leu-1</i>	KH5(r) ALS12 33757	4196		C R R	EK
<i>acr-2 met-8 leu-1</i>	KH5(r) P53 33757	7177		C R R	DDP
<i>acr-2 leu-1 his-7</i>	KH5(r) leu-1 his-7	7160	7178	C R R	DDP
<i>acr-2 leu-1 trp-1 dow</i>	KH5(r) 33757 10575 P616	4117	4118	C R R R	EK
<i>acr-2 trp-1 mus-21</i>	KH5(r) 10575 FK120	6420	6421	C R R	EK
<i>acr-2 trp-1 nit-7 dow</i>	KH5(r) 10575 <u>V</u> 1M59 P616	6018		C R R R	DDP
<i>acr-2 trp-1 dow</i>	KH5(r) 10575 P616	4119	4120	C R R	EK
<i>acr-2 dow</i>	KH5(r) P616	2036	2037	C R	DDP
<i>sc trp-1</i>	5801 10575	190	239	C R	DDP
<i>ad-4 pro-1</i>	Y155M13(F10) 21863		468	R R	MEC
<i>ad-4 leu-1</i>	44206t 33757	7161		R R	DDP
<i>ad-4 leu-1</i>	Y112M160(F4) 33757		463	R R	MEC
<i>uvs-4 leu-1</i>	ALS12 33757		4197	R R	EK
<i>leu-1 thi-2</i>	33757 9185		7162	R R	DDP
<i>acr-6 shg</i>	KH19 KH160	2325	2326	R R	KSH
<i>trp-1 mus-21</i>	10575 FK121	6416	6417	R R	EK
<i>trp-1 vel</i>	10575 B18	173	298	R R	DDP
<i>nit-7 dow</i>	<u>V</u> 1M59 P616	7163		R R	DDP
<i>nit-7 erg-3</i>	<u>V</u> 1M59 UV41	7247	7248	R R	DDP
<i>vel tyr-1</i>	B18 Y6994	7179	7180	R R	DDP
<i>dow erg-3</i>	P616 UV41	7243	7244	R R	DDP

Linkage Group IV

<i>uvs-3 trp-4 pan-1</i>	ALS11 Y2198 5531	4194	4195	L R R	EK
<i>cys-10 cut pyr-1</i>	39816 LLM1 H263	2707		L R R	DDP
<i>cys-10 pdx-1 pan-1</i>	39816 37803 5531	4121	4122	L R R	EK
<i>cys-10 pdx-1 pan-1 uvs-2</i>	39816 37803 5531 no#	4123	4124	L R R R	EK
<i>cys-10 col-4</i>	39816 70007c	1534		L C	DDP
<i>cys-10 col-4 cot-1</i>	39816 70007c C102(t)	2752	2753	L R R	DDP
<i>cys-10 cot-1 uvs-2</i>	39816 C102(t) no#	2017	2018	L R R	DDP
<i>cys-10rug</i>	39816 B57	2615	2616	L R	DDP
<i>cys-10 uvs-2</i>	39816 no#	1989	2266	L R	DDP
<i>cys-10 pmb</i>	39816 cnr-37(r)	6884	6885	L R	DDP
<i>cut psi-1</i>	LLM1 34C	8253	8254	L R	DDP
<i>psi-1 pdx-1</i>	34C, 37803	8255	8256	R R	DDP
<i>pyr-1 col-4 pyr-3</i>	H263 70007c 37815(t)	390		R R R	MBM
<i>pyr-1 arg-2</i>	H263 33442	394		R R	MBM
<i>pyr-1 rug</i>	H263 B57	186	187	R R	DDP
<i>pyr-1, pyr-3</i>	DFC33, DFC3		8392	R R	RHD
<i>pdx-1 col-4</i>	35405 70007c		388	R R	MBM
<i>pdx-1 col-4</i>	37803 70007c	404		R R	MBM
<i>pdx-1 col-4</i>	39106p 70007c		345	R R	MBM
<i>pdx-1 col-4 ad-6 pan-1 rug</i>	37803 B148 28610 5531 B57	4962		R R R R R	BDM
<i>pdx-1 tol</i>	37803 N83	1948		R R	DNP
<i>pdx-1 pan-1 pyr-2</i>	37803 5531 38502	161	170	R R R	DDP
<i>pdx-1 pan-1 cys-4</i>	37803 5531 K7	4125	4126	R R R	EK
<i>pdx-1 pan-1 cys-4 uvs-2</i>	37803 5531 K7 no#	4127	4128	R R R R	EK
<i>pdx-1 cot-1 cys-4</i>	37803 C102(t) K7	4151	4152	R R R	EK
<i>pdx-1 cys-4</i>	37803 K7	1291		R R	DDP
<i>mtr pmb</i>	Pm-22(r) cnr-37(r)		2276	R R	LW
<i>col-4 arg-2</i>	70007c 33442		389	R R	MBM
<i>col-4 pyr-3</i>	70007c 37815(t)	392		R R	MBM
<i>col-4 pyr-3</i>	70007c 45502		344	R R	MBM

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

Linkage Group V

<i>dgr-1 lys-1</i>	KHY15 33933	7238	7239	L L	CTY
<i>dgr-1 at al-3 his-6</i>	KHY15 M111 RP100 Y152M105	7587	7560	L C R R	DDP
<i>dgr-1 al-3 his-6</i>	KHY15 RP100 Y152M105	7150	7151	L C R	DDP
<i>caf-1 lys-1</i>	KH101 33933	7164		L L	DDP
<i>caf-1 lys-1 cyt-9 at cyh-2 al-3</i>	KH101 33933 17 NM221 KH53 RP100	7182		L L L C R R	DDP
<i>caf-1 at</i>	KH101(r) M111	3657	3658	L C	DDP
<i>caf-1 at al-3</i>	KH101 M111 RP100		7165	L C R	DDP
<i>caf-1 al-3 his-6</i>	KH101(r)(t) RP100 Y152M105	3752	3753	L R R	DDP
<i>lys-1 cyt-9</i>	33933 17		7183	L L	DDP
<i>lys-1 at</i>	33933 M111	7166	7184	L C	DDP
<i>lys-1 cyh-2 al-3 his-6</i>	33933 KH53 RP100 Y152M105	4130		C R R R	EK
<i>lys-1 cyh-2 al-3</i>	33933 KH53(r) RP100	4135		C R R R R	EK
<i>inl his-6</i>	83201(t) Y152M105				
<i>lys-1 cyh-2 al-3</i>	33933 KH53(r) RP100		4132	C R R R R	EK
<i>inl pab-2</i>	83201(t) H193				
<i>lys-1 cyh-2 al-3</i>	33933 KH53(r) RP100		4129	C R R R R R	EK
<i>inl pab-2 his-6</i>	83201(t) H193 Y152M105				
<i>lys-1 al-3 inl pab-2</i>	33933 RP100 83201(t) H193	4131		C R R R	EK
<i>lys-1 inl</i>	33933 37401	209	1097	C R	DDP
<i>lys-1 inl his-6</i>	33933 37401 Y152M105	1535	4136	C R R	DDP
<i>lys-1 pk</i>	33933 B6	192		C R	DDP
<i>lys-1 asn</i>	33933 S1007	1181	1182	C R	DDP
<i>lys-1 mus-11</i>	33933 FK117	6413		L R	EK
<i>cyt-9 at</i>	17 M111	7185		L C	DDP
<i>at cyh-2 al-3</i>	M111 KH53 RP100	7186	7167	C R R	DDP
<i>at al-3 his-6</i>	M111 RP100 Y152M105	2089	2090	C R R	DDP
<i>at his-6</i>	M111 Y152M105	1991	1992	C R	DDP
<i>ilv(?6201) inl</i>	?6201 37401	204	311	R R	DDP
<i>ilv-1 inl</i>	16117 64001	676		R R	MEC
<i>rol-3 inl</i>	R2498 89601	1354		R R	ELT
<i>cyh-2 leu-5</i>	KH53(r) 45208		7168	R R	DDP

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
Linkage Group V, continued					
<i>cyh-2 sp al-3</i>	KH53(r) B132 RP100	7187	7188	R R R	DDP
<i>cyh-2 al-3</i>	KH53(r) RP100	7169		R R	DDP
<i>cyh-2 al-3 inl pab-2</i>	KH53(r) RP100 83201(t) H193	4133	4134	R R R R	EK
<i>md cl</i>	MW 84 CL11		1297	R R	AS
<i>ndc-1 inl</i>	1(t) 89601		3441	R R	DRS
<i>cot-4 inl</i>	R2101(t) 89601	1357		R R	ELT
<i>ure-2 am</i>	47 32213		4299	R R	HGK
<i>am inl</i>	am132 37401	6649		R R	JAK
<i>ure-1 his-1</i>	9 C91		4298	R R	HGK
<i>spe-1 inl</i>	462JM 89601	4265	4266	R R	RHD
<i>spe-1 inl</i>	TP-138 89601	4267		R R	RHD
<i>his-1 al-3</i>	C84 Y234M470		7170	R R	DDP
<i>his-1 al-3 inl</i>	C84 RP100 89601	8257		R R R	DDP
<i>his-1 met-3</i>	K744 36104		780	R R	DGC
<i>erg(RES208) al-3</i>	RES208(r) al-3		3155	R R	RES
<i>al-3 inl</i>	RP100 83201(t)	2309	2300	R R	DDP
<i>al-3 inl</i>	RP100 89601	2308	2301	R R	DDP
<i>al-3 pab-1</i>	RP100 1633	7171	7172	R R	DDP
<i>al-3 ad-7</i>	RP100 P73B171	7173	7174	R R	DDP
<i>al-3 pyr-6 oak</i>	RP100 DFC37 R2358	7175		R R R	DDP
<i>udk uc-4</i>	FB-D425 RW341	4284	4285	R R	FPB
<i>inl gln-1</i>	89601 R1015	1450		R R	ER
<i>inl met-3</i>	37401 92935	2159		R R	GAM
<i>inl pk pab-2</i>	37401 B6 H193	242		R R R	WNS
<i>inl col-9</i>	89601 R2417		1385	R R	ELT
<i>inl ro-4</i>	89601 R2428	1356		R R	ELT
<i>inl asn</i>	37401 C123	284		R R	WNS
<i>inl acu-1</i>	R233 JI48	1731		R R	RBF
<i>inl his-6</i>	37401 Y152M105	1285	1286	R R	DDP
<i>pk asp</i>	B6 S1007		243	R R	DDP
<i>pk¹¹ pab-1</i>	17-575 1633?	3420	3421	R R	AMS
<i>pk¹² pab-1</i>	19-773(peak) 1633?	3422	3423	R R	AMS
<i>ro-4 inv</i>	B38 no#		7176	R R	DDP
<i>un-9 his-6</i>	T54M96 Y152M105		7189	R R	DDP
<i>met(152C) inl</i>	152C(t) 89601		3759	(?) R	DRS
<i>un(20J) inl</i>	20J(t) 89601		3778	R R	DRS
<i>un(21T) inl</i>	21T(t) 89601		3782	R R	DRS
<i>un(121C) inl</i>	121C(t) 89601		3769	R R	DRS
<i>un(134C) inl</i>	134C(t) 89601		3770	R R	DRS
<i>un(165C) inl</i>	165C(t) 89601		3772	R R	DRS
<i>un(16J) inl</i>	16J(t) 89601		3777	R R	DRS
<i>un(181C) inl</i>	181C(t) 89601		3787	R R	DRS
<i>un(58E) inl</i>	58E(t) 89601		3775	(?) VR	DRS

Linkage Group VI

<i>chol-2 nit-6</i>	47904(t) OP4	7212		L L	DDP
<i>chol-2 nit-6 ser-6 het-8^{PA}</i>	47904 OP4 DK42 het-8 ^{PA}	7470	7471	L L L L	JFL
<i>chol-2 nit-6 ser-6 het-8^{HO}</i>	47904 OP4 DK42 het-8 ^{P516}	7485	7486	L L L L	JFL
<i>chol-2 nit-6 het-8^{OR} ser-6 ad-8</i>	47904 OP4 no# DK42 Y112M343	7404	7405	L L L L L	JFL
<i>chol-2 ad-8 lys-5</i>	47904(t) Y226M58 DS6-85	3251	3252	L L L L R	OMM
<i>un-4 pan-2</i>	66204(t) Y153M96				
<i>chol-2 trp-2</i>	47904(t) 75001	1087	1088	L R	DDP
<i>chol-2 ylo-1 rib-1 pan-2</i>	47904(t) Y30539y 51602(t)		5179	L L R R R	EK
<i>trp-2</i>	Y153M96 41				
<i>chol-2 ylo-1 trp-2</i>	47904(t) Y30539y 41	5180	5181	L L R	EK
<i>chol-2 ylo-1 ws-1</i>	47904(t) Y30539y RP99	3519	3520	L L R	DDP

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

Linkage Group VII

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

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
<u>B. Two Linkage Groups Marked</u>					
I;II					
<i>fr;arg-5</i>	B110;27947	328	279	IL;IIC	DDP
<i>sod-1;fl</i>	3C;P	7439	7440	IL;IIL	DON
<i>ylo-2;eas</i>	Y256M230;UCLA191	4671	4672	IL;IIR	MLS
<i>rg-1 cr-1;pe fl</i>	B53 B123;Y8743m L	331		IC R;IIR R	DDP
<i>sn cr-1;pe fl</i>	C136 B123;Y8743m L	4162	4163	IC R;IIR R	EK
<i>ad-3B;pe fl</i>	2-17-51;Y8743m L	5537	5536	IR;IIR R	FJD
<i>ad-3B;pe fl</i>	2-17-74;Y8743m L	5535		IR;IIR R	FJD
<i>ad-3B;pe fl</i>	2-17-75;Y8743m L	5534		IR;IIR R	FJD
<i>al-1;arg-5</i>	34508;27947	1205	1206	IR;IIC	DDP
<i>al-1;pe</i>	34508;Y8743m	1203	1204	IR;IIR	DDP
<i>cr-1;pe fl</i>	B123;Y8743m L	4167	4168	IR;IIC R	EK
<i>Fsp-2;Fsp-1</i>	DL709;ALS141	5069	5070	IR;IIR	NBR
<i>nuc-1;nuc-2</i>	<u>T</u> 28-M1; <u>T</u> 28-M2	1998		IR;IIR	TI
<i>uc-2;pyr-4 uc-1</i>	RW135;36601 RW57	2203		I;IIL II	LGW
<i>wc-2;fl</i>	ER33 P	7203	7204	IR;IIR	FRL
I;III					
<i>acr-4;shg</i>	KH16(r);KH160	2322		IL;IIR	KSH
<i>leu-4;leu-1</i>	FLR92;D221	1501		IL;IIR	SRG
<i>sn cr-1;acr-2 leu-1 dow</i>	C136 B123;KH5(r) 33757 P616	5177	5178	IC R;IIIC R R	EK
<i>sn cr-1;acr-2 leu-1 trp-1 dow</i>	C136 B123;KH5(r) 33757 10575 P616	5174	5175	IC R;IIIC R R R	EK
<i>sn cr-1;acr-2 trp-1 dow</i>	C136 B123;KH5(r) 10575 P616		5176	IC R;IIIC R R	EK
<i>su(mtr);fpr-3</i>	18;no#	2999		IC;IIR	JAK
<i>al(Y234M468);ad-2</i>	Y234M468a1;Y175M256	956		IR;IIR	AMK
<i>arg-3 ad-3A nic-2;ad-2</i>	30300 1-112-13 43002;1-175-256	5553		IL R R;IIR	FJD
<i>arg-3 ad-3A ad-3B nic-2</i>	30300 1-112-13 35203 43002; 5555			IL R R R R;	FJD
<i>al-1;ad-2</i>	1-234-471;1-175-256			IIR	
<i>ff-3;ty-3(T22)</i>	no#;135-333(T22)	2962		IR;IIR	JFF
<i>his-2 ad-3A ad-3B nic-2;ad-2</i>	C94 1-112-13 35203 43002; 1-175-256	5307		IR R R R;IIR	FJD
<i>his-2 ad-3A ad-3B nic-2</i>	C94 1-112-13 35203 43002	5539	5540	IR R R R R;	FJD
<i>al-1;ad-2</i>	1-234-471;1-175-256			IIR	
<i>his-2 ad-3A ad-3B nic-2</i>	C94 1-112-13 35203 43002	5532		IR R R R R;	FJD
<i>al-2;ad-2</i>	1-112-38;1-175-256			IIR	
<i>nuc-1;pgov^c</i>	<u>T</u> 28-M1;R42	3480		IR;IIR	RLM
I;IV					
<i>acr-3 nic-1 pdx-1</i>	KH14(r) S1413;37803		4630	IL R;IVR	JL
<i>ad-5 nic-2 thi-1;cot-1</i>	Y152M40 43002;56501;C102(t)	256		IL R R;IVR	DDP
<i>arg-3; arg-2, pyr-3</i>	CD186; CD80, DFC3	8393		IL; IVR, IVR	RHD
<i>csp-1;bd</i>	UCLA37;no#	2948	4547	IL;IVR	SB
<i>csp-1;cel bd</i>	UCLA37;R2366o no#	3484		IL;IVR R	SB
<i>En(pdx-1);pdx-1</i>	K30;44602p	422		IL;IVR	DDP
<i>fmf-1;pyr-3</i>	PB-J6;KS43	3108		IL;IVR	TEJ
<i>fmf-1;tol pan-1</i>	PB-J6;N83 5531	3109	3110	IL;IVR R	TEJ
<i>leu-3 arg-1 ad-3B</i>	R156 36703 2-17-114		3819	IL L R R;IVR	AJG
<i>al-1 tol C D</i>	car-10 N83				
<i>leu-3;cot-1</i>	R156;C102(t)	2253		IL;IVR	RKL
<i>leu-3 cyt-1 arg-3;tol</i>	R156 C115 30300;N83	7337		IL L L;IVR	DDP
<i>leu-3 suc;tol pan-1</i>	R156 66702;N83 5531		7322	IL L;IVR R	DDP
<i>leu-3 his-2 cr-1</i>	R156 Y152M14 B123		249	IL C I I;IVR	DDP
<i>al-1 cot-1</i>	34508;C102(t)				
<i>mei-3;tol</i>	N289;N83		2765	IL;IVR	DNP
<i>mei-3;uvs-2</i>	N289;no#	4616	4617	IL;IVR	ALS

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

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

Loci	Alleles	FGSC #		Linkage group	Obtained from
		A	a		
I;VI, continued					
<i>ssu-8 ad-3B al-2;pan-2</i>	Y319-37;12-21-22 Y112M38; 2487 Y153M96			IR R R;VIR	AJG
<i>ssu-8 ad-3B al-2;pan-2</i>	Y319-37;12-21-76 Y112M38; 2488 Y153M96			IR R R;VIR	AJG
I;VII					
<i>csp-1;nic-3</i>	UCLA37;Y31881	2514		IL;VIIL	CPS
<i>fr;nic-3</i>	B110;Y31881		254	IL;VIIL	DDP
<i>fs-3;nic-3</i>	52-2;Y31881		3239	IL;VIIL	OMM
<i>sn cr-1;csp-2</i>	C136 B123;UCLA101	2697	2002	IC R;VII	REN
<i>sn cr-1;csp-2</i>	C136 B123;UCLA101	4157		IC;VII	EK
<i>sn cr-1;nic-3 met-7 arg-10</i>	C136 B123;Y31881 4894 B317	5219		IC R;VIII R R	EK
<i>is-3;hlp-2</i>	K458;HC114		2319	IR;VIIR	HCC
<i>his-3 aga</i>	Y155M261; UM906		8387	IR;VIIR	RHD
<i>nic-2;csp-2</i>	43002;FS590	2515		IR;VII	CPS
<i>nic-2;csp-2</i>	43002;UCLA102	3871		IR;VII	CPS
<i>uvs-6;nic-3</i>	ALS35;Y31881	4199		IR;VIIL	EK
I;--					
<i>arg-3;mei-4</i>	30300;N395	2763		IL;--	DNP
<i>tyr(LW101);glt</i>	LW101(s);D240(r)	2736		IL;--	GAM
<i>ad-3B;ssu-5</i>	2-17-34;Y319-45	2483		IR;--	AJG
<i>ad-3B;ssu-5</i>	2-17-34;Y319-45	2484		IR;--	AJG
<i>suc;ma-1</i>	46005;M20	1112		IR;--	KDM
<i>suc;ma-2</i>	46005;M24	1113		IR;--	KDM
II;III					
<i>arg-5 pe fl;acr-2</i>	27947 Y8743m L;KH53(r)	5169	5170	IIR R R;IIIC	EK
<i>aro-1;trp-1</i>	Y7655;10575a	1145		IIR;IIIR	RBC
<i>fl;Sk-2</i>	P;no#	3297	3298	IIR;III	DDP
<i>fl;Sk-3</i>	P;no#	3579	3580	IIR;IIIC	DDP
<i>trp-3;su(trp-3^{td2})-2</i>	S1952;su2		6136	IIR;III	ELT
II;IV					
<i>pmg;pmb</i>	no#;can-37(r)	4810	4811	IIL;IVR	RMD
<i>pmg;pmn</i>	no#;Pm-22(r)	4808	4809	IIL;IVR	RMD
<i>arg-12^S;pyr-3</i>	37301s;37301p		894	IIR;IVR	RHD
<i>col-1;pe</i>	Y8743c;Y8743m		535	IIR;IVR	ELT
<i>fl;dn</i>	P;38502d	3517	3518	IIR;IVR	DDP
<i>pe fl cot-1</i>	Y8743m L;C102(t)		639	IIR R;IVR	RWB
<i>pe fl;le-1</i>	Y8743m L;S4355		1402	IIR R;IVR	ELT
<i>pe fl;gul-3 pt cot-1</i>	Y8743m L;845 NS1(t) C102(t)		1174	IIR R;IVR R R	HFT
<i>pe fl;pan-1</i>	Y8743m L;5531		3532	IIR R;IVR	ELT
II;V					
<i>cyb-3;his-6</i>	A10;Y175M16		3427	IIL;VR	DVW
<i>ro-3;inl</i>	R2354;89601	2311		IIL;VR	ELT
<i>aro-3;inl</i>	R2202;89601	1098		IIR;VR	MEC
<i>aro-4;inl</i>	R2219;89601	1105		IIR;VR	MEC
<i>en(am)-2;am</i>	C24;32213	1624		IIR;VR	MS
<i>fl;his-6</i>	P605;Y152M105	1537	1538	IIR;VR	DDP

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

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

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

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

C. Three Linkage Groups Marked

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;IIC 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 5594 5593 IR;IIR;IVR R FJD
C102(t)
al-1;ad-2;cot-1 1-234-471;1-175-256;C102(t) 5588 5589 IR;IIR;IVR FJD
al-1;ad-2;mtr col-4 1-234-471;1-175-256;17-1-64 5605 IR;IIR;IVR FJD
cot-1 70007c C102(t) R R
al-2;ser-5;cot-1 15300;JBM9;C102(t) 2612 IR;IIR;IVR JBM
his-3 al-1;ad-2;col-4 1-152-111 1-234-471;1-175-256; 5595 5596 IR R;IIR; IVR R FJD
cot-1 70007c C102(t)
his-3 al-1;ad-2;cot-1 1-152-111 1-234-471;1-175-256; 5590 IR R;IIR;IVR FJD
C102(t)
his-3 al-1;ad-2;mtr 1-152-111 1-234-471;1-175-256; 5601 5602 IR R;IIR;IVR R FJD
col-4 17-1-64 70007c
sn cr-1;acr-2;cys-10 C136 B123;KH5(r);39816 5188 IC R;IIC;IVL EK
pdx-1 pan-1 uvs-2 37803 5531 no# R R R

I;III;V

al-2;sc;lys-1 15300;5801;33933 230 231 IR;IIR;VC DDP
arg-3 ad-3A ad-3B nic-2; 30300 1-112-13 35203 43002; 5556 IL R R R;IIR FJD
ad-2;inl 1-175-256;JH319 VR
arg-3 ad-3A ad-3B nic-2 30300 1-112-13 35203 43002; 5554 5552 IL R R R R FJD
al-1;ad-2;inl 1-234-471 1-175-256;JH319 IIR;VR

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

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

Loci	Alleles	FGSC #		Linkage group	Obtained from
		mating type A	a		
II;IV;V					
<i>acr-2;uvs-2;his-6</i>	KH5(r);no#;Y 152M 105	4190		IIC;IVR;VR	EK
<i>ff-1;ylo-1;inl</i>	744;Y 30539y;83201(t)	2967		IIR;IVL;VR	JBC
<i>fl;dn;inl</i>	P;38502d;37401	3633	3634	IIR;IVR;VR	DDP
II;V;VII					
<i>aro-9;qa-2;inl</i>	M6-11;89601;M246	3952		IIR;VR;VIIR	MEC
II;VI;VII					
<i>bal;ylo-1;met-7</i>	B56;4894;Y30539y		330	IIL;VIL;VIIR	DDP
<i>arg-5;sit-2;sit-5</i>	no#;GN328;GN218		4223	IIR;--;--	GWC
III;IV;V					
<i>acr-2;uvs-2;his-6</i>	KH5(r);no#;Y 152M 105		4190	IIIC;IVR;VR	EK
III;IV;VI					
<i>trp-1;cot-1;ylo-1</i>	10575;C102(t);Y30539y	1095		IIIR;IVR;VIL	DDP
III;--;--					
<i>ota;sit-2;sit-3</i>	UM728;GN328;GN235		4219	IIIR;--;--	GWC
<i>ota;sit-2;sit-5</i>	UM728;GN328;GN218		4224	IIIR;--;--	GWC
VI;VII;--					
<i>pan-2;nic-3;fs-2</i>	Y153M96;Y31881;10-4(t)	3238		VIR;VIIL;--	OMM
<u>D. Four Linkage Groups Marked</u>					
<i>sn cr-1 cyh-1;ad-2;uvs-2;trp-2</i>		7880		IC R R;IIIR;IVR;VIR	DRS
<i>al-1;arg-5;trp-1;ylo-1</i>	34508;27947;10575;Y30539y	2124	1888	IR;IIC;IIIR;VIL	DDP
<i>al-1;arg-5;cot-1;inl</i>	34508;27947;C102(t);37401	1885	1886	IR;IIC;IVR;VR	DDP
<i>al-2;fl;cot-1;inl</i>	1-112-38;L;C102(t);JH319	5621		IR;IIR;IVR;VR	FJD
<i>al-2;pe fl;cot-1;pan-2</i>	1-112-38;L L;C102(t);1-153-96	5516		IR;IIIR;IVR;VIR	FJD
<i>cr-1 al-2;fl;cot-1;inl</i>	B123 1-112-38;L;C102(t);JH319	5622		IR;IIR;IVR;VR	FJD
<i>nic-2 cyh-1 al-2;arg-5;</i> <i>pan-1;met-7</i>	43002 KH53(r) 15300;27947; 5521;4894	5152		IR R R;IIIR;IVR VIIR	
<i>al-2;uvs-4;cot-1;pan-2</i>	Y112M38;ALS12;C102(t);Y153M96	4585	4586	IR;IIIR;IVR;VIR	FJD
<i>al-2;uvs-5;cot-1;pan-2</i>	Y112M38;ALS13;C102(t);Y153M96	4587	4588	IR;IIIR;IVR;VIR	FJD
<i>al-2;uvs-5;cot-1;pan-2</i>	Y112M38;ALS13;C102(t); Y387-15.7	2716	2717	IR;IIIR;IVR;VIR	FJD
<i>al-2;cot-1;inl;pan-2</i>	1-112-38;C102(t);JH319;1-153-96	5542		IR;IVR;VR;VIR	FJD
<i>arg-3 al-2;cot-1;inl;pan-2</i>	30300 1-112-38;C102(t);JH319; 1-153-96	5614		IL R;IVR;VR;VIR	FJD
<i>cr-1 al-2;cot-1;inl;</i> <i>pan-2</i>	B123 1-112-38;C102(t);JH319; 1-153-96	5615		IR R;IVR;VR;VIR	FJD
<i>his-3 al-2 cot-1 inl pan-2</i>	1-152-111 1-112-38;C102(t); JH319;1-153-96	5040		IR R;IVR;VR;VIR	FJD
<i>lys-4 al-2 cot-1</i> <i>inl pan-2</i>	ST3954 1-112-38;C102(t); JH319;1-153-96	5039	5048	IR R;IVR;VR;VIR	FJD
<i>nic-1 al-2;cot-1;inl;pan-2</i> <i>1-153-96</i>	39113 1-112-38;C102(t);JH319;	5623	5625	IR R;IVR;VR;VIR	FJD
<i>cyh-1 al-2 al-1;bd;inl</i> <i>al-3;csp-2</i>	KH52(r) 15300 34508;no# 83201(t);RP100(t);UCLA101		4554	IR R R;IVR VR R;VIIL	DDP

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

E. Five Linkage Groups Marked

<i>al-2;fl;cot-1;inl;pan-2</i>	1-112-38;L;C102(t);JH319;1-153-96		5620	IR;IIR;IVR;VR;VIR	FJD
<i>al-2;cot-1;inl;pan-2; arg-10</i>	1-112-38;C102(t);JH319; 1-153-96;B317	5627	5626	IR;IVR;VR;VIR; VIIR	FJD
<i>acr-2;pdx-1;at;ylo-1;wc-1</i>	KH5(r)37803 M111 Y30539y P829	1985	1986	IIIC;IVC;VC;VIL;VIIR	DDP
<i>sn cr-1;arg-5;acr-2;pdx-1 mtr pan-1;al-3 inl</i>	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

<i>arg-5;acr-2;mtr;al-3 inl; rib-1;met-7</i>	27947;KH53(r);15;RP100 83201(t);51602(t);4894	5205	5206	IIR;IIIC;IVR; VR R;VIR;VIIR	EK
<i>bal;acr-2;pdx-1;at; ylo-1;wc-1</i>	B56;KH5(r);37803;M111; Y30539y;P829	2014	2015	IIR;IIIR;IVR; VC;VIR;VIIR	DDP
<i>arg-5;acr-2;psi-1;at; ylo-1;wc-1</i>	27947;KH5;34C(t);M111; Y30539y;P829	6828	6829	IIR;IIIL;IVR VC;VIL;VIIR	DDP

G. Seven Linkage Groups Marked

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

PART III. Mitochondrial Mutant Stocks

Symbol	Isolation designation or stock #	MT	FGSC #	Nuclear gene markers present	Genetic back-ground	Obtained from
--------	----------------------------------	----	--------	------------------------------	---------------------	---------------

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

ABNORMAL

[<i>abn-1</i>]	no#	<i>a</i>	1448	<i>inl</i> (37401)	M	DJL
[<i>abn-2</i>]	no#	<i>A</i>	1458		M	JFW

CYANIDE INSENSITIVE

[<i>cni-3</i>]	<u>1</u>	<i>A</i>	3304	<i>inl</i> (89601)	M	DLE
------------------	----------	----------	------	--------------------	---	-----

EXTRANUCLEAR

[<i>exn-1</i>]	N4-9-4	<i>a</i>	2475	<i>pan-2</i> (B3)		HB
[<i>exn-2</i>]	X-21	<i>a</i>	2476	<i>al-2</i> (15300); <i>nic-1</i> (3416)	M	HB
[<i>exn-4</i>]	P85	<i>a</i>	2477	<i>al-2</i> (15300); <i>pan-2</i> (B3)	M	HB
[<i>exn-5</i>]	exn-5-1	<i>a</i>	2478		M	HB
[<i>exn</i> (C93)]*	C93	<i>A</i>	3557		SL	THP

* Probably ATPase mutant; complements in heterokaryon with [*poky*].

MATERNAL INHERITANCE

[<i>mi-2</i>]	mi-2-3.3	<i>A</i>	1580		SL3	PSL
[<i>mi-2</i>]	mi-2-3.5	<i>a</i>	1581		SL3	PSL
[<i>mi-2</i>]	mi-2R1	<i>a</i>	1233		M	MBM
[<i>mi-2</i>]	mi-2-3.1	<i>A</i>	1579	<i>ad-4</i> (F4)	SL3	PSL
[<i>mi-2</i>]	mi-2-3.7	<i>a</i>	1582	<i>ad-4</i> (F4)	SL3	PSL
[<i>mi-3</i>]	no#	<i>A</i>	1729		SL	NJW
[<i>mi-3</i>]	2543	<i>A</i>	2472	<i>su-1</i> ([<i>mi-3</i>])(CR-52A)	M	HB
[<i>mi-3</i>]	2543	<i>a</i>	7595	<i>su-1</i> ([<i>mi-3</i>])(CR-52A) <i>pan-2</i> -B3	M	FEN
[<i>mi-3</i>]	3754	<i>a</i>	382		M	MBM
[<i>mi-3</i>]	3754	<i>A</i>	4691	<i>eas</i> (UCLA 191)		MLS
[<i>mi-3</i>]	3754	<i>a</i>	4692	<i>eas</i> (UCLA 191)		MLS
[<i>mi-4</i>]	mi-4	<i>A</i>	1234		M	MBM
[<i>mi-4</i>]	mi-4-3.1	<i>A</i>	1583		SL3	PSL
[<i>mi-4</i>]	mi-4-3.5	<i>a</i>	1585		SL3	PSL
[<i>mi-4</i>]	mi-4-3.3	<i>A</i>	1584	<i>pan-1</i> (5531)	SL3	PSL
[<i>mi-4</i>]	mi-4-3.7	<i>a</i>	1586	<i>pan-1</i> (5531)	SL3	PSL
[<i>mi-5</i>]	mi-5-1.2	<i>A</i>	1587		SL3	PSL
[<i>mi-5</i>]	mi-5-1.4	<i>a</i>	1588		SL3	PSL
[<i>mi-5</i>]	mi-5R1	<i>A</i>	1235		M	MBM
[<i>mi-5</i>]	mi-5-1.6	<i>a</i>	1589	(F4)	SL3	PSL
[<i>mi-5</i>]	mi-5-1.8	<i>A</i>	1590	(F4)	SL3	PSL
[<i>mi-6</i>]	mi-6-2.2	<i>a</i>	1591		SL3	PSL
[<i>mi-6</i>]	mi-6-2.8	<i>A</i>	1594		SL3	PSL
[<i>mi-6</i>]	mi-6R1	<i>A</i>	1236		M	MBM
[<i>mi-6</i>]	mi-6-2.2	<i>a</i>	1592	<i>ad-4</i> (F4)	SL3	PSL
[<i>mi-7</i>]	mi-7	<i>A</i>	1237		M	MBM
[<i>mi-7</i>]	mi-7-4.2	<i>a</i>	1595		SL4	PSL
[<i>mi-7</i>]	mi-7-4.6	<i>A</i>	1597		SL4	PSL
[<i>mi-7</i>]	mi-7-4.4	<i>a</i>	1596	<i>ad-4</i> (F4)	SL4	PSL
[<i>mi-7</i>]	mi-7-4.8	<i>A</i>	1598	<i>ad-4</i> (F4)	SL4	PSL
[<i>mi-8</i>]	mi-8-1.4	<i>a</i>	1600		SL3	PSL
[<i>mi-8</i>]	mi-8-1.6	<i>A</i>	1601		SL3	PSL
[<i>mi-8</i>]	mi-8R6*	<i>a</i>	1238		M	MBM
[<i>mi-8</i>]	mi-8-1.2	<i>a</i>	1599	<i>ad-4</i> (F4)	SL3	PSL
[<i>mi-8</i>]	mi-8-1.8	<i>A</i>	1602	<i>ad-4</i> (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 ¹	Isolation designation or stock #	MT	FGSC #	Nuclear gene markers present	Genetic back-ground	Obtained from
POKY (also called [<i>mi-1</i>])						
[<i>poky</i>]	3627-2	A	384		M	MBM
[<i>poky</i>]	mi-1-1.4	A	1575		SL3	PSL
[<i>poky</i>]	mi-1-1.8	a	1578		SL	PSL
[<i>poky</i>]	[13-5]	A	3485	<i>bd</i> (no#); <i>inl</i> (89601?)		SB
[<i>poky</i>]	3627-4	A	4693	<i>eas</i> (UCLA 191)		MLS
[<i>poky</i>]	3627-4	a	4694	<i>eas</i> (UCLA 191)		MLS
[<i>poky</i>]	mi-1-1.6	a	1577	<i>nic-2</i> (?)	SL3	PSL
[<i>poky</i>]	mi-1-1.2	A	1576	<i>nic-2</i> (?)	SL3	PSL
[<i>poky</i>]	3627-3	a	386	<i>su</i> (<i>[mi-1]</i>)-f	M	MBM
[<i>poky</i>]	3627-4	A	385	<i>su</i> (<i>[mi-1]</i>)-f	M	MBM
RESPIRATORY DEFECTIVE						
[<i>rsp-1</i>]	<u>1</u>	A	3233		M	DLE
[<i>rsp-2</i>]	<u>1</u>	A	3301	<i>inl</i> (89601)	M	DLE
[<i>rsp-3</i>]	<u>1</u>	A	3303	<i>inl</i> (89601)	M	DLE
[<i>rsp-4</i>]	<u>1</u>	A	3302	<i>inl</i> (89601)	M	DLE
SLOW GROWTH						
[<i>SG-1</i>]	RL 3202-23	a	1702		SL	AMS
[<i>SG-3</i>]	RL 3120-10	a	1452		M	AMS
STOPPER						
[<i>stp-B1</i>]	30a-1	A	1574	<i>al-2</i> (15300); <i>ad-4</i> (F4)	M	HB
[<i>stp</i>]	17-2 a-1	A	1573	<i>al-2</i> (15300); <i>ad-4</i> (F4)	M	HB
[<i>stp</i>]	E35	A	5061	<i>al-3</i> (RP100); <i>inl</i> (89601)		HDV
[<i>stp</i>]	Iar155	A	6654	<i>met-2</i> (no#); <i>inl</i> (89601)	M	SRG
[<i>stp</i>]	ER-3	A	6716	<i>inl</i> (89601)	RL	AA
ULTRAVIOLET SENSITIVE (NON-NUCLEAR)						
[<i>uvs</i> (<i>cyt</i>)]	no#	A	1631	<i>cr-1</i> (B 123), <i>rg-1</i> (B 53); <i>pe</i> (Y 8743m, <i>fl</i> (L))	M	RWT

Strains shown to contain Mitochondrial Plasmids

<i>N. crassa</i>	FGSC #	Reference	<i>N. intermedia</i>	FGSC #	Reference
Mauriceville-1c	2225	1,6	Fiji N6-6	435	2
Mauriceville M2-8	6008	6	LaBelle-1b	1940	2
Mauriceville M3-24	6009	6	Varkud-1c	1823	3,6
Roanoke-1	2228	5	Varkud 1-2	6006	6
			Varkud V2-7	6037	6
			Varkud V3-8	6007	6

<i>N. tetrasperma</i>	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, especially numbers 7-10.

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

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.

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
NEUROSPORA AFRICANA						
Africana N200	1740		Nsukka, Eastern Nigeria	N200		DPM
	(homothallic)					
NEUROSPORA CRASSA						
Standard reference strains and derived wild types. For a detailed pedigree showing origins and relationships, see Newmeyer <i>et al.</i> 1987. <i>FGN</i> 34:46-51. The following stocks are indicated not to be authentic: 351,354,424,541, 687,739,1757 and 1758						
ABBOTT						
Abbott 4 <i>mei-1</i>	1228			Abbott 4A		MBM
Abbott	757		(Possibly 4A)	832		DGC
Abb4	1757			10336		ATCC
Abbott 12		351*			12a	MBM
Abb12		1758	contains <i>un(P8319)</i> 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						
Em 5256	424		progeny of Abbott X Lindegren			RF
Em 5297		352				
Em 5296;Em 5297	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		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
LINDEGREN						
Lindegren 1A;25a	5222*	353*	Beadle and Tatum wild type			MBM
(+)	853		Presumably orig. Lindegren (+)	#239.37		CBS
ROCKEFELLER-LINDEGREN (<i>het C D E</i>)						
RL3-8;RL21	2218*	2219*	From 1A X 25a	RL3-8A	RL21a	ELT
* contain <i>scot</i> (VR)						
ST. LAWRENCE (<i>het C d e</i>)						
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 compatibility locus. ST73a not compatible with other OR stocks						
YALE (TATUM)						
SY4f3a		621	contains <i>scot</i> (VR)		SY4f3a	RWB
SY7A	622		contains <i>scot</i> (VR)	SY7A		RWB
HC462		2556			H462	HCC
Other <i>N. crassa</i> wild types						
1-2A;1-77a	5729	5730	Fast growing isolates.	*See Mullaney E.J. and K.E. Papa		
2A;43a	5731	5732	Slow growing isolates	* J. Hered. <u>73</u> :245-246. 1982		
Original <i>N. crassa</i> 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	7833	7834	Louisiana	P4448	P4449	BCT
Fred-2		3225	Texas 1977		P828	DDP
Georgia Plantation		8104	Louisiana		P4506	BCT
Groveland-1c		1945	Florida 1970 (<i>pts-1</i>)	P438		DDP
Homestead-2	3970	3971	Florida 1980	P1409	P1405	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
CONTINENTAL UNITED STATES, continued from previous page						
Houma-11		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
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
HAITI						
Bas Quartier		4707	1984		P3471	DDP
Berard	4708	4709	1984	P3479	P3478	DDP
Carrefour Dufort	4710		1984	P3424		DDP
Carrefour Mme. Gras	4824		1984	P3491		DDP
Haut Diquini	4711		1984	P3420		DDP
Leogane		4712	1984		P3433	DDP
Merger	4713		1984	P3437		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
Dagguluru-1	3360	3361	Andhra Pradesh 1978 (N.B. Raju)	P1120	P1121	NBR
Lankala Koderu-1; -2	3358 [†]	3359	Andhra Pradesh 1978 (N.B. Raju)	P1105	P1117	NBR
Madurai	4717	4718	Tamil Nadu 1984	P2540	P2533	DDP
Mallilintham		4719	Tamil Nadu 1984		P2565	DDP
Vallancheri	4720	4721	Tamil Nadu 1984	P2560	P2559	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
INDIA, continued						
Vehar		8316	Vehar-1j		P675	
Venkatavarum		4722	Tamil Nadu 1984		P2576	DDP
Vickramam	6688		Tamil Nadu 1976 (R. Maheshwari)			DDP
* Senescent, due to maranhar plasmid - see Court <i>et al.</i> 1991. <i>Curr. Genet.</i> <u>19</u> :129-137.						
† Requires thiamine						
IVORY COAST						
Adiopodoume	430		D. Muller, 1955 (Called North Africa I)			NHH
Asikro		4828	1985		P3753	DDP
Foro-Foro		4829	1985		P3720	DDP
Golikro	4830		1985		P3726	DDP
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
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
Kabah	6638	6637	Yucatan 1988 (R. Metzenberg)	P4127	P4125	DDP
PAKISTAN						
Lahore-1; -1b	1824	1825	1969	P349	P350	DDP
PANAMA						
Panama		1165	1944 (Hutchinson)		QM#4834	EGS
Panama CZ30.6	1131		<i>het-5, -6, -8, -9</i> . 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
PUERTO RICO						
Colonia Paraiso	3693	3694	1979	P1295	P1291	DDP
Puerto Rico 18		429	(H. Teas)			NHH

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
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
Tucumanduba	7556		Brazil 1992 (N. Giles)	P4592		BCT
Tucumanduba-2	7851		Brazil	P4607		BCT
THAILAND						
Khao Eto	6490	6797	1984	P4085	P4248	DDP
Klong Rangsit-57	6488		1984	P2913		DDP
TRINIDAD						
Caroni Swamp	8147		(N. Giles)	P4585		BCT
NEUROSPORA DISCRETA						
Bandipur		6789	India 1974 (R. Maheshwari)		P2511	DDP
Gouana	6794		Ivory Coast 1985	P3642		DDP
Hiri	6788		Papua New Guinea 1983	P1992		DDP
Homestead-1k		3268	Florida 1970		P390	DDP
Homestead 8143;8144	5064	5065	7th backcross P390 to P851	8143	8144	DDP
Kang Koi		6792	Thailand 1983		P3016	DDP
Khao Yai-4		6790	Thailand 1983		P3002	DDP
Kirbyville-6, -1	3228	3229	Texas 1977	P851	P846	DDP
Kirbyville 8127		4378	4th backcross P846 to P851		P8127	DDP
lwn (lawn)	5922	5923	Morph. variant in Homestead-1k	8240	8241	DDP
Marinville	6785		Papua New Guinea 1983	P1859		DDP
Pakchong-2		6791	Thailand 1983		P3004	DDP
Rouna-8		6787	Papua New Guinea 1983		P1966	DDP
Santa Maria		3319	Guatemala 1972 (N. Franklin)		P755	DDP
Santa Maria 8161;8162	5066	5067	5th backcross P755 to P851	8161	8162	DDP
Serra Araca	6793		Brazil 1984 (G. Samuels)	P3388		DDP
Sogeri Road-1	6786		Papua New Guinea 1983	P1913		DDP
Wau-6		6784	Papua New Guinea 1983		P1692	DDP
NEUROSPORA DISCRETA-like						
Brabadougou	8317		Ivory Coast	P4297		DDP
Fougbesso		8318	Ivory Coast		P3660	DDP
NEUROSPORA DODGEI						
PR 300	1692		Luquillo Mtns., Puerto Rico,		15509	ATCC
			(homothallic)			
NEUROSPORA GALAPAGOSENSIS						
G 349	1739		Isla Santa Cruz, Galapagos Islands		18746	ATCC
			(homothallic)			
var. dominicana						
D 301	4628		From soil, Dominica		D301	DDP
			(homothallic) Island (L.H. Huang)			

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
NEUROSPORA INTERMEDIA						
Reference strains; derived wild types						
<i>N. intermedia</i> 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 (corn cob), 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)			
<i>fl^P</i>	5798	5799	<i>fl^P</i> from <i>N. crassa</i> introgressed via 7 backcrosses to ShP	8238	8239	DDP
Original <i>N. intermedia</i> strains collected from nature						
AUSTRALIA						
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
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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
CENTRAL AMERICA and MEXICO						
Coba-2		6645	Mexico 1988 (R. Metzberg) >50% white spores x <i>N. intermedia</i> 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
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
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
Madingo		6274	1985		P3839	DDP
Madingo Market	6275		1985, yellow ecotype	P3848		DDP
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
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
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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
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
Talayag	6544	6543	1984	P3200	P3199	DDP
Taleysay	6552		1984	P3226		DDP
Taleytae	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
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
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	
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
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
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
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
Kampung 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 <i>T(I;IV)P170</i>	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 <i>nit-4</i> , <i>Sk-2^K</i>		P8108	DDP
14151	2613		ontjom, Bandung, Java 1959	14151		ATCC
IVORY COAST						
Adiopodoume-1	6262		1985	P3758		DDP
Adiopodoume-4		6263	1985		P3770	DDP
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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
JAPAN						
Unzen	1768		Kyushu 1968	P3		DDP
LIBERIA						
Liberia 4	434		H. Teas			NHH
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
Gertak Sangul	5353	5354	Penang 1984	P2655	P2656	DDP
Kajang	5249	5250	1984	P2825	P2829	DDP
Kampung Cempaka	5238	5237	1984	P2746	P2743	DDP
Kampung 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
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
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
South Coast	6595	5123	Tahiti 1983	P2427	P2421	DDP
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	Auckland 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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
PAPUA NEW GUINEA						
Baiyer River-1	4857	4858	1983	P1786	P1789	DDP
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
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
Wau-2	4853	4854	1983	P1656	P1651	DDP
Yalu	4855	4856	1983	P1561	P1560	DDP
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
Philippine Islands 4		433	PI-4 Srb (from Everett?)			NHH
X	629		E. Quisumbing	11513		ATCC
X-1		630	E. Quisumbing		11514	ATCC
X-2	631		E. Quisumbing	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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
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
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
Tapei-1c; -1g	1766	1767	1968	P13	P17	DDP
THAILAND						
Bangkok-5	5257	5258	1984	P2880	P2883	DDP
Bangkok Airport	5260	5259	1984	P2892	P2887	DDP
Ban Phru Mao	6806		1989 (J. Leslie)	P4344		DDP
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* New sl. 25:25)

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

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

Strain designation	FGSC #		Comments	Number in other culture collection		Obtained from
	A	a		A	a	

NEUROSPORA LINEOLATA

A-236 1910 near Lahore, Pakistan 18966 ATCC
homothallic

NEUROSPORA PANNONICA

TRTC 51327 7221 near Hortobagyi, Hungary CBS 270.91 JCK
homothallic

NEUROSPORA SITOPHILA

Reference strains, derived wild types, and mutants

P8085;P8086	2216	2217	sitophila reference strain	P8085	P8086	DDP
f1(P1012);Sk-1 ^K	4762	4763	fluffy reference stocks (Sk-1 ^K)	8222	8223	DDP
f1 ^P ;Sk-1 ^S	4887	4888	fluffy reference stocks (Sk-1 ^S)	8226	8227	DDP
P8097 <i>acon</i> ;P8098 <i>acon</i>	2664	2665		P8097	P8098	DDP
56.1-aPc		581				BBG
56.8;56.4	2019	2020		P8066	P8067	DDP
56.6-Apc	583			CU 108		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			CU 104		BBG
B		964	f ₁ from FGSC 963 X standard Dodge isolate			JW
Beale APC	415			CU 110		BBG
HSS	586					BBG
HSSf ₁ 22aPC		412			CU 101	BBG
HSSf ₁ 32aPC	414			CU 103		BBG

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
MNHN504	1137		From Museum Natural History, Paris no source data	QM #8194		EGS
WA;W a no#	346	2983	2984 Whitehouse wild types	P8106	P8107	DDP MBM
<i>pdx(299)</i>		348	pyridoxine mutant 299			MBM
<i>rg-2 thi(1090)</i>	3886			SFT-5		NCM
<i>rg-1(B53) pdx(299)</i>	3888			M-17		NCM
<i>rg-2</i>	4643	4644		8221	8220	DDP
<i>rg-2</i>		3887			SFT-9	NCM
<i>rg-2 su-2</i>	3891	3892		NSA	Nsa	NCM
<i>rg-2 su-2</i>		3889			15-6	NCM
<i>rg-2 su-2 cr-1</i>	3890			15-7		NCM
<i>Sk-1^S</i>	5940	5941		P2443	P2444	DDP
<i>Sk-1</i>		7866			P4689	BCT
<i>thi(1090)</i>	3959	347		P504		DDP
<i>(rg-2 thi(1090) + rg-1(B53) pdx(299))</i>	3895		Heterokaryon of 3886 + 3888			NCM
Original collected <i>N. sitophila</i> 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		Roslyn, Virginia 1927 (<i>Sk-1^K</i>)	178.27		CBS
Bayou Chicot-2		3215	Louisiana 1977 (<i>Sk-1^K</i>)		P871	DDP
Belen	8580		New Mexico	W 684		DJJ
Coon-9		3216	Louisiana 1977 (<i>Sk-1^K</i>)		P887	DDP
Elizabeth-2	3214		Louisiana 1977 (<i>Sk-1^K</i>)	P862		DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
CONTINENTAL UNITED STATES, continued						
El Paso		4201	Texas 1980 (H. Luscombe) (<i>Sk-I^K</i>)	P1502		DDP
Everglades		4202	Florida 1980	P1503		DDP
Ithaca, N.Y.	3999		1979 (O. Yoder) (<i>Sk-I^K</i>)	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 (<i>Sk-I^K</i>)	P472	P475	DDP
Palo Alto-1		2494	(<i>Sk-I^K</i>) California 1973 (M.R. Smith)		P653 ^{SK}	DDP
Palo Alto-2	2684		California 1973 (M.R. Smith)	P756		DDP
Ravenswood-2		3217	Louisiana 1977 (<i>Sk-I^K</i>)		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, <i>r(Sk-I)</i>	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
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
Mercara		4800	from soil 1975 (R. Maheshwari)		P2515	DDP
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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
IVORY COAST, continued						
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
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
Gabiokoko	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
Yopougou-2	6857		Ivory Coast 1989 (D. Le Pierres)	P4270		DDP
JAPAN						
Obama-1; -1b	1764	1765	Kyushu 1968 (<i>Sk-I^K</i>)	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 (<i>Sk-I^K</i>)	P2500	P2502	DDP
Baie D'O Punohu		4733	Moorea 1983		P2476	DDP
Haapape	4745		Tahiti 1983	P2377		DDP
Haapiti-1	5936		Tahiti 1983 (<i>Sk-I^K</i>)	P2454		DDP
Haapiti-2	5937	4734	Moorea 1983 (5937 is <i>Sk-I^K</i>)	P2466	P2461	DDP
Hitiaa	4746	4747	Tahiti 1983	P2400	P2394	DDP
Musee Gauguin		4748	Tahiti 1983		P2430	DDP
North Road	4749	4750	Tahiti 1983 (4750 is <i>Sk-I^K</i>)	P2372	P2374	DDP
Papenoo	4751	4752	Tahiti 1983	P2380	P2379	DDP
Papetoia	5939	5938	Moorea 1983 (<i>Sk-I^K</i>)	P2483	P2482	DDP
Plateau de Taravao		4753	Tahiti 1983		P2408	DDP
Plateau de Taravao	5934	5933	Tahiti 1983 (<i>Sk-I^K</i>)	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 <i>Sk-I^K</i>)	P2495	P2492	DDP
Temae		4738	Moorea 1983 (<i>Sk-I^K</i>)		P2451	DDP
Teoharao		4739	Moorea 1983 (<i>Sk-I^K</i>)		P2490	DDP
Tiarei-1	4758	4759	Tahiti 1983	P2387	P2386	DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
NIGERIA						
Nigeria 243; 112	2009	2010	Nsukka, Eastern Nigeria 1965	P8064	P8065	DDP
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
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 (<i>Sk-I^K</i>)		P3245	DDP
Moen-4		6554	Moen, Truk (<i>Sk-I^K</i>)		P3249	DDP
Songsong-1		6213	Rota, 1984		P3150	DDP
Tonga	4203	4204	Tonga 1981 (L. Olive) (<i>Sk-I^K</i>)	P1544	P1543	DDP
Vanuatu		4806	1975 (R.E. Beever)		P3409	DDP
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
TURKEY						
Gebze		6232	1984 (Ali Sazci)		P3957	DDP
Other <i>N. sitophila</i> 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
<i>NEUROSPORA SUBLINEOLATA</i> Furuya et Udagawa						
(= <i>Anixiella sublineolata</i>)						
SANK 17876	5508		From soil, Iriomote Island, Okinawa pref., Japan, March 1973 (K. Furuya)			KF
<i>NEUROSPORA TERRICOLA</i>						
WFS 5000	1889		Spring Green, Wisconsin 1961	14941		ATCC
		homothallic				

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
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
<i>N. tetrasperma</i> 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						
Beerburum		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
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
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
Ekw arun		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

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
CONTINENTAL UNITED STATES						
18 Mile post	8557		Sula, MT	W474		DJJ
Belen	8579	8578	New Mexico	W 683	W 682	DJJ
Blodgett Trailhead	8558		Montana	W 477		DJJ
Chapin	3329 ^{PS}		South Carolina 1978	P 1132		DDP
Cobalt	8567	8568	Idaho	W 593	W 594	DJJ
Coleville	8583	8584	California	W 09	W 710	DJJ
Columbia	3330 ^{PS}		South Carolina 1978	P 1133		DDP
Elizabeth-5	3203 ^{PS}		Louisiana 1977	P 865		DDP
Empire-1v2; -1ba	2501	2502	Louisiana 1972	P 665	P 471	DDP
Franklin	8102 ^{PS}		Louisiana	P 4458		BCT
Georgia Plantation	8105 ^{PS}		Louisiana	P 4511		BCT
Groveland-1	1942 ^{PS}		Florida 1970	P 436		DDP
Homestead-1f	1943 ^{PS}		Florida 1970	P 388		DDP
Kennedy Meadows	8561	8560	California	W 514	W 512	DJJ
LaBelle-1	1941 ^{PS}		Florida 1970	P 404		DDP
Laird Creek	8556	8555	Sula, Montana	W 467	W 466	DJJ
La Joya	8581	8582	New Mexico	W 693	W 694	DJJ
Lake Alfred-1b	1944 ^{PS}		Florida 1970	P 425		DDP
Los Alamos #1	8591		New Mexico	W 776		DJJ
Los Alamos #2	8588	8589	New Mexico	W 755	W 756	DJJ
Los Lunas	8577	8576	New Mexico	W 648	W 645	DJJ
Manter Meadow	8562	8563	California	W 531	W 532	DJJ
Moss Hill-5	3205 ^{PS}		Texas 1977	P 815		DDP
Napais Creek	8554	8553	Idaho	W 458	W 457	DJJ
Northside Planting	8139 ^{PS}		Louisiana	P 4516		BCT
Northwest Peak	8548		Montana	W 441		DJJ
Panther Creek Road	8550		Idaho	W 443		DJJ
Pecos #1	8585		New Mexico	W 736		DJJ
Pecos #2	8587	8586	New Mexico	W 741	W 740	DJJ
Perkins Colony-1	3327 ^{PS}		Georgia 1978	P 1130		DDP
Perkins Colony-2	3328 ^{PS}		Georgia 1978	P 1131		DDP
Perkins-1v2	2505		Louisiana 1972	P 654		DDP
Perma #1	8569	8570	Montana	W 606	W 607	DJJ
Perma #2	8573	8572	Montana	W 621	W 620	DJJ
Plumas		8564	California		W 538	DJJ
Raleigh	3998	4245	North Carolina 1981	P 1534	P 1535	DDP
Ramey Creek		8551	Idaho		W 449	DJJ
Sugartown-5	3204 ^{PS}		Louisiana 1977	P 856		DDP
Sweetwater-1m		2507	Florida 1970		P 403	DDP
Turner Creek Road	8549		Montana	W 442		DJJ
Wells	8565	8566	Nevada	W 564	W 565	DJJ
Welsh-1bv1; -1bv2	2503	2504	Louisiana 1972	P 658	P 663	DDP
Yankee Fork	8552		Idaho	W 452		DJJ
HAWAII						
Hanalei-1bv1; -1bv3	2510	2511	Kauai, 1972	P 664	P 659	DDP
Lihue-1v1; -1v2	2508	2509	Kauai, 1972	P 657	P 656	DDP
Waimea Falls-2		3296 ^{PS}	Oahu, 1976	P 771		DDP
INDONESIA						
Gianjor-1		1794 ^{PS}	Bali 1969	P 202		DDP
MALAYA						
Batu Ferringi-2		6578 ^{PS}	Penang	P 2687		DDP

Strain designation	FGSC # and mating type		Comments	Number in other culture collection		Obtained from
	A	a		A	a	
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
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

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.

Strain designation	FGSC # and mating type		Bisexual heterokaryons	FGSC #
	A	a		
86.9		615 ^{PS}	Dwarf 16-ade	597
NS-130		425	H3-aI	599
394.4-Ae	608		Dwarf 16-aDP+C4-Ad	598
394.5-ae		609 ^{PS}	H3-aI+D4-AI	601
616-Ae	616		16-ade + 10-Ade	603
2521.12-ae		604	343.6AE + 340.6-a	607
J3C3		617	394.4-Ae+ 394.5-ae	610
343.6-AE		606	343.6-AE + 394.5-ae	611
N-aD-wild type		590	343.6-AE + 2521.12-ae	612
ND=dwarf		596	343.6-AE + 395.-ae	613
S1-aD		593	2521.12-ae + 87.11-AE	619
10-Ade	602			
16-ade		595		
C4-Ad	591			
C8-ad		592		
D6-AI	600			

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 mostly 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 #		L.G.	Allele	Obtained from
	A	a			
ACRIFLAVINE RESISTANCE					
<i>acr(111)</i>	1251		I	111	HBH
<i>acr(112)</i>	1252	7858	III	112	HBH/DDP
<i>acr(112); E</i>	7292	7293			DDP
ADENINE					
<i>ad(101)</i>	1255		V	101	HBH
ALBINO					
<i>al(102)</i>	1256		I	102	HBH
<i>al(102);E</i>	7234				DDP
<i>al-2; lys-1</i>	8605		IR; VL	102; 33933*	DDP
<i>al-2; cys-10; E</i>	8607		IR; IVL	102; 39816*	DDP
* from <i>N. crassa</i>					
COLONIAL					
<i>col(105)</i>	1260		IV	105	HBH
<i>col(118)</i>	1261		V	118	HBH
<i>col(119)</i>	1262		VII	119	HBH
<i>col(119);E</i>	7480				DDP
CYCLOHEXIMIDE RESISTANCE					
<i>cyh(113)</i>	1253	6691	V	113	HBH/DDP
<i>cyh(113);E</i>		7235			DDP
<i>cyh(114)</i>	1254		I	114	HBH
<i>cyh(114);E</i>	7233				DDP
CYSTEINE*					
<i>cys(123)</i>	1265	6707	VI	123	HBH/DDP
<i>cys(123);E</i>	7236				DDP
<i>cys-10</i>		8606	IVL	39816 [#]	DDP
*Responds to cysteine or methionine, not to sulfite. Formerly called <i>met(123)</i>					
[#] from <i>N. crassa</i>					
EIGHT SPORE					
<i>E</i>	7502	7503	VI	E	DDP
<i>E(f₈)*</i>	8114	8115			DDP
* Progeny of eight sib-matings. Asci with eight viable spores more frequent but still low.					
LAWN					
<i>lwn(P2612)</i>		7282	VII	P2612	DDP
<i>lwn;al(102)</i>	7281				DDP
<i>lwn;E</i>		7284			DDP
<i>lwn;al(102);E</i>	7283				DDP
LYSINE					
<i>lys(122)</i>	1264			122	HBH
<i>lys(122);E</i>		7237			DDP
<i>lys-1</i>		8606	V	33933*	DDP
* from <i>N. crassa</i>					

Locus	FGSC #		L.G.	Allele	Obtained from
	A	a			
NITRATE NON-UTILIZER					
<i>nit(VP1)</i>		7877	IV	VP1	DDP
<i>nit(VP1);al(102)</i>		7876	I;IV		DDP
<i>nit(VP1);E</i>		7865			DDP
<i>nit(VP1);al(102);E</i>	7864				DDP
OSMOTIC					
<i>os(P2610)</i>	6692		I	P2610	DDP
<i>os;E</i>	8116	8117	I;VI	P4519	DDP
PANTOTHENATE					
<i>pan(124)</i>	1266	7859	IV	124	HBH/DDP
<i>pan(124);E</i>	7860	7861			DDP
TRYPTOPHAN					
<i>trp(126)</i>	1268		II	126	HBH
UNKNOWN					
<i>un(127)</i>	1269		IV	127	HBH

Strains for testing linkage *

<i>(al(102);pan(124);col(119) A + met(123) E A)</i>	FGSC # 7568	DDP (Tests I, IV, VII)
<i>(pan(124);col(119) a + lys(112) E a)</i>	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 #		L.G.	Allele	Obtained from
	A	a			
<i>T(IR;IIR)4637al-1</i>		7878	IR,IIR		DDP
FLUFFY					
<i>fl^P</i>	7084	7085	IIR		DDP
<i>fl^P;E</i>	7136	7087			DDP
PEACH					
<i>pe;E</i>	7862	7863	IIR		DDP
PEAK					
<i>pk</i>		7879	VR		DDP

NEUROSPORA TOROI* = *N. tetrasperma

Strain designation	FGSC #		Collection date, comments	Number in other collection		Obtained from
	A	a		A	a	
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 #		Collection date, comments	Number in other collection		Obtained from
	A	a		A	a	
New Zealand M-1		643	J.H. Warcup (<i>N. discreta?</i>)			MJM
New Zealand S-3		644	J.H. Warcup			MJM
N2798		588	Beadle (1943) → Dodge			BBG
Tiaba-8		3269	Tiaba, Papua New Guinea 1968 (<i>N. discreta?</i>)	P47		DDP
Carrefour Dufort	8225		DDP, 1984, Haiti	P3426		BCT
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. <i>N. discreta?</i>	P4297		DDP
Fougbesso		8318	Ivory Coast. <i>N. discreta?</i>	P3660		DDP
Fougbesso		8334	Ivory Coast. <i>N. discreta?</i>	P3655		BCT
Agbanou	8335		Ivory Coast. <i>N. discreta?</i>	P3748		BCT
Asikro	8336		Ivory Coast. <i>N. discreta?</i>	P3750		BCT
Brabadougou	8338	8337	Ivory Coast. <i>N. discreta?</i>	P4527	P4288	BCT
Brabadougou	8339		Ivory Coast. <i>N. discreta?</i>	P4528		BCT

GENES TRANSFERRED AMONG NEUROSPORA SPECIES

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

'Foreign' genes now in *N. intermedia*

<i>fl^P</i>	5798	5799	from <i>N. crassa</i> , 7th BC	DDP
<i>A^C</i>	1755		m.t. from <i>N. crassa</i> , 10th BC	AMS
<i>al-3</i> RP100	6567	6568	from <i>N. crassa</i> , 6th BC	DDP
<i>acr-2</i> KH5	8743	8742	from <i>N. crassa</i> , 6th BC	DDP

'Foreign' genes now in *N. sitophila*

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

'Foreign' genes now in *N. tetrasperma*

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

HYBRID STRAINS USEFUL FOR INTERSPECIFIC GENE TRANSFERsee Metzenberg and Ahlgren 1969 NN 15:9-10Metzenberg and Ahlgren 1973 Can. J. Genet. Cytol. 15:571-576Perkins 1991 FGN 38:84

FGSC

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

APPARENTLY HYBRID STRAINS

FGSC

Strain designation	A	a	Comments
Madurai		8198	Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i> , Tamil Nadu India
Georgetown-8	8199		Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>
Carrefour Dufort	8200		Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>
Merida-1		8201	P4157, Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>
Merida-1		8202	P4158, Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>
Mallilintham		8203	Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>
Nosy Be	8204	8205	Possible hybrid of <i>N. crassa</i> and <i>N. intermedia</i>

OTHER GENERA RELATED TO NEUROSPORA

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

Mating Type Notes PS - Pseudohomothallic H - Homothallic

ASCOBOLUS

Strain designation	Genotype	FGSC #	Mating type	Collection place (collector:comments)
<i>Ascobolus stercorarius</i>	C^1D^1	7799	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^1D^2	7800	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^2D^1	7801	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^2D^2	7802	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^1D^1	7803	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^1D^2	7804	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^2D^1	7805	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	C^2D^2	7806	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^1 meth^-$	7807	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^2 meth^-$	7808	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^1 meth^-$	7809	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^2 meth^-$	7810	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^1 meth^-$	7811	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^2 meth^-$	7812	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^1 meth^-$	7813	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^2 meth^-$	7814	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^1 nic^-$	7815	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^2 nic^-$	7816	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^1 nic^-$	7817	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^2 nic^-$	7818	a	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^1 nic^-$	7819	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^1D^2 nic^-$	7820	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^1 nic^-$	7821	A	GNB, NY-NJ, Herbivore Dung
<i>Ascobolus stercorarius</i>	$C^2D^2 nic^-$	7822	A	GNB, NY-NJ, Herbivore Dung

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, SB: 7504	
	7406-7413	

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-interrupted arabic numeral following the parentheses. Digits subsequent to an interruption or letter are ignored unless needed for secondary ordering.

Genotype (isolation numbers of separable markers)	FGSC stock #		Genotype (isolation numbers of separable markers)	FGSC stock #	
	matin type	A a		mating type	A a

A. Reciprocal Translocations. Single Translocation stocks.

<i>T(III;VI)1</i>	976	975	<i>T(I;IV)TLd9-2</i>	5804	5805
<i>T(III;VI)V1M44n</i>	4255	4256	<i>T(IV;V)TLd9-6</i>	5806	5807
<i>T(IV;VI)V1M44o os-2</i>	4286	4287	<i>T(IR;VIL)UK9-13</i>	7285	7286
<i>T(III;IVR)RLM02 pho-5^C</i>	7869		<i>T(II;III)UK9-15</i>	6816	6817
<i>T(III;IVR)RLM04 pho-5^C</i>		7870	<i>T(II;V)UK9-17</i>	7070	8258
<i>T(IIR;VL)UK4-22</i>	7129	7130	<i>T(I;VR)UK9-18 am</i>	6871	6872
<i>T(II;IV)UK4-33</i>	6864	6865	<i>T(II;III)UK9-25</i>	6818	6819
<i>T(II;IV)D5</i>	2393	1554	<i>T(I;IV)UK9-30</i>	6873	6874
<i>T(IL;IIR)KH5-9 eas</i>	7143	7144	<i>T(IVR;VIIR)AR10</i>	2007	2008
<i>T(III;VII)UK5-20</i>	6836	6837	<i>T(IR;IVR)Z10</i>	5808	5809
<i>T(IR;VI)UK5-27</i>	6912	6913	<i>T(IVR;VR)AR11r</i>	2093	2094
<i>T(II;V)UK5-31</i>	6916	6917	<i>T(IL;VR)AR12</i>	2006	1462
<i>T(VI.VII)UK5-32</i>	6866	6867	<i>T(IR;VIL)AR13</i>	1913	1914
<i>T(I;IVR)RLM06 pho-5^C</i>		7871	<i>T(II;VR)UK14-3</i>	7038	7039
<i>T(VIR;VIIR)ALS7</i>	1993	2016	<i>T(I;II;VI)UK14-7</i>	7031	7032
<i>T(I;VI)UK7-11</i>	6838	6839	<i>T(I;V)UK15-1</i>	7082	7083
<i>T(IV;VI)B8</i>	2394	2395	<i>T(IV;VII)UK19-4</i>	7047	7048
<i>T(III;IVR)RLM08 pho-5^C</i>	7872	7873	<i>T(IL;VI)UK19-37</i>		7051
<i>T(IVR;VII)RLM09 pho-5^C</i>		7874	<i>T(VI;VII)UK19-65</i>	7049	7050
<i>T(IIR;VIL)AR9r</i>	2131	2132	<i>T(VR;VII)17-088 Pk</i>	3672	3418
<i>T(IVR;VIL)MN9 cpc-1 (MN9)</i>	6700	6699	<i>T(I;VI)UK17-51</i>		7073

Genotype (isolation numbers of separable markers)	FGSC stock # mating type		Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a		A	a
<i>T(I;VI)UK17-51,al-1^S</i>		7072	<i>T(IIR;IIR)ALS132</i>	3041	3042
<i>T(III;VII)AR19</i>	1915	1916	<i>T(IR;IV)NM132</i>	7339	
<i>T(IL;IVR)MEP24 arg-2</i>	3170	3171	<i>T(II;VII)NM134</i>	1919	1920
<i>T(IVR;VR)RLM25 pho-5^C</i>	7875		<i>T(I;II)NM135</i>	2023	2024
<i>T(IL;V)T27M9</i>	2095		<i>T(I;IV)Z135</i>	5814	
<i>T(IIL;VL)AR30</i>	2004	2005	<i>T(I;III)NM136</i>	2639	2588
<i>T(IIL;VL)AR30,caf-1 at</i>	3950	3951	<i>T(I;IV)NM137</i>	1874	1875
<i>T(IIL;VL)AR30,fl(P)</i>	3948	3949	<i>T(IR;IVR)NM139 bs</i>	1565	1566
<i>T(V->IV)AR33, acon-3</i>	8603	8604	<i>T(IR;IVR)NM140</i>	1759	1548
<i>T(IV;V)T33M8</i>	2397	2398	<i>T(IVR;VR)NM141</i>	2025	1479
<i>T(IVR;VR)MEP35d</i>	4526	4527	<i>T(IR;VR)NM143</i>	1549	1550
<i>T(III;IV)T42M36</i>	2443	2444	<i>T(IR;IVR)NM144</i>	1336	1335
<i>T(III;VII)LO44</i>	5789	5790	<i>T(IVR;VR)NM145</i>	2098	2099
<i>T(VL;VII)AR45</i>	1760	1761	<i>T(I;III)NM146</i>	2449	2450
<i>T(IV;V)L046</i>	4639	4640	<i>T(I;IIR)NM150</i>	2060	2061
<i>T(IIR;VIIR)T51M143</i>	2399	2400	<i>T(I;VIR)NM152d</i>	4697	4698
<i>T(I;VI)T51M158</i>	2759	2760	<i>T(IIR;VR)ALS154,mei-3(JL102)</i>		2062
<i>T(I;VI)T51M166</i>	2401	2402	<i>T(IIR;VR)ALS154</i>		2063
<i>T(IIIIR;VR)Z52,inl(89601)</i>	5810	5111	<i>T(IIR;VR)ALS154,mei-3;fl(JL102;P)</i>		4629
<i>T(I;IVL)HK53 cut</i>	2272	2068	<i>T(IR;VIIR)NM155</i>	1877	1878
<i>T(I;IVL)HK53 cut,mei-1</i>	176		<i>T(IV;VII)NM156</i>	1921	1922
<i>T(IR;VI)P54</i>	2445	2446	<i>T(VR;VIR)NM157</i>	2648	2649
<i>T(IR;IVR)T54M19</i>	2135	2136	<i>T(IVR;VIIR)NM158</i>	2026	2027
<i>T(VR;VI)T54M117 un</i>	3055	3056	<i>T(V;VII)NM159</i>	2411	2412
<i>T(II;III)T54M140b</i>	2941	2942	<i>T(IR;IVR)NM160</i>	1338	1337
<i>T(IIR;IIR)AR62</i>	1545	1546	<i>T(IIR;IIR)C161 aro(C161)</i>	2106	2107
<i>T(I;II)B66</i>	1464	1465	<i>T(IIR;IIR)NM161</i>	2028	2029
<i>T(IV;VIL)P73B12</i>	2623	2624	<i>T(VR;VI)NM162b</i>	2591	2592
<i>T(IR;IIR)P73B101</i>	2645	2646	<i>T(IR;VIL)NM163</i>	2030	2756
<i>T(IIR;VIIR)P73B169</i>	2625	2626	<i>T(IR;IVR)NM164</i>	1341	1340
<i>T(IR;IIR)STL76</i>	2096	2097	<i>T(I;VII)ALS167,rg-1 cr-1(B53,B123)</i>	2413	2529
<i>T(I;VIIR)K79 met-7</i>	2297	2298	<i>T(I;IIR)NM168</i>	1923	1924
<i>T(II;IV)SG81 mb</i>	4532	4533	<i>T(IIIIR;VIIR)NM169r</i>	1816	1817
<i>T(I;VI)C84</i>	3437	3438	<i>T(I;IV)NM170</i>		1489
<i>T(VIL;VII)MN86</i>	3185	3186	<i>T(I;IV)P170</i>	4497	4498
<i>T(VI;VII)NCRL91 plm</i>	4243	4244	<i>T(V;VI)NM171</i>	2451	2452
<i>T(I;II)UK93D1</i>	7566	7567	<i>T(IR;IIL)ALS172</i>	3035	3036
<i>T(IIIIR;VI)UK93 D3</i>	8112	8113	<i>T(IR;IVR)NM172</i>	1345	1518
<i>T(I;V)UK93E1</i>	7660	7661	<i>T(VR;VI)AR174</i>	2678	2679
<i>T(II;VI)Z99,aro-9(Y325M6)</i>	5812	5813	<i>T(I;VR)AR175</i>	2593	2594
<i>T(III;V)NM101</i>	1879	1880	<i>T(VIR;VIR)NM175</i>	2295	2293
<i>T(I;III)NM107</i>	2058	2059	<i>T(IV;V)Y175M253</i>	3521	3522
<i>T(III;VII)JL108</i>	6632	6633	<i>T(VR;VII)Z175</i>	5902	5903
<i>T(IL;IIR)NM109</i>	2627	2628	<i>T(V;VII)Z175,inl(89601)</i>	5815	5816
<i>T(IR;VR)ALS111</i>	2629	2630	<i>T(IIIIR;VL)AR177</i>	2680	2681
<i>T(III;VII)Y112M4r</i>	2631	2632	<i>T(I;IVR)AR180b</i>	2754	2755
<i>T(IV;VII)NM113</i>	1917	1918	<i>T(IR;IIIIR)AR180r</i>	2939	2940
<i>T(III;IV)NM118</i>	2403	2404	<i>T(IIR;VR)NM180</i>	2031	1491
<i>T(IR;IVR)NM119</i>	1447	1334	<i>T(IIR;VI)AR181</i>	2453	2454
<i>T(I;III)Z119</i>	5870	5871	<i>T(I;IVR)NM181</i>	2933	2934
<i>T(I;VII)Z121</i>	6570	6571	<i>T(I;VI)AR182</i>	2597	2598
<i>T(IV;VII)ALS122</i>	2986	2987	<i>T(III;VL)NM183</i>	2633	2634
<i>T(VI;VII)NM124</i>	2214	1472	<i>T(V;VI)AR184</i>	2416	2417
<i>T(IVR;VR)NM125</i>	2447	2448	<i>T(III;VI)AR186</i>	1925	1926
<i>T(IIR;IVR)NM126</i>	1611	1612	<i>T(I;IV)AR193</i>	2470	2471
<i>T(I;III)NM127</i>	2405	2406	<i>T(IIL;VI)Z194</i>	5862	5863
<i>T(I;IVR)NM128</i>	7338		<i>T(IVR;VI)AR207</i>	1927	1928
<i>T(I;II)NM129</i>	2330	2331	<i>T(IR;III)AR208</i>	1929	1930
<i>T(I;VL)NM130</i>	2407	2408	<i>T(III;IV)AR211</i>	1933	1934
<i>T(III;IV)NM131</i>	2409	2410	<i>T(IR;IVR)AR212</i>	1521	1522

Genotype (isolation numbers of separable markers)	FGSC stock # mating type		Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a		A	a
<i>T(IR;IIL)AR216</i>	1950		<i>T(IVR;VR)R2355; ylo-1; wc-1</i>		
<i>T(IR;IIL)AR216, al(AR216)</i>	1606	1607	(Y30539y; P829)	221	
<i>T(IVR;VR)AR221</i>	2034	2035	<i>T(II;V)R2497</i>	4290	4291
<i>T(I;VI)Y234M419</i>	2635	2636	<i>T(I;II)EB2501</i>	3047	3048
<i>T(I;VIL)Y234M470</i>	6019	6020	<i>T(IR;III)P2648</i>	1492	2032
<i>T(I;VR)Z252</i>	5920	5921	<i>T(II;VI)P3340</i>	3123	3124
<i>T(II;IV)Y256M230</i>	1556		<i>T(IR;VR)P3427</i>	5796	5797
<i>T(II;IV)Y256M230; ylo-2(Y256M230)</i>	917		<i>T(I;IIIR)3717 vis</i>	2682	2683
<i>T(I;IV)D304</i>	1443	1444	<i>T(I;VR)P4038^s</i>	5872	5873
<i>T(I;II)OY324</i>	3835	3836	<i>T(IR;IIR)4637 al-1</i>	253	252
<i>T(VL;VIL)OY325 ser-6</i>	3737	3738	<i>T(IR;IIR)4637 al-1; pan-1; het-1</i>		
<i>T(II;VI)OY326</i>	3676	3677	(4637; 5531; no#)	7342	
<i>T(IR;VR)OY327</i>	3663		<i>T(I;IIR)P4704</i>	2425	2426
<i>T(IR;VR)OY327, al-2(15300)</i>		3664	<i>T(IR;VR)P5166</i>	2185	2186
<i>T(I;VI)OY328</i>	3678	3679	<i>T(IL;IIL)P5390</i>	2455	2456
<i>T(I;VI)OY331</i>	3680	3681	<i>T(IL;VR)P5401</i>	2427	2428
<i>T(I;II)OY332</i>		3682	<i>T(IIIR;VI)P6070</i>	2601	2602
<i>T(IL;VIIR)SB332 cla-1; bd</i>		7504	<i>T(IR;IIL)P7889</i>	3316	3317
<i>T(II;IV)OY334</i>	3683	3684	<i>T(I;VR)P7987</i>	3221	3222
<i>T(I;III)OY335</i>		3686	<i>T(III;VII)P8804</i>	6684	6685
<i>T(I;III)OY335; ylo-1 (Y30539y)</i>	3685		<i>T(V;VII)P9103</i>	4699	4700
<i>T(II;V)OY336</i>	3797	3798	<i>T(IR;IVR)P9329</i>	3851	3852
<i>T(IL;IIR)OY338 arg/lys</i>	3837	3838	<i>T(III;IV)P9673</i>	3828	3829
<i>T(IIIL;VR)OY339</i>	3687	3688	<i>T(IR;VIIL)17084 thi-1</i>	216	509
<i>T(II;IV)OY340</i>	3689	3690	<i>T(IR;VR)36703</i>	1445	1446
<i>T(IR;IIR)OY341</i>		3692	<i>T(IR;VR)36703, arg-1 (36703)</i>	273	529
<i>T(IR;IIR)OY341, al-2 (15300)</i>	3691		<i>T(IL;III)36703b</i>	1552	1553
<i>T(III;IV)OY342d</i>	7492	7493	<i>T(IVR;VIR)45502</i>	1067	1876
<i>T(I;III)OY344</i>	3748	3749	<i>T(IVR;VIR)45502, pyr-3 (45502)</i>	208	207
<i>T(I;III)OY345</i>	3799	3800	<i>T(VR;VIL)46802 inl</i>	670	1199
<i>T(IV;VI)P347</i>	4258	4259	<i>T(VR;VIL)46802 inl, his-1, pk; chol-2, ad-8</i>		
<i>T(III;VI)OY352</i>	5791	5792	(C84, B6; 47904, Y226M58)	1283	1284
<i>T(I;II)OY353</i>		5793	<i>T(IL;VR)47711</i>	226	223
<i>T(III;VI)OY354</i>	5895	5896	<i>T(II;IV)P50391</i>	7591	7592
<i>T(I;III)OY355</i>	5866	5867	<i>T(IV;VII)P50392</i>	7531	7532
<i>T(VI;VII)OY356</i>	5904	5905			
<i>T(I;IIIR)OY357</i>	6138	6139			
<i>T(I;VI)OY358</i>	6021	6022			
<i>T(IIL;VIL)B362r</i>	3011	3012			
<i>T(IVR;VIIR)STL384b</i>	2421	2422			
<i>T(IVR;VIL)STL384r</i>	2419	2420			
<i>T(IIIL;VL)MB412</i>	5794	5795			
<i>T(III;VII)MB414</i>	7134	7135			
<i>T(V;VI)A420</i>	2334	2335			
<i>T(IR;VII)TM429 his-3</i>	2530	2531			
<i>T(IR;VIL)P649</i>	1608	1609			
<i>T(IL;VII)MB727</i>	3944	3945			
<i>T(I;VI)RLM940, ylo-1 (30539y)</i>	7494	7495			
<i>T(I;VII)S1007</i>	227	224			
<i>T(I;VII)S1007, asn (S1007)</i>		484			
<i>T(III;IV)S1302 col-6</i>		1400			
<i>T(IR;VR)C-1670 pk</i>	483	2761			
<i>T(I;VII)P1676</i>	1935	1936			
<i>T(II;III)P1831</i>	5930	5931			
<i>T(V;VI)JH2003</i>	2423	2424			
<i>T(I;II)P2006</i>	7496	7497			
<i>T(III;IV)P2089</i>	6781	6782			
<i>T(I;II)P2117</i>	6300	6668			
<i>T(III;VI)P2190</i>	6491	6492			
<i>T(IVR;VR)R2355</i>		222			

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

Stocks with two or more reciprocal translocations

<i>T(III;VL)AR30 T(IIIR;VR)ALS154, acf-3;arg-5 fl;ilv</i>	4633	4634	KH24(r),27947,P,STL3
<i>T(III;VL)AR30 T(IIIR;VR)ALS154 fl</i>		4635	P
<i>T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1 (=alcoy linkage tester)</i>	997	998	C102(t);Y30539y
<i>T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1;csp-2 (alcoy;csp-2)</i>	3661	3434	C102(t);Y30539y;UCLA101
<i>T(I;II)4637 al-1;T(IV;V)R2355,cot-1; T(III;VI)1,ylo-1;inl;csp-2 (alcoy;csp-2)</i>		3717	C102(t);Y30539y;37401;UCLA101
<i>T(I;II)4637 al-1;T(IV;VI)45502,pyr-3</i>		2196	45502
<i>T(I;VII)17084 thi-1; T(IV;VI)45002,pyr-3</i>	1079	1080	45502
<i>T(I;VII)S1007,un-3;T(V;VI)46802</i>		1071	55701(t)
<i>T(I;II)4637 al-1; T(IV;V)R 2355; T(VI;VII)MN 86</i>		8610	

B. Complex translocations involving more than two linkage groups

<i>In(IL;IR)T(IL;IIIR)SLm-1</i>	5413	5414	
<i>T(III;IV;VI)TLd4-4</i>	5924	5925	
<i>T(VI;VII)TLd5-7</i>	5802	5803	
<i>T(I;IV;VR)UK8-21</i>	7068		
<i>T(I;IV;VR)UK8-21,at</i>		7069	M111
<i>T(III;IV;VII)UK14-5</i>	7080	7081	
<i>T(IIIR-[IR;IIIR])AR17</i>	2442	1463	
<i>T(IL;IVR;IVR;VR)MEP35 arg-3</i>	3844	3845	
<i>T(III;VR;VII)ALS169</i>	3197	3198	
<i>T(IR-VII;IR;V;VII)AR173</i>	2468	2469	
<i>T(IVR;VIL;VIIR)ALS175</i>	2931	2932	
<i>T(I;III;VI;VII)AR176</i>	2708	2709	
<i>T(I;III;VR;VI)ALS178,rg-1 cr-1</i>		7501	B53 B123
<i>T(III-[I;IV;V])AR179</i>	2595	2596	
<i>T(I;IVR;IR;IIIR)AR180</i>	7491		
<i>T(IR-II;I;VII)AR217</i>	3033	3034	
<i>T(IR-II;I;VII)AR217,ad-9 cyh-1</i>		3149	Y154M37,KH52(r)
<i>T(IIIR-[I;IIIR;VIL]D305</i>	2139	2140	
<i>T(IIIR-[I;IIIR;VIL]D305,dow</i>	3150	3151	P616
<i>T(IIIR;V;VIIR)P1156</i>	2599	2600	
<i>T(IVR-VIIL;IL;IIIR;IVR)S1229 arg-14,pe</i>	2946	268	Y16329,Y8743m
<i>T(VIL-[I;IIIR])Y16329</i>	2710	2711	
<i>T(VIL-[I;III]R)Y16329,phe-2</i>	870		

C. Inversions that do not generate viable duplications
see Barry and Leslie, 1982; Turner and Perkins, 1982

<i>In(IL;IR)OY323</i>	3793	3794	
<i>In(IL;IR)OY323,al-2</i>	4257	3796	15300
<i>In(IL;IR)OY323,arg-1,al-2</i>	3795		B369,15300
<i>ro-10 In(IL;IR)OY323,al-2,arg-13</i>	7481	7482	AR7,15300
<i>In(IL;IR)OY348</i>	3839	3840	

D. Insertional translocations that do not generate viable duplications

<i>T(IR-IV)Y112M15 ad-3A</i>	2957		
<i>T(IR-VR)S1325 nic-2</i>	1558	1557	

Genotype (isolation numbers of separable markers)	FGSC stock #		Genotype (isolation numbers of separable markers)	FGSC stock #	
	A	a		A	a
E. Rearrangements that produce viable duplications when crossed by normal					
<i>T(VIR→IVR)CJS1</i>	2676	2677	<i>T(IR→VIR)NM103,cyh-1 al-1^Y arg-13 R</i>		
<i>T(IR→VL)UK1-35</i>	6881	6882	(<i>KH52(r),ALS4,RU3,35408</i>)	3135	
<i>T(IR→IIR)MD2</i>	3826	3827	<i>T(IR→IIR)Y112M4i ad-3B</i>	2637	2638
<i>T(VR→VL)UK2-y,am</i>	7245	7246	<i>T(I→IV)Y112M115 ad-3A</i>	2957	
<i>T(VR→VL)UK2-y,am al-3 inl</i>			<i>T(IIL→VR)NM149,hct-c (no#)</i>	1483	1482
<i>UK2-y,RP100 89601</i>	7589	7590	<i>T(IIL→VR)NM149,hct-C (no#)</i>	3879	3880
<i>T(IR→VII)UK2-26,al-1(34508)</i>		7030	<i>T(IIL→VR)NM149,hct-c^{PA} (no#)</i>	2647	2188
<i>T(IVR→VL)UK2-32</i>	7294	7295	<i>T(IIL→VR)NM149,hct-6^{PA} (no#)</i>	7352	7353
<i>T(VR→VIL)UK3-41,inl (37401)</i>	6869	6870	<i>T(IIL→VR)NM149,hct-c^{AD} (no#)</i>	2191	2192
<i>T(VR→VII)EB4</i>	3046	2180	<i>T(IIL→VR)NM149,hct-c^{AD} pyr-4</i>		
<i>T(VIL→IR)IBj5 cpc-1</i>	4433	4434	(<i>no# 36601</i>)	7314	7315
<i>T(IIIR→IL)UK8-18</i>	7037	7131	<i>T(IIL→VR)NM149,hct-c^{GR} (no#)</i>	2193	2194
<i>T(IIIR→IL)UK8-18,ro-2 (B20)</i>		7133	<i>T(IIL→VR)NM149,hct-C pyr-4</i>		
<i>T(VR→IIIR)DBL9</i>	5926	5927	(<i>no#,36601</i>)		3136
<i>T(VR→IIIR)DBL9,inv (DBL9)</i>	5928	5929	<i>T(IIL→VR)NM149,hct-C ro-3</i>		
<i>T(IR→VIR)UKT12</i>	6926	6927	(<i>no#,R2354</i>)	2011	2012
<i>T(IR→VIR)UKT12,un-1 (44409)</i>	7036		<i>T(IVR→I)NM152</i>	1752	1753
<i>In(IL→IR)AR16</i>	3315	1614	<i>T(IR;IIR;III)Y155M64 ad-3A</i>	3037	3038
<i>In(IL→IR)AR16,leu-3 (R156)</i>		3129	<i>T(IVR→VIR)ALS159</i>	2100	2101
<i>T(IIIR→[IR,IIR])AR17</i>	2442	1463	<i>T(IVR→VIR)ALS159,cot-1 cys-4;ylo-1</i>		
<i>T(IIL→IIIR)AR18</i>	2643	2644	(<i>C102(t),K7,Y3053</i>)		3138
<i>T(VL→IVL)AR33</i>	2021	2396	<i>T(IVR→VIR)ALS159,cys-4;ylo-1</i>		
<i>T(VL→IVL)AR33,caf-1 (KH101)</i>	5220	5221	(<i>K7,Y30539y</i>)	3137	
<i>T(IL;IVR;IVR;VR) MEP35 arg-3</i>	3844	3845	<i>T(IVR→VIR)ALS159,met-2 pan-1;ylo-1</i>		
<i>T(VIL→IR)T39M777</i>	2133	2134	(<i>P159,5531,Y30539</i>)		3189
<i>T(VIL→IR)T39M777,ad-8</i>			<i>T(IVR→VIR)ALS159,trp-4 met-2;</i>		
(<i>Y112M343</i>)	3187	3188	<i>ylo-1 (Y2198,K43,Y30539)</i>	3190	
<i>T(VIL→IR)T39M777,chol-2 (47904)</i>		3131	<i>T(IR→VL)NM169d</i>	2279	2280
<i>T(VIL→IR)T39M777,chol-2;arg-13</i>			<i>T(IR→VII;IR;V;VII)AR173</i>	2468	2469
(<i>47404;RU3</i>)	3130		<i>T(IVR;VIL;VIIR)ALS175</i>	2931	2932
<i>T(VIL→IR)T39M777 het-8^{HO}</i>	7411	7410	<i>T(IIR→VL)ALS176</i>	2102	2103
<i>T(VIL→IR)T39M777 het-8^{PA}</i>	7413	7412	<i>T(IIR→VL)ALS176,hct-C het-D</i>	2414	3014
<i>T(VIL→IR)T39M777,nit-6,hct-8^{OR}</i>			<i>T(IIR→VL)ALS176 ,het-C het-d</i>	3013	2415
(<i>OP4</i>)	7409	7408	<i>T(IIR→VL)ALS176,fl (L)</i>		3139
<i>T(VIL→IR)T39M777,ser-6,hct-8^{OR}</i>			<i>T(IIR→VL)ALS176,pe (Y8743m)</i>		3140
(<i>DK42</i>)		7406	<i>T(IIR→VL)ALS176,pe fl</i>		
7407			(<i>Y8743m,L</i>)	3141	3142
<i>T(IL→VIL)T51M156 un</i>	2270	2271	<i>T(I;III;VI;VII)AR176</i>	2708	2709
<i>T(VIIL→IVR)T54M50,hct-e (no#)</i>	2466	2467	<i>In(IL→IR)NM176</i>	3267	1613
<i>T(VIIL→IVR)T54M50,hct-E (no#)</i>	2603	2604	<i>In(IL→IR)NM176,ser-3 (47903)</i>		3143
<i>T(VIIL→IVR)T54M50,hct-e nic-3</i>			<i>T(IIR→IL)NM177</i>	1610	2003
(<i>no#,Y31881</i>)	3132	3133	<i>T(IIR→IL)NM177,aro-1 (Y7655)</i>	3158	
<i>Tp(IR→IR)T54M94</i>		2928	<i>T(IIR→IL)NM177,cys-11 (85518)</i>	3159	3160
<i>Tp(IR→IR)T54M94,al-2 cyh-1</i>			<i>T(IIR→IL)NM177,leu-3 (R156)</i>		3161
(<i>RIP-15300 KH52</i>)		7565	<i>T(IIR→IL)NM177,leu-3 leu-4</i>		
<i>Tp(IR→IR)T54M94,un-18</i>			(<i>R156,R108</i>)		3162
(<i>T54M94(t)</i>)	2943		<i>T(IIR→IL)NM177,nuc-2 (RLM38)</i>	3165	
<i>T(I;III;III;II)T54M140 un</i>	4528		<i>T(IIR→IL)NM177,pcon^{c-2} nuc-2^{(t)35}</i>		
<i>T(VL→)MB67</i>	6714	6715	(<i>c-2,35(t)</i>)		3166
<i>T(II→VIIR)P73B159 wc-1</i>	3039	3040	<i>T(IIR→IL)NM177,pcon^c (c-2)</i>	2533	3163
<i>T(VIIR→IR)Z88</i>	6298	6299	<i>T(IIR→IL)NM177,preg^c (c-1)</i>	2537	3164
<i>T(IR→VIR)NM103</i>	2137	2138	<i>T(VIIL→IVR)ALS179</i>	2264	2265
<i>T(IR→VIR)NM103 het-5^{PA}</i>	7346	7347	<i>T(VIIL→IVR)ALS179,cya-8A +</i>		
<i>T(IR→VIR)NM103,ad-9 cyh-1 al-2</i>			<i>a^{m1} ad-3B cyh-1</i>		
(<i>Y154M36,KH52(r),15300</i>)		3134	(<i>P9178 + 1,B114,KH52</i>)	4557	

Genotype (isolation numbers of separable markers)	FGSC stock # mating type		Genotype (isolation numbers of separable markers)	FGSC stock # mating type	
	A	a		A	a
<i>T(IIL→[IV;V])AR17</i>	2595	2596	<i>T(IR→VIR)OY343,al-2 arg-13</i>		
<i>T(IR→VL)ALS182</i>	2973	2974	(15300,RU3)	6704	
<i>T(IR→VL)ALS182,al-2 (15300)</i>		3929	<i>T(IL→VIL)OY347</i>		3870
<i>T(IR→VL)ALS182,met-6 (35809)</i>		3146	<i>T(VIL→IVR)OY349</i>	5868	5869
<i>T(IR→VL)ALS182,thi-1 cyh-1 aur</i>			<i>T(VIL→IR)OY350</i>	4641	4642
(56501,KH52(r),34508)	3144		<i>T(VIL→IR)OY350 chol-2</i>	8277	8278
<i>T(IR→VL)AR190</i>	1951	1952	<i>T(IVR→I)B362i</i>	2935	2988
<i>T(IR→VL)AR190,lys-1 (66202)</i>	3174	3175	<i>T(IIIR;VR;VII)P1156</i>	2599	2600
<i>T(IR→VL)AR190,met-6 al-1^Y</i>			(IVR→VIII;IL;IIR;IVR)S1229		
(35809,ALS4)		3167	<i>arg-14,pe (S1229,Y8743m)</i>	2946	268
<i>T(IR→VL)AR190,nic-2 (43002)</i>	3172	3173	<i>T(I→VIL)S1425</i>	5011	5012
<i>T(IR→VL)AR190,nic-2 cyh-1 al-1</i>			<i>T(IIL→IV)R2394</i>	2757	2758
(43002,KH52(r),JH216)	3176	3177	<i>T(IL→IIIR)R2472 pro</i>	3284	3285
<i>T(IR→VL)AR190,nic-2 ad-9 cyh-1 al-2</i>			<i>T(IIR;VIR)R2459</i>	7287	7288
(43002,Y154M37,KH52(r),MN58p)	3180	3181	<i>T(IIL→VI)P2869</i>	1828	1829
<i>T(IR→VL)AR190,nic-2 al-2 lys-1</i>			<i>T(IIL→VI)P2869,ylo-1 (Y30539y)</i>	3125	3126
(43002,MN58,66202)	3178	3179	<i>In(IL→IR)H4250</i>	1563	1564
<i>T(IR→VL)AR190,thi-1 (56501)</i>	3169	3168	<i>In(IL→IR)H4250,arg-1 (H4250)</i>	1160	1161
<i>T(VIR→IVR)AR209</i>	1931	1932	<i>In(IL→IR)H4250,aur R</i>		
<i>T(VIR→IVR)AR209,pan-2</i>			(34508,35408R)	3156	
(Y154M64)	3147	3148	<i>In(IL→IR)H4250,leu-3;tol</i>		
<i>T(IR→II;I;VII)AR217</i>	3033	3034	(R156;N83)	3253	3254
<i>T(IR→II;I;VII)AR217,ad-9 cyh-1</i>			<i>In(IL→IR)H4250;tol (N83)</i>	1947	2975
(Y154M37,KH52(r))		3149	<i>T(IVR→IIIR)S4342</i>	2064	2065
<i>T(IIIR→ ;IIIR;VIL)D305</i>	2139	2140	<i>T(IVR→IIIR)S4342,pt (S4342)</i>	109	
<i>T(IIIR→ ;IIIR;VIL)D305,dow (P616)</i>	3150	3151	<i>T(IR→IIIR)4540 nic-2</i>	766	767
<i>T(VIR→IIIR)OY320</i>	3635	3636	<i>T(VIIR→IL)5936</i>	2104	2105
<i>T(IL→VL)OY321</i>	3746	3747	<i>T(VIIR→IL)5936,arg-10 (B317)</i>	3152	3153
<i>T(IL→VL)OY321,nit-2 leu-3</i>			<i>T(VIIR→IL)5936,leu-3 (5936)</i>	217	
(nr37,R156)	4288	4289	<i>T(VIIR→IL)5936,nt (65001)</i>	3154	
<i>Dp(VL→IL)QNS-1 (OY321)</i>	5380		<i>T(IR→VII)P7442 mo</i>	3208	3209
<i>Dp(VL→IL)QNS-2 (OY321)</i>	6572		<i>T(VIL→[I;IIIR])Y16329</i>	2710	2711
<i>Dp(VL→IL)QNS-6 (OY321),nit-2 leu-3;</i>			<i>T(VIL→[I;IIIR])Y16329,phe-2</i>	870	
<i>caf-1 at (nr37,R156;KH101,M111)</i>		5381	<i>T(IL→IIR)39311</i>	1245	1246
<i>T(IL→IVR)OY322</i>	3662		<i>T(IL→IIR)39311 a^{m33}</i>		6705
<i>T(VIR→IIIR)OY329</i>	3670	3671	<i>T(IL→IIR)39311,ser-3 arg-1;tol</i>		
<i>T(IL→VR)OY330</i>	3665		(47903,B369,N83)		3220
<i>T(IVR→IL)OY333 met</i>	3666	3667	<i>T(IL→IIR)39311,suc (39311)</i>		41
<i>T(IIR→IVR)OY337</i>	3669		<i>T(IL→IIR)39311,suc (39311)</i>		1247
<i>T(IIR→IVR)OY337;al-2 (15300)</i>	3668		<i>T(IL→IIR)39311;tol trp-4</i>		
<i>T(IIR→IVR)OY337,fl trp-3 (P,td24)</i>		4886	(N83,Y2198)	2985	2976
<i>T(IIR→IVR)OY337 het-D</i>	7472	7473			
<i>T(IR→VIR)OY343</i>	3881	3882			

F. Heteromorphic chromosome stocks

SATELLITE-LESS

sat no # VL 944 945

G. Mini-chromosome stocks

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

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. 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*

	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
alcoy	997	998	alcoy; <i>csp-2</i> (VII marked)	3661	3434

Follow-up testers for use with alcoy

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

2. Multiply marked centromere testers

<i>multicent-1</i> (Perkins NN 19:30)			<i>multicent-2</i> (Metzenberg <i>et al.</i> NN 31:35)		
<i>acr-2;pdx-1;at;ylo-1;wc-1</i>	1985	1986	<i>un-2;arg-5;thi-4;pyr-1;</i>		
<i>bal;acr-2;pdx-1;at;ylo-1;wc-1</i>	2014	2015	<i>lys-1 inl;nic-3 ars-1;</i>		4488
<i>multicent-3</i> (Perkins FGN 37:31)			<i>multicent-4</i> (Perkins FGN 37:31)		
<i>In(IL;IR)OY323;arg-5;acr-2;</i>			<i>arg-5;acr-2;psi;at;ylo-1;wc-1</i>	6828	6829
<i>pdx-1;at;ylo-1;wc-1</i>	6824	6825			
<i>multicent-5</i> (Perkins FGN 37:31) <i>In(IL;IR)OY323;arg-5;acr-2;psi;at;ylo-1;wc-1</i>				6832	6833

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

Mt	Strain designation										FGSC#									
<i>a</i>	+	+	;	<i>rip-1</i>	+	;	<i>acr-2 dow</i>	;	+	+	;	<i>ylo-1 ;nic-3 arg-10</i>	5200							
<i>a</i>	<i>cyh-1</i>	<i>al-2</i>	;	+	<i>ro-7</i>	;	+	+	;	<i>pan-1 cys-4</i>	;	+	;	+	5201					
<i>A</i>	+	+	;	<i>rip-1</i>	+	;	<i>acr-2 dow</i>	;	+	+	;	<i>ylo-1 ;nic-3 arg-10</i>	5199							
<i>A</i>		<i>un-5</i>	+	;	<i>cys-10 uvs-2</i>	;	<i>al-3 inl^f</i>	+	<i>his-6</i>	;	+	+	+	5202						
<i>a</i>		<i>un-5</i>	+	;	<i>cys-10 uvs-2</i>	;	<i>al-3 inl^f</i>	+	<i>his-6</i>	;	+	+	+	5203						
<i>a</i>		+	<i>un-18</i>	;	+	;	+	+	<i>cyh-2</i>	+	;	<i>chol-2 ylo-1 trp-2</i>	5204							
<i>A</i>	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>mtr</i>	;	+	+	<i>al-3 inl^f</i>	;	+	+	<i>rib-1</i>	+	;	<i>met-7</i>	5205			
<i>A</i>	+	;	+	;	+	;	<i>lys-1 cyh-2</i>	+	+	;	<i>chol-2 ylo-1</i>	+	<i>trp-2</i>	;	+	5207				
<i>a</i>	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>mtr</i>	;	+	+	<i>al-3 inl^f</i>	;	+	+	<i>rib-1</i>	+	;	<i>met-7</i>	5206			
<i>a</i>	+	;	+	;	+	;	<i>lys-1 cyh-2</i>	+	+	;	<i>chol-2 ylo-1</i>	+	<i>trp-2</i>	;	+	5208				
<i>A</i>	+	;	+	;	+	;	<i>lys-1</i>	+	;	+	;	<i>ylo-1 pan-2;</i>	<i>nic-3 met-7</i>	5210						
<i>A</i>	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>pdx-1 mtr;</i>	<i>pan-1;</i>	+	<i>al-3 inl^f;</i>	+	;	+	;	+	+	5209					
<i>A</i>	<i>sn cr-1</i>	;	+	;	+	;	;	+	;	<i>lys-1 cyh-2</i>	+	+	;	<i>ylo-1 + pan-2 ;nic-3</i>	+	5211				
<i>A</i>	+	+	;	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>mtr</i>	;	+	+	<i>al-3 inl^f</i>	;	+	<i>rib-1</i>	+	;	+	<i>met-7</i>	5205
<i>a</i>	<i>sn cr-1</i>	;	+	;	+	;	;	+	;	<i>lys-1 cyh-2</i>	+	+	;	<i>chol-2 ylo-1 trp-2;</i>	+	5213				
<i>a</i>	<i>sn cr-1</i>	;	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>mtr</i>	;	+	+	<i>al-3 inl^f</i>	;	+	+	+	;	<i>met-7</i>	5212		
<i>A</i>	<i>sn cr-1</i>	;	+	;	+	;	+	;	+	;	<i>lys-1</i>	+	+	;	<i>ylo-1 pan-2</i>	;	<i>nic-3 met-7</i>	5215		
<i>A</i>	<i>sn cr-1</i>	;	<i>arg-5</i>	;	<i>acr-2</i>	;	<i>pdx-1 mtr;</i>	<i>pan-1</i>	;	+	<i>al-3 inl^f</i>	;	+	+	;	+	+	5214		

4. Testers for linkage in distal regions

Linkage Group					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>ro-10</i>	3618	3619	<i>un-5 al-2 arg-13</i>	2282	2283
<i>ro-10 un-5</i>	7222	7223	<i>un-5 al-1 R</i>	2177	2178
<i>ro-10 al-2 un-18</i>	3789	3790	<i>In(IL;IR)OY323 al-2</i>		3796
<i>ro-10 nit-2 leu-3</i>	7224	7225	<i>al-2 R un-18</i>	7232	
<i>fr al-1 un-18</i>	2617	2618	<i>R un-18</i>	7242	
Linkage Group II					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>ro-7 arg-5 rip-1</i>	6563	6564	<i>trp-3 un-15</i>	7201	7202
<i>ro-7 rip-1</i>	3467	3468			
Linkage Group III					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>cum cyt-22 r(Sk-2)-1</i>	7154		<i>Sk-2^K phe-2 dow</i>	4538	4539
<i>cum r(Sk-2)-1 acr-7</i>		7155	<i>Sk-2^K dow</i>	4260	4261
<i>cum acr-7</i>	7156	7157	<i>acr-2 trp-1 dow</i>	4119	4120
<i>cum acr-7 dow</i>	4540	4541	<i>nit-7 dow</i>	7163	
<i>cum dow</i>	4542	4543	<i>nit-7 erg-3</i>	7247	7248
			<i>dow erg-3</i>	7243	7244
Linkage Group IV					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>cys-10 pdx-1 pan-1 uvs-2</i>	4123	4124	<i>cys-10 mat</i>	2615	2616
<i>cys-10 cot-1 uvs-2</i>	2017	2018	<i>cys-10 uvs-2</i>	1989	2266
Linkage Group V					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>dgr-1 lys-1</i>	7238	7239	<i>caf-1 al-3 his-6</i>	3752	3753
<i>dgr-1 at al-3 his-6</i>	7152	7560	<i>un-9 his-6</i>		7189
<i>dgr-1 al-3 his-6</i>	7150	7151			
Linkage Group VI					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>chol-2 ylo-1 ws-1</i>	3519	3520	<i>chol-2 ylo-1 trp-2</i>	4137	4138
<i>chol-2 nit-6</i>	7212		<i>nit-6 ylo-1 un-23</i>	7563	7564
Linkage Group VII					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>(cya-8A)+(a^{ml} ad-3B cyh-1)</i>	4524	4525	<i>nic-3 wc-1 arg-10</i>	157	
<i>sppo-4 wc-1 nt</i>	2284	2285	<i>nic-3 wc-1 sk</i>	2073	2074
<i>nic-3 met-7 arg-10</i>	4141	4142	<i>arg-10 nt</i>	7217	
Linkage Groups IIIL R;VIL R					
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>acr-2 dow;chol-2 ylo-1 trp-2</i>	4153		<i>acr-2 dow;chol-2 trp-2</i>		4154
<i>T(III;VI)I acr-2 leu-1 dow;ylo-1</i>	4145				
Linkage Groups IL R;IIL;IVL			Linkage Groups IR;IVR;VR		
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>un-5 al-2;pi;cys-10</i>	2922	2923	<i>un-18;mat;his-6</i>	2944	2945
Linkage Groups IIR;IIIR;VIR			Linkage Groups VII;VIIL R R		
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>rip-1;dow;trp-2</i>	3313	3314	<i>chol-2;sppo-4 wc-1 nt</i>	2924	2925

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

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

OR23-1VA	<u>A</u>	2489	ORS-6a	<u>a</u>	4200	<i>fl</i>	<u>A</u>	4317	<u>a</u>	4347
----------	----------	------	--------	----------	------	-----------	----------	------	----------	------

C. Species testers and reference strains

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

<i>Neurospora crassa</i>			<i>Neurospora intermedia</i>			<i>Neurospora sitophila</i>		
	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>fl^P</i> (OR)	4317	4347	Shp-1A/-1a	3416	3417	<i>fl^P;Sk-I^K</i>	4762	4763
OR23-1VA	2489		P13A	1766		P8085A (<i>Sk-I^K</i>)		2216
ORS-6a		4200	P17a		1767	P8086a (<i>Sk-I^K</i>)		2217
			P420A	2316		<i>fl^P;Sk-I^S</i>	4887	4888
<i>Neurospora discreta</i>			P405a		1940	P2443A (<i>Sk-I^S</i>)	5940	
P851A	3228					P2444a (<i>Sk-I^S</i>)		5941
P8127a		4378						
<i>Neurospora tetrasperma</i>								
85A		1270						
85a			1271					

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.

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

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.

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

het-6 (IIL)

Where not specified, the strain is *het-C*. Duplications from translocation NM 149 include both the *het-c* locus and the *het-6* locus. Whether *het-6* heterozygosity contributes to an incompatible phenotype detected using NM 149 can be determined by progeny-testing with AR 18 or P2869.

Genotype	FGSC#	
	A	a
<i>het-6^{PA}</i> (Panama CZ30.6, CZ30.4) (<i>het-C?</i>)	1131	1130
<i>het-6^{PA}</i> (Probably <i>het-C</i>)	2189	2190
<i>het-6^{PA} arg-12</i> (b ₉ from Spurger P836)	7350	7351
<i>het-6^{PA} thr-2</i>	8236	8237
<i>T(IIL→VR)NM149 het-6^{PA}</i> (b ₇ from P836)	7352	7353
<i>T(IIL→VR)NM149 het-6^{PA}</i> (Probably <i>het-C</i>)	2647	2188
<i>het-6^{OR}</i> (OR wild types)	2489	4200
<i>un-24 het-6^{OR}</i>	7354	—
<i>T(IIL→IIR)AR18 het-6^{OR}</i>	1561	1562
<i>T(IIL→VI)P2869 het-6^{OR}</i>	1828	1829
<i>T(IIL→VR)NM149 het-6^{OR}</i>	3879	3880
<i>T(IIL→VR)NM149 het-6^{OR}</i> (<i>het-c</i>)	1483	1482

Genotype	FGSC #	
	A	a
<u><i>het-9 (VIR)</i></u>		
<i>het-9^{PA}</i> (Panama CZ30.6)	1131	—
<i>het-9^{OR}</i> (OR wild types)	2489	4200
<i>T(VIR→IVR)AR209 het-9^{OR}</i>	1931	1932

het-10 (VIIR)

Genotype	FGSC #	
	A	a
<i>het-10^{CR}</i> (Costa Rica UFC 205 a)	851	—
<i>het-10^{OR}</i> (OR wild types)	2489	4200
<i>T(VIIR→IL)5936 het-10^{OR}</i>	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 recessive suppressor of *A/a het*-incompatibility.)

E. Strains for mutant enrichment and replication

Strains for selective enrichment of mutants

	A		a	
<i>al-3 inl</i> (89601)	2308	2301		
<i>sn cr-1; al-3 inl</i> (89601)	2303	2306		
Strains for replica-plating				
<i>sn cr-1</i>	4158	4159		
<i>sn cr-1; csp-2</i>	4157			
<i>sn cr-1; pe fl</i>	4162	4163		
<i>sn cr-1; al-3 inl(t)</i>	4160	4161		
<i>sn cr-1; pe fl al-3 inl(t)</i>	4164	4165		
<i>cot-1</i>	4065	4066		

FGSC#

Genotype	FGSC#	
	A	a
<i>T(IIL→VR)NM149 het-6^{OR} pyr-4</i>	—	3136
<i>T(IIL→VR)NM149 het-6^{OR} ro-3</i>	2011	2012

het-7 (IIR)

Genotype	FGSC#	
	A	a
<i>het-7^{LI}</i> (Liberia UA-1)	961	—
<i>het-7^{OR}</i> (OR wild types)	2489	4200
<i>T(IIR→X; IIR; VII)D305 het-7^{OR}</i>	2139	2140
<i>T(IIR→X; IIR; VII)D305 het-7^{OR} dow</i>	3150	3151

het-8 (VIL)

Genotype	FGSC#	
	A	a
<i>het-8^{PA}</i> (Panama CZ30.6, Marrero-1d)	1131	2224
<i>T(VIL→IR)T39M777 het-8^{PA}</i>	7413	7412
<i>het-8^{OR}</i> (OR wild types)	2489	4200
<i>chol-2 nit-6 het-8^{OR}</i>	7212	—
<i>ser-6 het-8^{OR} ad-8</i>	—	7213
<i>T(VIL→IR)T39M777 het-8^{OR}</i>	2133	2134
<i>T(VIL→IR)T39M777 nit-6 het-8^{OR}</i>	7409	7408
<i>T(VIL→IR)T39M777 ser-6 het-8^{OR}</i>	7406	7407
<i>T(VIL→IR)T39M777 ad-8 het-8^{OR}</i>	3187	3188
<i>het-8^{HO}</i> (Houma-1n, 1l)	2220	3943
<i>chol-2 nit-6 ser-6 het-8^{HO}</i>	7485	7486
<i>T(VIL→IR)T39M777 het-8^{HO}</i>	7411	—

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

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: Metzberg et al. 1984. Neurospora Newsletter 31:35-40. The genotype of RLM 1-33 is as follows:

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

FGSC#	<i>mt</i>	<i>al-2</i>	<i>arg-12</i>	<i>nuc-2</i>	<i>cot-1</i>	<i>inl</i>	FGSC#	<i>mt</i>	<i>al-2</i>	<i>arg-12</i>	<i>nuc-2</i>	<i>cot-1</i>	<i>inl</i>
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: Metzberg 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 no.	I <i>mt</i>	I <i>un-2</i>	II <i>arg-5</i>	III <i>thi-4</i>	IV <i>pyr-1</i>	V <i>lys-1</i>	VR <i>inl</i>	VIII <i>nic-3</i>	VII <i>ars</i>	FGSC no.	I <i>mt</i>	I <i>un-2</i>	II <i>arg-5</i>	III <i>thi-4</i>	IV <i>pyr-1</i>	V <i>lys-1</i>	VR <i>inl</i>	VIII <i>nic-3</i>	VII <i>ars</i>
4450	A	+	+	-	+	+	+	+	-	* 4470	A	+	+	+	+	+	-	-	-
4451	a	+	+	-	+	+	+	-	-	* 4471	A	+	+	+	+	+	+	-	-
4452	A	+	-	-	+	-	-	-	-	* 4472	a	-	+	-	+	+	+	-	-
4453	A	+	-	-	-	-	-	-	-	* 4473	a	-	+	-	+	+	-	-	-
4454	a	-	+	+	+	-	+	+	+	* 4474	a	-	+	-	+	-	-	-	+
4455	a	-	+	+	+	-	-	+	+	* 4475	a	-	+	-	+	-	+	+	+
4456	A	+	-	+	-	-	-	+	+	* 4476	a	-	+	-	+	+	+	+	+
4457	A	+	-	-	-	-	+	+	+	* 4477	a	-	+	-	+	+	+	-	+
4458	A	+	+	-	+	-	-	-	-	* 4478	a	-	-	+	-	-	-	-	-
4459	A	+	+	-	+	-	-	-	-	* 4479	a	-	-	+	-	-	+	-	-
4460	a	-	-	+	-	+	+	+	+	* 4480	a	-	-	+	-	+	-	+	+
4461	a	-	-	+	-	+	+	+	+	* 4481	A	+	-	+	-	+	+	+	+
4462	A	+	-	+	-	+	+	-	-	* 4482	a	-	-	+	+	+	+	-	-
4463	A	+	-	+	-	+	-	-	-	* 4483	A	-	-	-	-	+	+	-	-
4464	A	+	+	+	+	-	-	-	-	* 4484	a	-	+	+	+	+	-	+	+
4465	A	+	+	+	+	-	-	+	-	* 4485	a	-	+	+	-	+	+	+	+
4466	a	+	+	+	-	+	+	-	-	* 4486	A	+	-	-	+	-	+	-	-
4467	A	+	+	+	-	+	+	-	-	* 4487	A	+	-	-	+	-	-	-	-
4468	a	+	+	-	+	-	-	+	-	* 4488	a	-	-	-	-	-	-	-	-
4469	A	+	+	-	+	-	+	-	-										

H. Strains for obtaining protoplasts or spheroplasts

	<u>A</u>	<u>a</u>	
slime in heterokaryon A/A		327	Emerson 1963 <i>Genetica</i> 34:162; Nelson <u>et al.</u> 1975 NN 23:15.
slime-like	1118		Scarborough 1978 <i>Meth. Cell. Biol.</i> 20:117
slime-like (fast variant)	4761		Scarborough 1985 <i>Exp. Mycol.</i> 9:275
<i>inl</i> (allele 37401)	3659	3660	Wooton <u>et al.</u> 1980 <i>Neurospora Newsl.</i> 27:33
<i>os-1</i> (allele E11200)	47	34	Emerson and Emerson 1958 <i>PNAS</i> 44:668
<i>os-1</i> (allele M16)	812	813	Hamilton and Calvet 1964 <i>J. Bact.</i> 88:1084
<i>os-1</i> (allele NM233t)	4493	4494	Selitrennikoff <u>et al.</u> 1981 <i>Exp. Mycol</i> 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	<u>a</u> ^{m33}	<i>nic-2 cyh-1; inl inv mei-2</i>	VVM
7252	II H	<u>a</u>	<i>thr-3 arg-12^s; pyr-3; inl inv mei-2</i>	VVM + thr + urid
7253	III H	<u>a</u>	<i>acr-2 trp-1; inl inv mei-2</i>	VVM + trp
7254	IV H	<u>a</u>	<i>pan-1 mtr; inl inv mei-2</i>	VVM
7255	V H	<u>a</u>	<i>cyh-2 lys-2 leu-5 mei-2</i>	VVM + lys + leu
7256	VI H	<u>a</u>	<i>pan-2 Bml; inl inv mei-2</i>	VVM
7257	VII H	<u>a</u>	<i>nic-3 oli; inl inv mei-2</i>	VVM
7258	II H, alt	<u>a</u>	<i>pyr-4; inl inv mei-2</i>	VVM + urid
7259	V H, alt	<u>a</u>	<i>cyh-2 am₁₃₂ inl inv mei-2</i>	VVM + leu
7260	VI H, alt	<u>a</u>	<i>pan-2 fpr-6; inl inv mei-2</i>	VVM
7270	IV H, alt	<u>a</u>	<i>pyr-1 mtr; inl inv mei-2</i>	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	<u>A</u>	<i>ad-3A; am₁₃₂ inl inv mei-2</i>	min
7262	II M	<u>A</u>	<i>pyr-3; trp-3; am₁₃₂ inl inv mei-2</i>	min
7263	III M	<u>A</u>	<i>ad-2; am₁₃₂ inl inv mei-2</i>	min
7264	IV M	<u>A</u>	<i>trp-4; am₁₃₂ inl inv mei-2</i>	min
7265	V M	<u>A</u>	<i>am₁₃₂ inl inv mei-2</i>	min
7266	VI M	<u>A</u>	<i>ad-1; am₁₃₂ inl inv mei-2</i>	min
7267	VII M	<u>A</u>	<i>met-7; am₁₃₂ inl inv mei-2</i>	min
7268	II M, alt.	<u>A</u>	<i>arg-12; am₁₃₂ inl inv mei-2</i>	min
7269	V M, alt.	<u>A</u>	<i>inl met-3 inv mei-2</i>	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	<i>a</i>	<i>ad-3A; am₁₃₂ inl inv mei-2</i>	7251
7272	II C	<i>a</i>	<i>pyr-3; trp-3; am₁₃₂ inl inv mei-2</i>	7252
7273	III C	<i>a</i>	<i>ad-2; am₁₃₂ inl inv mei-2</i>	7253
7274	IV C	<i>a</i>	<i>trp-4; am₁₃₂ inl inv mei-2</i>	7254
7275	V C	<i>a</i>	<i>am₁₃₂ inl inv mei-2</i>	7255
7276	VI C	<i>a</i>	<i>ad-1; am₁₃₂ inl inv mei-2</i>	7256
7277	VII C	<i>a</i>	<i>met-7; am₁₃₂ inl inv mei-2</i>	7257
7278	II C, alt.	<i>a</i>	<i>arg-12; am₁₃₂ inl inv mei-2</i>	7258
7279	VC, alt.	<i>a</i>	<i>inl met-3 inv mei-2</i>	7259
7280	VIC, alt.	<i>a</i>	<i>ad-1; am₁₃₂ inl inv mei-2</i>	7260

Alleles used in this work

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

	<u>A</u>	<u>a</u>		<u>A</u>	<u>a</u>
<i>fl;dn</i>	3517	3518	<i>pe fl</i>	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.

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

Strains containing *eas*

The presence of *eas* (*UCLA191*) greatly reduces dispersal of conidia. See Sargent, M.L. 1985. Neurospora Newsl. **32**:12-13. *eas* is present in each strain listed below in addition to the mutant gene shown.

Locus	Allele	FGSC #		Locus	Allele	FGSC #	
		A	a			A	a
<i>ad-3A</i>	38701	4651	4642	<i>al-2</i>	MN58p	4673	4674
<i>cot-2</i>	R1006(t)	4653	4654	<i>al-3^{pos}</i>	Y234M470	4675	4676
<i>trp-4</i>	Y2198	4655	4656	<i>arg-1</i>	B369	4677	4678
<i>al-1</i>	JP45-2	4657	4658	<i>arg-2</i>	CD80	4679	4680
<i>al-2</i>	Y254M165	4659	4660	<i>arg-5</i>	CD6	4681	4682
<i>al-3</i>	P7775	4661	4662	<i>arg-6</i>	CD25	4683	4684
<i>al-1</i>	34508	4663	4664	<i>inl</i>	37401	4685	4686
<i>al-1 (pale)</i>	80-96	4665	4666	<i>pan-2</i>	B2(Y153M66)	4687	4688
<i>al-1 (lemon)</i>	RWT-y1o	4667	4668	<i>cys-3</i>	NM27(t)	4689	4690
<i>ylo-1</i>	P1193	4669	4670	<i>[mi-3]</i>	3754	4691	4692
<i>ylo-2</i>	Y256M230	4671	4672	<i>[poky]</i>	3627-4	4693	4694
<i>ace-1</i>	Y2492, JD105	8111		<i>trp-3</i>	TD24, JD105	8596	
<i>fl</i>	DE1	8601	8602				

L. Strains for photobiology and circadian rhythms

Strain designation	FGSC #		Strain designation	FGSC #	
	A	a		A	a
<i>bd</i>	1858	1859	<i>csp-1;cel bd</i>	3485	
<i>csp-1;bd</i>	2948	4547	<i>cyh-1 al-2 al-1</i>	4550	4551
<i>bd;csp-2</i>	4548	4549	<i>al-2 al-1;al-3</i>	4552	
<i>csp-1;bd;oli</i>	3483		<i>cyh-1 al-2 al-1;al-3</i>		4553
<i>frq¹;bd</i>	2670	2671	<i>cyh-1 al-2 al-1;al-3 inl;bd;csp-2</i>		4554
<i>frq²;bd</i>	2672	2673	<i>bd cel</i>		2947
<i>frq³;bd</i>	2674	2675	<i>chr;bd</i>	4908	
<i>frq⁴;bd</i>	2958	2959	<i>prd-1;bd</i>		4902
<i>frq⁶;bd</i>	4897		<i>prd-2;bd</i>	4903	4904
<i>frq⁷;bd</i>	4898	4899	<i>prd-3;bd</i>	4905	4906
<i>frq⁸;bd</i>	4900	4901	<i>prd-4;bd</i>		4907
<i>frq¹⁰ bd</i>	7490		<i>wc-1 al-2 al-1(aur);al-3</i>	5140	5141
<i>bd;rib-1</i>		7543	<i>bd rib-2</i>		7544

M. Spore-killer tester strains

In heterozygous crosses of $Sk^K \times Sk^S$, 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.* 137:416-429; Turner and Perkins 1993, *Fungal Genet. Newsletter* 40:76-78.

Species and genotype	Origin of allele*	FGSC #		Comment†
		A	a	
<i>Neurospora crassa</i>				
$Sk-2^K$	B	6648	6647	10th backcross to <i>N. crassa</i> , mixed background
$Sk-2^K$	B	3114	3115	10th backcross to <i>N. crassa</i> , inbred to OR wild type
<i>cum Sk-2^K acr-7</i>	B	—	7432	
$Sk-2^K acr-7$	B	6930	—	10th backcross to <i>N. crassa</i>
$Sk-2^K acr-7 leu-1 his-7$	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 <i>N. crassa</i>
$Sk-2^K$	P	7368	7367	12th backcross to <i>N. crassa</i>
$Sk-2^K acr-2$	P	7385	7386	
$Sk-2^K$	J	7369	7370	12th backcross to <i>N. crassa</i>
<i>cum Sk-2^K acr-2</i>	J	7383	7384	
$Sk-2^K acr-2$	J	6928	6929	15th backcross to <i>N. crassa</i>
$Sk-2^K$	J	7392	7393	Used for testing <i>N. crassa</i> from India
$r(Sk-2)-1$	-	2222	—	Iowa-1, LA (P527)
$r(Sk-2)-1 cum$	-	7379	7380	
<i>cum r(Sk-2)-1 acr-7</i>	-	—	7389	
$r(Sk-2)-2$	-	—	7398	Derived from <i>N. crassa</i> P2604, Georgetown, Malaya. See 8275
$Sk-3^K$	P	3577	3578	10th backcross to <i>N. crassa</i>
<i>cum Sk-3^K</i>	P	7382	7381	
<i>cum Sk-3^K his-7</i>	P	7390	7391	
$Sk-3^K acr-2$	P	—	7077	
$Sk-3^K acr-7$	P	6931	6932	15th backcross to <i>N. crassa</i>
$Sk-3^K fl$	P	3579	3580	10th backcross to <i>N. crassa</i>
$Sk-2^S Sk-3^S fl^S$		6682	6683	fl^P (RL) testers
$r(Sk-3)$		7395	—	6th backcross to <i>N. crassa</i>
<i>cum r(Sk-3)</i>		—	7396	6th backcross to <i>N. crassa</i>
<i>cum r(Sk-3) leu-1</i>		—	7394	9th backcross to <i>N. crassa</i>
$r(Sk-3) acr-7 ser-1$		7397	—	6th backcross to <i>N. crassa</i>
<i>mod(pr) ad-4</i>		8272		
<i>pr(sk-2) ser-1</i>			8273	
<i>pr(sk-2) mod(pr) ser-1</i>		8274		
<i>pr(sk-2) mod(pr)</i>		8276	8275	Combined loci formerly called $r(sk-2)-2$. See 7398

Species and genotype	Origin of allele*	FGSC #		Comment†
		A	a	
<i>Neurospora intermedia</i>				
<i>Sk-2^K</i>	B	7401	7402	3rd and 4th backcross to Taipei background
<i>Sk-2^K</i>	P	7429	—	3rd backcross to Taipei background
<i>Sk-2^K</i>	J	7399	7400	f ₁ of Tjiawi-2d (P162) × Taipei-1c (P13)
<i>Sk-2^K</i>	SA	7426	—	Menggatal, Sabah (P3126)
<i>r(Sk-2)</i>		1832	1833	Townsville-1b (P113), Townsville-1 (P112)
<i>Sk-3^K</i>	P	3193	3194	Derived from Rouna-1 (P32)
<i>r(Sk-3)</i>		6595	5123	Tahiti (P2427, P2421)
<i>Sk-2^S Sk-3^S‡</i>		3416	3417	Shew wild types (Taipei background)
<i>Sk-2^S Sk-3^S fl[‡]</i>		5798	5799	7th backcross of fl ^P from <i>N. crassa</i> to Shew wild types

Neurospora sitophila

<i>Sk-1^K</i>		2216	2217	Derived from Dodge's Arlington stocks
<i>Sk-1^K</i>			7866	Purified from mixed collection near Brisbane Australia
<i>Sk-1^K; fl</i>		4762	4763	fl P(1012) from Whitehouse <i>N. sitophila</i> , 3rd backcross to Dodge stocks
<i>Sk-1^S</i>		5940	5941	Tahiti (P2443, P2444)
<i>Sk-1^S; fl</i> or derivative		4887	4888	5th backcross of fl ^P from <i>N. crassa</i> to Panama VP203
<i>r(Sk-1)</i>		6850	—	Makokou-1 (P3914)

Neurospora tetrasperma

(See Raju and Perkins 1991 *Genetics* 129: 25-37. *E*: 8-spored ascus.)

<i>Sk-2^K acr-2</i>	J	6934	6935	8th-9th backcross to <i>N. tetrasperma</i>
<i>Sk-2^K acr-2; E</i>	J	6936	6937	4th backcross to <i>N. tetrasperma</i>
<i>Sk-3^K acr-7</i>	P	6938	6939	7th-8th backcross to <i>N. tetrasperma</i>
<i>Sk-3^K acr-7; E</i>	P	6940	6941	8th backcross to <i>N. tetrasperma</i>
<i>Sk-2^S</i>		1270	1271	Wild types 85A, 85a (also <i>Sk-3^S</i>)
<i>Sk-2^S; E</i>		5897	5901	85A, 85a background (also <i>Sk-3^S</i>)

* 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

Strain designation	FGSC number		Strain designation	FGSC number	
	A	a		A	a
<i>pmb</i>	4814	4815	<i>pmg</i>	4613	4614
<i>mtr*</i>	4812	4813	<i>pmb pmg</i>	4810	4811
<i>pmb mtr</i>		2276	<i>pmg mtr</i>	4808	4809
<i>mtr pmb pmg</i>	4607	4608			

* 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 I

Transport or putative transport mutants for other metabolites

<u>metabolite</u>	<u>mutant</u>	<u>metabolite</u>	<u>mutant</u>	<u>metabolite</u>	<u>mutant</u>
acetate	<i>acpⁱ</i>	oligopeptides	<i>glt</i>	pyrimidine bases	<i>uc-5</i>
ammonium	<i>mea-1</i>	phosphate	<i>pho-4</i>	pyrimidine nucleotides	<i>ud-1</i>
glucose	<i>car</i>	potassium	<i>trk</i>	siderophores	<i>sit</i>
isopropylmalate	<i>ipm-1, -2</i>	sulfate	<i>cys-13, 14</i>	sorbose	<i>sor</i>

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

ad-3B

<u>Genotype and mutant number</u>	<u>Complon coverage</u>	<u>FGSC #</u>
<i>ad-3B (2-17-118)</i>	1	4936
<i>ad-3B (2-17-128)</i>	2	4765
<i>ad-3B (2-31-8)</i>	10-11	4926
<i>ad-3B (2-32-3)</i>	15	4766
<i>ad-3B (2-32-5)</i>	16-17	4767
<i>ad-3A (1-68-13)</i>	-	4764
<i>ad-3B (1-112-2)</i>	NC	4937
<i>his-2 nic-2 al-2</i>	-	4933
<i>ad-2 inl</i>	-	4768

Mating type a

ad-3B

<u>Genotype and mutant number</u>	<u>Complon coverage</u>	<u>FGSC #</u>
<i>ad-3B (2-17-258)</i>	1	5853
<i>ad-3B (2-17-128)</i>	2	885
<i>ad-3B (2-31-8)</i>	10-11	6501
<i>ad-3B (2-32-3)</i>	15	6506
<i>ad-3B (2-32-5)</i>	16-17	6507
<i>ad-3A (1-68-13)</i>	-	5041
<i>ad-3B (1-112-2)</i>	NC	677
<i>his-2 nic-2 al-2</i>	-	5509
<i>ad-2 inl</i>	-	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	<i>ad-3A^R</i>	5016
11-1-5	<i>ad-3A^{IR}</i>	5017
11-1-6	<i>ad-3A^{IR}</i>	5018
11-1-8	<i>ad-3A^{IR}</i>	5019
11-1-13	<i>ad-3A^{IR}</i>	5020
11-1-122	<i>ad-3A^{IR}</i>	5021
11-1-121	<i>ad-3B^{IR}</i>	5026
11-1-1	<i>ad-3B^R</i>	5022
11-1-2	<i>ad-3B^{IR}</i>	5023
11-1-7	<i>ad-3B^{IR}</i>	5024
11-1-10	<i>ad-3B^{IR}</i>	5025
11-1-121	<i>ad-3B^{IR}</i>	5026
11-1-123	<i>ad-3B^{IR}</i>	5027

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

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

R. Strains for testing reverse mutation rates

Reversion by base substitution:

Genotype	FGSC #
<i>ad-3A(N23) al-2 cot-1 pan-2 A</i>	3331 ^A
<i>ad-8(E193) al-2 cot-1 pan-2 a</i>	5072 ^B

Reversion by frameshift

Genotype	FGSC #
<i>ad-3A(N24) al-2 cot-1 pan-2 a</i>	3332 ^A
<i>ad-8(E146) al-2 cot-1 pan-2 a</i>	5071 ^B

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

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

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

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

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

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

Genotype	FGSC #
<i>his-2 nic-2 al-2 pan-2 inl cot-1</i>	
<i>lys-4 al-2 pan-2 inl cot-1</i>	5039
<i>his-3 al-2 pan-2 inl cot-1</i>	5040
<i>ad-3B + RL^{CL}</i>	5035
<i>ad-3A + RL^{CL}</i>	5031
<i>ad-3B + RL^{CL}</i>	5053
<i>ad-3A + RL^{CL}</i>	5054
<i>ad-3A + RL^{CL}</i>	5030
<i>ad-3B + RL^{CL}</i>	5055
<i>ad-3A + RL^{CL}</i>	5056
<i>ad-3B + RL^{CL}</i>	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	<i>al-2;pan-2;cot-1 A</i>	2583
wt	<i>al-2;pan-2;cot-1 a</i>	4934
<i>uvs-1</i>	<i>al-2;pan-2;cot-1;uvs-1 A</i>	4581
	<i>al-2;pan-2;cot-1;uvs-1 a</i>	4582
<i>uvs-2</i>	<i>al-2;pan-2;cot-1;uvs-2 A</i>	4583
	<i>al-2;pan-2;cot-1;uvs-2 a</i>	4584
<i>uvs-3</i>	<i>al-2;pan-2;cot-1;uvs-3 A</i>	4778
	<i>al-2;pan-2;cot-1;uvs-3 a</i>	4779

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

Strains used as heterokaryon testers

74-OR24 a	<i>his-2(C94) nic-2(43002)</i>	5058	74-OR17-69A	<i>his-2(C94) nic-2(43002)</i>	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	<i>(ad-3A ad-3B nic-2^{IR})</i>	5037
12-7-215	21	<i>(ad-3A)^{IR}</i>	5029
12-5-182	38	<i>(ad-3B)^{IR}</i>	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-OR17-24a	<i>his-2 nic-2</i>	5058
74-OR17-69A	<i>his-2 nic-2</i>	5059
68306-OR6-5a	<i>ad-3A</i>	5043
68306-OR6-6A	<i>ad-3A</i>	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 (FGSC 2581)	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl A</i> <i>al-2;pan-2;cot-1 A</i>	2582 2583
59	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-2 A</i> <i>al-2;pan-2;cot-1;uvs-2 A</i>	4773 4583
72	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-3 A</i> <i>al-2;pan-2;cot-1;uvs-3 A</i>	4959 4778
57	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-4 A</i> <i>al-2;pan-2;cot-1;uvs-4 A</i>	4774 4585
73	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-5 A</i> <i>al-2;pan-2;cot-1;uvs-5 A</i>	4775 4587
63	<i>upr-1 his-2 ad-3A ad-3B nic-2;ad-2;inl A</i> <i>upr-1 al-2;pan-2;cot-1;uvs-2 A</i>	4772 4935
71	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl A</i> <i>al-2;pan-2;cot-1;uvs-2 A</i>	2582 4583
70	<i>his-2 ad-3A ad-3B nic-2;ad-2;inl;uvs-2 A</i> <i>al-2;pan-2;cot-1 A</i>	4773 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#
<i>ad-3B nic-2</i>	2-17-17 43002	5316	<i>arg-3 ad-3B</i>	30300 2-17-124	5297 ⁺
<i>ad-3B nic-2</i>	2-17-19 43002	5296	<i>arg-3 ad-3B</i>	30300 2-17-128	5337 ⁺
<i>ad-3B nic-2</i>	2-17-37 43002	5286	<i>arg-3 ad-3B</i>	30300 2-17-158	5529 ⁺
<i>ad-3B;pe fl</i>	2-17-51;Y8743m L	5536	<i>arg-3 ad-3B</i>	30300 2-17-17	5314 ⁺
<i>ad-3B;pe fl</i>	2-17-74;Y8743m L	5535	<i>arg-3 ad-3B</i>	30300 2-17-19	5295 ⁺
<i>ad-3B;pe fl</i>	2-17-75;Y8743m L	5534	<i>arg-3 ad-3B</i>	30300 2-17-233	5292 ⁺
<i>ad-3B nic-2</i>	2-17-79 43002	5313	<i>arg-3 ad-3B</i>	30300 2-17-37	5284 ⁺
<i>ad-3B nic-2</i>	2-17-124 43002	5298	<i>arg-3 ad-3B</i>	30300 2-17-79	5312 ⁺
<i>ad-3B nic-2</i>	2-17-233 43002	5294	<i>arg-3 ad-3B</i>	30300 2-17-793	5308 ⁺
<i>ad-3B nic-2</i>	2-17-793 43002	5310	<i>arg-3 ad-3B</i>	30300 2-17-799	5288 ⁺
<i>ad-3B nic-2</i>	2-17-799 43002	5290	<i>arg-3 ad-3B</i>	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
<i>ad-3A</i> 1-83-5	5657		<i>ad-3B</i> 1-112-9	5447	5446
<i>ad-3A</i> 1-83-10	5658		<i>ad-3B</i> 1-152-68	5659	5483
<i>ad-3A</i> 1-112-13	5648	5445	<i>ad-3B</i> 1-155-55	5660	
<i>ad-3A</i> 1-112-15	5649		<i>ad-3B</i> 1-155-55	5484	
<i>ad-3A</i> 1-152-36	5650		<i>ad-3B</i> 1-230-49	5485	
<i>ad-3A</i> 1-154-22	5651		<i>ad-3B</i> 1-230-83	5486	
<i>ad-3A</i> 1-154-28	5652		<i>ad-3B</i> 1-230-200	5460	
<i>ad-3A</i> 1-155-64	5653		<i>ad-3B</i> 1-234-148	5661	5461
<i>ad-3A</i> 1-155-314	5654		<i>ad-3B</i> 1-263-111	5662	
<i>ad-3A</i> 1-175-167	5655		<i>ad-3B</i> 2-11-6	5463	
<i>ad-3A</i> 1-230-47	5656		<i>ad-3B</i> 2-11-5	5462	
<i>ad-3A</i> 2-31-2	5628		<i>ad-3B</i> 2-11-163	5464	
<i>ad-3A</i> 2-32-10	5637		<i>ad-3B</i> 2-16-18	5727	
			<i>ad-3B</i> 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.

Allele	FGSC#			Allele	FGSC#			Allele	FGSC #		
	A	a	Mutagen		A	a	Mutagen		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 <i>ylo</i>	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

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

DD. Strains for Targetted transformation

From J. Kinsey, Described in Gene
142:219-224 (1994)

<u>Designation</u>	<u>FGSC #</u>	
	<u>A</u>	<u>a</u>
<i>am</i> target strain TEC39		8071
<i>am</i> target strain TEC41-1	8072	

EE. Strains for Assaying Aneuploidy

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

<u>Designation</u>	<u>FGSC #</u>	
	<u>A</u>	<u>a</u>
mtr::hph, trp-2	8288	8289
mtr::hph, trp-2, al-2	8290	
trp-2, arg-3 a ^{m33}		8291

FF. Stocks Maintained as Heterokaryons on Minimal Medium

Loci	Alleles	FGSC #		Obtained from
		Mating type A	a	
<i>(his-2 ad-3A ad-3B nic-2; inl A + al-2; cot-1; pan-2 A)</i>	C94 Y112M13 35203 43002; Y175M256; JH319 + Y112M38; C102(t); Y387-15.7a		2581	FJD
<i>(fmf-1; pyr-3 A + ad-2; per-1 A)</i>	PB-6; KS43 + STL2; AB-T8		3111	TEJ
<i>(fmf-1; tol pan-1 A + tol trp-4 A)</i>	PB-J6; N83 5531 + N83 Y2198		3112	TEJ
<i>(fz; sg; arg-1 cr-1 al-1 os-1 A + al-2 nic-1 lys-3 os-1 A)</i>	no#; no#; B369 B123 34508 B135 + 15300 1413 4545 E11200		327	SE
<i>(fz; sg; os-1 A + arg-1 cr-1 al-1 os-1 A)</i>	no#; no#; B135 + B369 B123 34508 B135	1119		SE
<i>(fz; sg; arg-1 cr-1 al-1 os-1 A + tol pan-1 a)</i>	no#; no#; B369 B123 34508 B135 + N83 5531		2713	REN
<i>(nd al-2 a + lys-1 a)</i>	no# 15300 + 4545		3572	KDM
<i>(nd al-2 a + lys-1 a)</i>	no# 15300 + 4545		3571	KDM
<i>(nd al-2 a + lys-1 a)</i>	no# 15300 + 4545		3570	KDM
<i>(nd al-2 nic-1 a + pan-2 a)</i>	no# 15300 S1413 + Y153M66		6868	BSR
<i>(cwl A + In(IL\leftrightarrowIR)H4250 arg-1 A)</i>	R2441 + H4250 H4250		3842	DDP
<i>(T(VII\rightarrowIV)ALS179, cya-8 + a^{ml} ad-3B cyh-1)</i>	ALS179, P9178	4557		DDP
<i>(cyt-7 wc-1 nt sk + a^{ml} ad-3B cyh-1)</i>	21 P829 65001 P1718	7474	7475	DDP
<i>(fr al-1^Y un-18 + a^{ml} ad-3B cyh-1)</i>	B110 ALS4 T54M90		4499	DDP
<i>(ro-7 arg-5 rip-1 + a^{ml} ad-3B cyh-1)</i>	R2470 27947 4m(t)	6565	6566	DDP
<i>(ro-10 al-2 un-18 + a^{ml} ad-3B cyh-1)</i>	AR7 15300 T54M94	4619	4620	DDP
<i>(ro-10 In(IR; IL)OY323 al-2 arg-13 + a^{ml} ad-3B cyh-1)</i>		7483	7484	DDP
<i>(ser-3 un-16 acr-3 + a^{ml} ad-3B cyh-1)</i>	47903 T42M69 KH14		5095	DDP
<i>(nic-3 wc-1 sk + a^{ml} ad-3B cyh-1)</i>	Y31881 P829 B234		7220	DDP
<i>(os-4; pan-2 + a^{ml} ad-3B cyh-1)</i>	NM2010; Y153M96		5894	DDP
<i>(acr-2 uvs-4 leu-1 + a^{ml} ad-3B cyh-1)</i>	KH5(r) ALS12 33757	7445	7446	DDP
<i>(uvs-5; al-3 inl + a^{ml} ad-3B cyh-1)</i>	ALS13; RP100 89601	7316	7317	DDP
<i>(dgr-1 at al-3 his-6 + a^{ml} ad-3B cyh-1)</i>	KHY15 M111 RP100 Y152M105	7588	7562	DDP
<i>(cyt-7 nic-3 + a^{ml} ad-3B cyh-1)</i>	20 Y31881		7581	DDP
<i>(fr nit-2 + a^{ml} ad-3B cyh-1)</i>	B110 nr7		7868	DDP
<i>(fl trp-3 + a^{ml} ad-3B cyh)</i>	P, TD24	8597	8598	DDP
<i>(T(III; IV)SI302 col-6 A + a^{ml} ad-3B cyh-1)</i>	S1302		8414	DDP

GG. Strains for Forcing and Resolving Heterokaryons

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

HH. Strains for studying MSUD

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

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*."

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., h₂; 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						
	<i>g⁺ mat/i₁</i>		6303			28
	<i>g⁺ mat/i₁ TL-1</i>		6324			43
	<i>g₆ mat</i>		6302			27
	<i>g₆ mat/i₁</i>		6305			30
	<i>h₅ mat</i>		6301			26
	<i>mat g₆ h₅</i>		6315			36a
	<i>mat g₆ h₅</i>		6316			36b
	<i>mat h₂ h₅</i>		6317			37a
	<i>mat h₂ h₅</i>		6318			37b
	<i>sp g⁺ cor</i>		6306			31a
	<i>sp g⁺ cor/i₁</i>		6307			32b
	<i>sp g₁ h₅ cor</i>		6319			38a
	<i>sp g₁ h₅ cor</i>		6320			38b
	<i>sp g₆ cor</i>		6321			39
	<i>sp g₆ h₅ cor</i>		6313			35a
	<i>sp g₆ h₅ cor/i₁</i>		6314			35b
	<i>sp g₇ cor</i>		6322			40
	<i>sp h_{4b} cor</i>		6310			33
	<i>sp h₅ cor</i>		6311			34a
	<i>sp h₅ cor/i₁</i>		6312			34b
LINKAGE II - m CHROMOSOME						
ABORTIVE						
	<i>a-3</i>	-	g ⁺	2792	X	7
MUMMY						
	<i>m₁</i>	-	g ⁺	2794	mummified spores, tawny color X	23-1
	<i>m₂</i>	-	g ⁺	2795	as above X	23-2
	<i>m₃</i>	-	g ⁺	2796	as above X	23-3
RESTRICTED GROWTH						
	<i>r-9</i>	-	g ⁺	2797	X	24
STERILITY						
	<i>st-412</i>	-	g ⁺	2793	self sterile X	22
LINKAGE III - t-y CHROMOSOME						
BLACKBERRY						
	<i>blb</i>	-	g ⁺	2669	bands of darkly pigmented hyphae radiating from colony edge toward center S	-
TAN						
	<i>t₁</i>	1	g ⁺	2799	tan ascospores, gene conversion frequency is low X	31-1
	<i>t₂</i>	2	g ⁺	2800	as above X	31-2
	<i>t₃</i>	3	g ⁺	2801	as above X	31-3
	<i>t₄</i>	4	g ⁺	2802	tan ascospores S	31-4
	<i>t₅</i>	5	g ⁺	2803	tan ascospores, slow growth cytosine	31-5
	<i>t₆</i>	6	g ⁺	2804	tan ascospores S	31-6
	<i>t₇</i>	7	g ⁺	2805	tan ascospores, gene conversion frequency is low X	31-7
	<i>t₈</i>	8	g ⁺	2806	tan ascospores ICR170	31-8
YELLOW						
	<i>y₁</i>	1	g ⁺	2807	yellow ascospores ICR170	32-1
	<i>y₂</i>	2	g ⁺	2808	as above UV	32-2
	<i>y₃</i>	3	g ⁺	2809	as above	32-3
	<i>y₄</i>	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						
<i>blu₃</i>	3	g ⁺	2813	blue ascospores	X	41-2
<i>blu₄</i>	4(?)	g ⁺	2814	blue ascospores	X	42
<i>blu₄ Hrec i</i>			6335			95a
<i>blu₄ Hrec i</i>			6336			95b
<i>blu₄ Hrec i</i>			6337			95c
<i>blu₄ Hrec i</i>			6338			95d
<i>blu₄ rec⁻</i>			6334			94
<i>blu₆</i>	6(?)	g ⁺	2816	bluish ascospores	UV	44
<i>blu₆</i>	-	g ⁺	2839	bluish-grey ascospores	ICR170	613
<i>blu₆ Rec⁺</i>			6328			92a
<i>blu₆ Rec⁺</i>			6329			92b
<i>blu₆ Rec⁺</i>			6330			92c
<i>blu₆ Rec⁺ i</i>			6331			92d
<i>blu₆ rec⁻</i>			6332			93a
<i>blu₆ Rec⁻ i</i>			6333			93b
<i>blu₇</i>	7(?)	g ⁺	2817	as above	S	45
<i>blu₉</i>	-	g ⁺	2836	dark-grey (cyan) ascospores	ICR170	610
<i>g⁺ Rec⁺</i>			6325			91a
<i>g⁺ Rec⁺</i>			6326			91b
<i>g⁺ Rec⁺</i>			6327			91c
INDIGO						
<i>i₁</i>	1	g ⁺	2811		X	41-1
<i>i₂</i>	2	g ⁺	2812	dark blue ascospores	X	41-2
<i>i₂</i>	2	g ⁺	6375			N38
<i>i₅</i>	5(?)	g ⁺	2815	as above		43
<i>i₈</i>	-	g ⁺	2840	greenish ascospores	S	614
<i>i₁₀</i>	-	g ⁺	2841	grey ascospores	UV	615
LINKAGE V (and some brown mutants)						
BROWN						
<i>br₁</i>	1(?)	g ⁺	2819	brown ascospores in homozygote	X	51
<i>br₂</i>	2(?)	g ⁺	2820	brown ascospores	S	52
<i>br₃</i>	3(?)	g ⁺	2821	as above	X	53
<i>br₅</i>	5(?)	g ⁺	2823	as above	UV	55
<i>br₆</i>	6(?)	g ⁺	2824	as above	X	56
<i>br₇</i>	7(?)	g ⁺	2825	as above	X	57
<i>brown</i>			6345		NG	N38
GROUP VI - COLOR MUTANTS						
AMBER						
<i>am</i>	-	g ⁺	2830	amber ascospores	ICR170	64
BLACK						
<i>bl</i>	-	g ⁺	2837	ascospores slightly lighter than wild type but look black and not as brown as wild type	X	611
CAMBRIDGE						
<i>cam</i>	-	g ⁺	2832	light tan ascospores	ICR170	66
CITRINE						
<i>ci</i>	-	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						
<i>col</i>	-	g ₁	2827	yellowish ascospores, no linkage with other y	UV	61
HAZEL						
<i>ha</i>	-	g ⁺	2833	hazel ascospores		67
KYO						
<i>kyo</i>	-	g ₁	2829	light grey ascospores	X	63
MOUSE-GREY						
<i>mo</i>	-	g ⁺	2834	mouse-grey ascospores	ICR170	68
OLIVE						
<i>o</i>	-	g ⁺	2828	olive-green ascospores	X	62
SMOKY						
<i>sm</i>	-	g ⁺	2838	smoky brownish-grey ascospores	X	612
SULPHUR						
<i>su</i>	-	g ⁺	2835	light and bright yellow ascospores	ICR170	69
GROUP VII - SPORE SHAPE (and other characters)						
PART I						
APICULATE						
<i>api-1</i>	-	g ⁺	2844	apiculate spores in homozygote	X	713
<i>api-2</i>	-	g ⁺	2845	as above	X	714
BANDED						
<i>band</i>	-	g ⁺	2848	band-like dark zone formation, mycelial pigment at band, dense perithecia	ICR170	726
NON-DISCHARGE						
<i>dis-1</i>	-	g ⁺	2846	poor ascospore discharge regardless of good fertility		724
<i>dis-2</i>	-	g ⁺	2849	poor ascospore discharge, fair fertility, light mycelial pigmentation		727
<i>dis-3</i>	-	g ⁺	2850	poor ascospore discharge and perithecial formation	ICR170	728
<i>dis-4</i>	-	g ⁺	2851	no spore discharge, few small perithecia	ICR170	729
<i>dis-5</i>	-	g ⁺	2852	as above	ICR170	730
DARK MYCELIUM						
<i>dm-1</i>	-	g ⁺	2853	mycelial color very dark; reduced fertility	ICR170	731
<i>dm-2</i>	-	g ⁺	2854	dark mycelium, rare fertile perithecia	ICR170	732
<i>dm-3</i>	-	g ⁺	2855	dark mycelium, self-sterile	S(?)	733
<i>dm-4</i>	-	g ⁺	2856	dark mycelium	S(?)	734
HALO						
<i>halo</i>	-	g ⁺	2847	halo formation around inoculum	S(?)	725
LOBED SPORES						
<i>lo</i>	-	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						
<i>ro</i>	-	g ⁺	2842	round spores in homozygote, wild type epistatic	X	711
PART II						
DENSE COLONIAL EDGE						
<i>ded</i>	-	g ⁺	2857	dense small perithecia at top of slant	ICR 170	735
PETIT PERITHECIA						
<i>pp</i>	-	g ⁺	2858	small perithecia with a few asci containing normal octads	S(?)	736
PERITHECIA SCATTERED						
<i>ps</i>	-	g ⁺	2859	perithecia of fair fertility scattered across mycelium	X	737
PERITHECIA VACANT						
<i>pv</i>	-	g ⁺	2860	normal size but empty perithecia	ICR 170	738
HYALOMYCELIUM						
<i>hym-1</i>	-	g ⁺	2861	mycelial pigmentation very light; self-sterile	ICR 170	739
<i>hym-2</i>	-	g ⁺	2862	slight mycelial pigmentation, dark spores		740
<i>hym-3</i>	-	g ⁺	2863	slight mycelial pigmentation; fertile, but a subnormal number of perithecia and spores discharged	UV	741
<i>hym-4</i>	-	g ⁺	2864	light mycelial pigmentation; spore pigmentation nearly normal, fertile	S(?)	742
<i>hym-5</i>	-	g ⁺	2865	slight mycelial pigmentation; fertile, spore pigmentation normal	S(?)	743
PARTIALLY FERTILE						
<i>pf-2</i>	-	g ⁺	2866	partial fertile perithecia	S(?)	744
<i>pf-3</i>	-	g ⁺	2867	almost sterile, but a few large partially fertile perithecia	S(?)	745
<i>pf-4</i>	-	g ⁺	2868	almost sterile, with small, partially fertile perithecia	ICR 170	746
<i>pf-5</i>	-	g ₁	2869	relatively poor spore discharge regardless of near normal fertility; smaller than normal	ICR170	747
GROUP VIII - DWARF and RESTRICTED GROWTH						
DWARF						
<i>dw-1</i>	-	g ⁺	2870	dark mycelium, fertile		811
<i>dw-2</i>	-	g ₁	2871	colony size smaller than dw-1, fertile		812
<i>dw-3</i>	-	g ₁	2872	each colony very small, very fertile	S	813
<i>dw-4</i>	-	g ⁺	2873	very slow growth, self-sterile	X	814
<i>dw-5</i>	-	g ⁺	2874	fertile, less dwarfed colonies	X	815
<i>dw-6</i>	-	g ⁺	2875	small, dense colony developing expanded growth, fertile	ICR170	816
<i>dw-7</i>	-	g ⁺	2876	self-sterile, slow growth, mycelium darkly pigmented along edge of primary growth, with thinner secondary growth several points on primary colony	ICR170	817
<i>dw-8</i>	-		6358		NG	N21
<i>dw-9</i>	-		6350		NG	N13
<i>dw-10</i>	-		6359		NG	N22
<i>dw-11</i>	-		6365		NG	N28

Symbol*	Allele number in locus	g locus allele	FGSC stock number	Comments	Mutagen	Number in other collection
<i>dw-12</i>	-		6366		NG	N29
<i>dw-13</i>	-		6367		NG	N30
<i>dw-14</i>	-		6368		NG	N31
<i>dw-15</i>	-		6369		NG	N32
<i>dw-16</i>	-		6371		NG	N34
<i>dw-17</i>	-		6372		NG	N35
<i>dw-19</i>	-		6378		NG	N41
<i>dw-20</i>	-		6379		NG	N42
<i>dw-21</i>	-		6380		NG	N43
RESTRICTED GROWTH						
<i>r-2</i>	-	g ⁺	2877	mycelium more dense than normal, X fertile		822
<i>r-3</i>	-	g ⁺	2878	dense and thin random growth, areas of densely clumped perithecia		823
<i>r-4</i>	-	g ⁺	2879	slow and dense growth, dark mycelium		824
<i>r-5</i>	-	g ⁺	2880	fertile perithecia densely produced, UV+ forming ringed zone about 1 cm from inoculum	5 bromo uracil	825
<i>r-6</i>	-	g ⁺	2881	thick, fertile mycelial growth	X	826
<i>r-7</i>	-	g ⁺	2882	dark, thick mycelial growth, makes small number of large perithecia	S(?)	827
<i>r-8</i>	-	g ₁	2883	fertile perithecia produced on small dense colony; germination of discharged spores from secondary colonies	X	828
<i>r-10</i>	-	g ⁺	2884	growth slow, fertility low, mycelia sparse	X	830
<i>r-11</i>	-	g ₁	2885	slow growth, fertile	UV	831
<i>r-12</i>	-	g ₁	2886	slow growth, very fertile	UV	832
<i>r-13</i>	-	g ⁺	2887	ascospore color in homozygote lighter than normal; slow growth, fertile	ICR170	833
<i>r-14</i>	-	g ⁺	2888	growth slow, colonies covered with an even density of fertile perithecia	ICR170	834
<i>r-15</i>	-	g ⁺	2889	fertile, dense, slow growth	S	835
<i>r-17</i>	-	g ⁺	2891	fertile, slow growth	ICR170	837
<i>r-18</i>	-	g ⁺	2892	early, irregular growth with dark and light mycelial zones	ICR170	838
<i>r-22</i>	-		6355		NG	N18
<i>r-26</i>	-		6352		NG	N15
<i>r-27</i>	-		6360		NG	N23
<i>r-29</i>	-		6361		NG	N24
<i>r-30</i>	-		6362		NG	N26
<i>r-31</i>	-		6363		NG	N26
<i>r-32</i>	-		6353		NG	N16
<i>r-34</i>	-		6364		NG	N27
<i>r-35</i>	-		6370		NG	N33
<i>r-36</i>	-		6356		NG	N19
<i>r-38</i>	-		6373		NG	N36
<i>r-39</i>	-		6374		NG	N37
<i>r-41</i>	-		6376		NG	N39
<i>r-43</i>	-		6347		NG	N8
<i>r-44</i>	-		6348		NG	N9
<i>r-45</i>	-		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

<i>a-4</i>	-	g ⁺	2893		S	92
<i>a-5</i>	-	g ⁺	2894	perithecia very small in homokaryon; large abortive perithecia produced in hybrid heterokaryon	ICR 170	93
<i>a-6</i>	-	g ₁	2895	relatively large perithecia, mostly empty asci		94
<i>a-7</i>	-	g ⁺	2896	growth and perithecial size normal; almost perfectly abortive	UV	95
<i>a-8</i>	-	g ⁺	2897	dwarf-like growth; zonation of perithecia	UV	96
<i>a-9</i>	-	g ⁺	2898	few relatively large perithecia	UV	97
<i>a-10</i>	-	g ⁺	2899	tan ascospores in homozygote, wild type color epistatic, various spore sizes in heterozygote	ICR170	98
<i>a-11</i>	-	g ⁺	2900	growth and perithecial size nearly normal; relatively large no. of spores, some viable	UV	99
<i>a-12</i>	-	g ⁺	2901	growth thin; few relatively large perithecia	ICR170	910
<i>a-13</i>	-	g ⁺	2902	growth and perithecial size normal, few in number	ICR170	911
<i>a-14</i>	-	g ⁺	2903	growth normal, rather small, abundant perithecia yielding relatively large number of spores	ICR170	912
<i>a-15</i>	-	g ⁺	2904	mycelial color very light; less than normal number of perithecia	ICR170	913
<i>a-16</i>	-	g ⁺	2905	mycelial color darker than normal; perithecial size varies	ICR170	914

GROUP X - TRANSLOCATION

TRANSLOCATION

<i>L-1</i>	-	g ⁺	2906		X	101
<i>L-2</i>	-	g ₁	2907		S	102
<i>L-3</i>	-	g ⁺	2908		X	103
<i>L-4</i>	-	g ⁺	2909		S	104
<i>L-5</i>	-	g ⁺	2910		S	105
<i>L-6</i>	-	g ₁	2911	with i ₁	S	106
<i>L-7</i>	-	g ₁	2912		UV(?)	107
<i>L-8</i>	-	g ⁺	2913		S(?)	108
<i>L-9</i>	-	g ⁺	2914		S(?)	109
<i>L-10</i>	-	g ⁺	2915		S(?)	110
<i>L-11</i>	-	g ₁	2916		S	111
<i>L-12</i>	-	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

Section B. Neurospora and Relatives

CLONED GENES

A limited selection of individual genes is available from the FGSC. Individual clones from cosmid and BAC libraries can also be supplied as described in Genbank and on the Whitehead Institute Center for Genome Research web-site.

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 requested are the same as for individual fungal strains: \$20.00 per clone to academic users, \$50.00 per clone for commercial concerns. **The fee cap applied to fungal strains does not apply to cloned genes.**

Neurospora crassa plasmids

<u>Cloned gene</u>	<u>Plasmid name</u>	<u>Reference</u>
acr-2	pAC203	Nakashima Biochim. Biophys. Acta 1307:187-192
al-1 (phytoene dehydrogenase)	pTJS342	Schmidhauser <u>et al.</u> 1990. Mol. Cell Biol. <u>10</u> :5064
al-2 (phytoene synthetase)	pTJS542	Schmidhauser <u>et al.</u> 1994. J. Biol. Chem. <u>269</u> :12060
am (glutamate dehydrogenase)	pJR1	Kinsey & Rambosek 1984. Mol. Cell. Biol. <u>4</u> :117
am (glutamate dehydrogenase)	pJR2	<u>ibid.</u>
arg-2 (CPS synthetase A)	pAB1	Orbach <u>et al.</u> 1990. J. Biol. Chem. <u>265</u> :10981
asn (asparagine synthetase)	pASN	F. Nargang (unpubl)
atp-1 (Mitochondrial ATP synthetase)	pF1 α G4	Bowman and Knock, 1992 Gene <u>114</u> :157-163
atp-2 (Mitochondrial ATP synthetase)	pF1 β 10A3	<u>ibid.</u>
Bml ^r (β -tubulin)	pBT6	Orbach <u>et al.</u> 1986. Mol. Cell. Biol. <u>6</u> :2452-2461
Bml ^r (β -tubulin)	pSV50 (cosmid)	Vollmer & Yanofsky 1986. PNAS <u>83</u> :4869
chs-2 (chitin synthase)	pAB22	Beth Din & Yarden 1994. Microbiology <u>140</u> :2189
chs-2 (chitin synthase)	pAB23	<u>ibid.</u>
chs-4 (chitin synthetase type IV)	pAB6	Beth Din, <u>et al.</u> Mol Gen Genet <u>250</u> :214-222.
chs-4 (chitin synthetase type IV)	pNCCSDE3	Beth Din, <u>et al.</u> Mol Gen Genet <u>250</u> :214-222.
cit-1 (citrate synthetase)	cit-1cDNA	Ferea <u>et al.</u> 1994 Mol Gen Genet <u>242</u> : 105-110
cit-1 (citrate synthetase)	cit-1genomic	<u>ibid.</u>
cot-1 (protein kinase)	pOY18	Yarden <u>et al.</u> 1992. EMBO J. <u>11</u> :2159-2166
cpc-1 (regulatory)	pCPC1-2	Paluh <u>et al.</u> 1988. PNAS <u>85</u> :3728-3732
cpc-1 (regulatory)	pMO31	<u>ibid.</u>
cys-3 (regulatory)	pCYS3	Paietta <u>et al.</u> 1987. Mol. Cell. Biol. <u>7</u> :2506-2511
cys-9	pCS907	Nakashima Genetics 146:101-110
cys-14 (sulfate permease II)	pJSK1	Ketter and Marzluf 1988 Mol.Cell.Biol <u>8</u> :1504-1508
cys-14 (sulfate permease II)	pJSK2	Ketter and Marzluf 1988 Mol.Cell.Biol <u>8</u> :1504-1508
cyt-18 (tyrosyl tRNA synthetase)	pRALcyt18	Ketter et al 1991 Biochemistry 30:1780-1787
cyt-20 (valyl tRNA synthetase)	pCyt20+	Akins and Lambowitz 1987. Cell <u>50</u> :331-345
cyt-21 (mitochon. ribosomal protein)	p297-4	Kubelik <u>et al.</u> 1991. Mol. Cell. Biol. <u>11</u> :4022-4035
cyt-22 (mitochon. ribosomal protein)	pCYT22	Kuiper <u>et al.</u> 1988. J. Biol. Chem. <u>263</u> :2840-2847
eas (ccg-2)	pLW1 Δ K	Kubelik 1989. Ph.D. thesis
erg-3 (C-14 reductase)	pKGP86	Bell-Pedersen <u>et al.</u> 1992. Genes Develop. <u>6</u> :2382
erg-3	pCHYG1	Papavinasundaram & Kasbekar 1994. J Genet <u>73</u> :33-41
erg-3	pCHYG2	Praksah et al. Microbiology 145:1443-1451
erg-3	pCHYG3	Praksah et al. Microbiology 145:1443-1451
frq (circadian periodicity)	pCRM101	Praksah et al. Microbiology 145:1443-1451
gdh-1	pVG1	McClung <u>et al.</u> 1989. Nature <u>339</u> :558-562
gdh-1	pVG2	Kapoor. Biochem. Cell. Biol. 71:205-219
gla-2 (glucoamylase)	pLMN1	Kapoor. Biochem. Cell. Biol. 71:205-219
ccg-1(=grg-1)	pGEM3/2D30	Ebbola and Madi, 1995 FGN <u>43</u> :23-24
het-c ^{GR}	het-cGR	McNally & Free 1988. Curr Genet <u>14</u> :545
het-c ^{PA}	het-cPA	Glass Genetics 146:1299-1309
het-c ^{OR}	het-cOR	Glass Genetics 146:1299-1309
his-3 (histidinol dehydrogenase)	pNH60 (CY)	Glass Genetics 143:1589-1600
his-3 (for targetting transformants)	pRAUW122	Legerton & Yanofsky 1985. Gene <u>39</u> :129-140
his-3 (for targetting transformants)	pBM60	Aramayo and Metzberg, 1995 FGN <u>43</u> :9-13
		Margolin <u>et al.</u> , 1996 FGN <u>44</u> :34-35

***Neurospora crassa* plasmids, continued**

Cloned gene

his-3 (for targetting transformants)
VR telomere, his-6
histones (H3, H4)
Hsp30
hsp-80
hsps-1
ilv-2
ilv-3
inl (inositol synthase)
inl
leu-1
leu-1
lys-4 (saccharopine cleaving)
met-7
met-10
mtA-1
mta-1
mtr (neutral amino transport)
mtr (neutral amino transport)
ncd-2
nic-1
nit-2 (regulatory)
nit-3 (nitrate reductase)
nit-4 (regulatory)
NiR (regulated by nit-4)
nmr (regulatory)
pan-2
pep-4 (Proteinase A, genomic)
pep-4 (Proteinase A, cDNA)
pho-2 (alkaline phosphatase)
pho-4 (phosphate permease)
pho-5 (phosphate permease)
pma-1 (H⁺-ATPase)
pph-1 (type 2A phosphoprotein phosphatase)
pph-1 (type 2A phosphoprotein phosphatase)
ppt-1 (serine/threonine protein phosphatase)
preg
pyr-4 (orotidine 5'-
monophosphate decarboxylase)
qa-2 (catab. dehydroquinase), qa-x
qa-2, qa-4 (dehydroshikimate dehydrase)
qa-3 (shikimate dehydrog.), qa-y
qa-y (quinic acid permease), qa-1S
qa-1F (regulatory)
Nc-ras2
Nc-ras2
rco-3
rgb-1
sod-1 (superoxide dismutase)
spe-1 (ornithine decarboxylase)
spe-3
T (tyrosinase)
thi-4
trp-1 (anthranilate synthetase)
3 (tryptophan synthetase)
un-3 (valyl tRNA synthetase)
un-18
ribosomal protein
vma-1 (genomic vacuolar ATPase)

Plasmid name

pBM61
pVRTEL1
pNcH3H4
pHSP30
pH807
pG6D
pHS503
pILV31
pINL-1-724593 (AL)
pOKE01
pLEU11
pLEU12
pSL4
pMET7
pMET10
pmtAG-2
pCSN4
pCVN2.9
pN846
pBNCD-2
pNIC-1
pNIT2
pNIT3
pNIT4B
pniR-1.11
pNMR
pOKE102
pep-4genomic
pep-4cDNA
pPL3
pBJ004
pWV01
pKH14
pphCos1
pEY24
pEY43
pPREG2.3[cDNA]
pFB6

pMSK338
pMSK374
pMSK381
pMSK363
pQA1F
pTY6
pTY7
pLMN1
pEY15
pCN101
pGS1
pTC102
pTYR103
pDC107(17:4B)
pNC2
pDB1
pUN3
pTS182
p1717
pvma-1g

Reference

Margolin *et al.* 1996 FGN 44:34-35
Schechtman 1987. Mol. Cell. Biol. 7:3168-3177
Woudt *et al.* 1983. Nucl. Acids Res. 11:5347-5360
Plesofsky and Brambl 1990 JBC 265:15432-15440
Kapoor. Biochem Cell Biol 70:1365-1367
Kapoor. J. Bacteriol. 177:212-221
Sista and Bowman 1992 Gene 120: 115-118
Jarai *et al.*, Mol. Gen. Genet. 224:383-388
Akins & Lambowitz 1985. Mol. Cell. Biol. 5:2272
R.L. Metzzenberg (unpubl)
Jarai *et al.*, Mol. Gen. Genet. 224:383-388
Jarai *et al.*, Mol. Gen. Genet. 224:383-388
R.L. Metzzenberg (unpubl)
Crawford *et al.* 1992. Gene 111:265-266
R.L. Metzzenberg (unpubl)
Glass *et al.* 1990. PNAS 87:4912-4916
Staben & Yanofsky 1990 PNAS 87:4917
Koo & Stuart 1991. Genome 34:644-651
Koo & Stuart 1991. Genome 34:644-651
Kurihara. Flavins and Flavoproteins, 1996 251-260
Akins & Lambowitz 1985. Mol. Cell. Biol. 5:2272
Fu and Marzluf 1987. Mol. Cell. Biol. 7:1691
Okamoto *et al* 1991 Mol Gen Genet 227:213-223
Fu *et al* 1989 J. Bact. 171:4067-4070
Colandene and Garrett 1996 FGN 44:11-12
Fu *et al.* 1988 Mol Gen Genet 214:74-79
R.L. Metzzenberg (unpubl)

Grotelueschen *et al.* 1994. Gene 144:147-148
Mann *et al.* 1988 Mol. Cell. Biol. 8:1376-1379
Versaw 1995 Gene 153:135-139
Hager *et al.* 1986 PNAS 83:7693
Yatzkan and Yarden 1995 Curr Genet 28:458-466
Yatzkan and Yarden 1995 Curr Genet 28:458-466
Yatzkan and Yarden 1997 BBA 1353:18-22
Kang and Metzzenberg 1993 Genetics 133:193-202
Buxton & Radford 1983 MGG 190:403

Geever *et al.* 1989 J. Mol. Biol. 207:15-34
Geever *et al.* 1989 J. Mol. Biol. 207:15-34
Geever *et al.* 1989 J. Mol. Biol. 207:15-34
Geever *et al.* 1989 J. Mol. Biol. 207:15-34
Geever *et al.* 1989 J. Mol. Biol. 207:15-34
Murayama. Mol. Gen. Genet. 254:427-432
Murayama. Mol. Gen. Genet. 254:427-432
Ebbola and Madi 1995 FGN 43:23-24
Yarden. Mol Microbiol. 31:197-209
Chary *et al.* 1990 JBC 265:18961-18967
Williams *et al.* 1992 Mol. Cell Biol. 12:347-359
Nakashima J. Biol Rhythm 13:452-460
Kothe *et al.* 1993 Fungal Genet. Newsl. 40:43-45
Nakashima. Curr Genet 30:62-67
Schechtman & Yanofsky 1983 J Mol Appl Genet 2:83
Burns and Yanofsky 1989. JBC 264:3840
Kubelik *et al.* 1991. Mol. Cell. Biol. 11:4022-4035
Nakashima. Mol. Gen. Genet. 259:264-271
Tarawneh, K. *et al.* 1990 Nucl Acids Res 18:7445
Bowman *et al.* 1988 JBC 263:13994-14001

***Neurospora crassa* plasmids, continued**

vma-1 (cDNA)	pRB34	Bowman <u>et al.</u> 1988 JBC <u>263</u> :13994-14001
vma-2 (genomic)	pBB4	Bowman <u>et al.</u> 1988 JBC <u>263</u> :14002-17007
vma-2 (genomic)	pMW1	Bowman <u>et al.</u> 1988 JBC <u>263</u> :14002-14007
vma-2 (cDNA)	pRB30	Bowman <u>et al.</u> 1988 JBC <u>263</u> :14002-17007
vma-3 (genomic)	pHS214	Sista <u>et al.</u> 1994 Mol Gen Genet <u>243</u> :82-90
vma-3, ilv-2 ((genomic)	pHS171	Sista <u>et al.</u> 1994 Mol Gen Genet <u>243</u> :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. <u>7</u> :3168-3177

Plasmids containing *Neurospora crassa* mtDNA

<u>Plasmid</u>	<u>Description</u>
pEco2	Eco2 fragment containing ND2, ND3, ND4 and part of ND5 in pBR322
pEco4	Eco4 fragment in pBR322
pEco6	Eco6 fragment in pBS ⁺
pHP2	<u>Pst</u> I-5a subfragment of <u>Eco</u> RI-1 containing 19S rRNA sequence in pBR322
pRH70	<u>Hind</u> III-7c fragment containing the <u>co</u> I gene in pBR322
pBX17	<u>Xba</u> I/ <u>Bam</u> HI subfragment of <u>Bam</u> HI-3 containing only 19S rRNA sequences
pHPR4a	large rRNA 5' exon probe in pBR322
pND3	<u>Kpn</u> I/ <u>Xba</u> I fragment behind T7 promoter in pBS ⁺
pUCB2 - pUCB11	<u>Eco</u> RI fragments of mtDNA in pBR325

Neurospora Genomic libraries

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. International users are requested to contact the FGSC regarding the availability and format for this library.

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 Whitehead Institute in their sequencing of the *Neurospora* genome.

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 follows:

<u>Locus</u>	<u>LG</u>	<u>Clone no.</u>	<u>Comments</u>
ace-2	IIR	1:6G, 11:1B, 18:12G	Nearby cosmids: 18:2C
ad-9	IR	6:3G	
al-1	IR	3:11H	<i>hom</i> also in this clone
al-3	VR	23:1A	<i>pho-2</i> also in this clone
am	VR	12:2A,15:1B,17:2A,32:3H	
aod-1	IV	23:7F	
arg-1	IL	9:11F,30:6G	
arg-2	IVR	6:7C, 11:7E, 20:5B, 24:8D	
arg-3	IL	9:12E,10:6C,13:6A,15:5E,26:11B,28:6G,28:12D	
arg-12	IIR	16:9H	
arg-13	IR	7:12B,21:10D, 24:10H	
aro-9	IIR	31:9G	
Bml (wt)	VIL	24:11A	24:11A & 22:11A overlap by >20 kb
cgg-1 (grg-1)		29:6C	
cpc-1	VIL	22:11A	22:11A & 24:11A overlap by >20 kb
cr-1	IR	1:10G, 4:7C	
cys-14	IV	16:2B	
for	VIIR	31:5E	23:9D and 26:1H are distal to <i>for</i>
frq	VIIR	6:5A,8:3B,26:2A,30:1A	
grg-1		29:6C	
his-2	IR	10:6F,6:11E	
his-3	IR	6:4E, 6:11C, 12:5C, 16:6F, 19:9A, 21:1D, 23:3H, 29:11F, 30:4C	
hom	IR	3:11H	<i>al-1</i> also in this clone
ilv-2	VR	30:5C, 30:10F	
ilv-3	IVR	2:4C	
inl	VR	13:10B,17:9D,18:6C,20:9B,21:8D	
leu-4	IL	9:7A	
met-5	IVR	18:5B	
met-6	IR	4:11C,7:10D,8:1F,8:4H	
mt(A)	IL	6:10A	<i>un-3</i> also present in this clone
mtr	IVR	5:10A,5:3B,5:4H	
nit-2	IL	6:9H	
nit-3	IVR	29:9H	
nit-4	IVR	9:11A	
os-1	IR	10:6B,12:4D,31:7G	21:5H nearby
pan-1	IVR	31:9C	
pep4	VIIR	6:5A, 31:5E	
pho-2	VR	23:1A	<i>al-3</i> also in this clone
pho-4 (van)	VIII	24:8F	
pmb	IVR	29:4H	This cosmid complements pmb but maps to linkage group VR
prd-4	IR	9:2H	
preg	IIR	2:8E,2:9F,5:2G,5:11C,10:5G,11:6D,21:2G,21:7F	
pro-1	IIR	13:10A, 18:2C, 21:6D	Nearby cosmids: 10:2D,18:10G,20:9A,21:12C,21:12D
rip-1	IIR	16:1D	Nearby cosmids: 3:11A, 4:9C, 13:7C
ser-1	IIR	14:1C, 22:4D, 25:3G, 27:10H	
T	IR	30:2D, 32:9A	
trp-2	VIR	2:5D	
trp-3	IIR	5:4G	possibly also in 1:9B
trp-4	IVR	32:2G	

un-3	IL	6:10A	mt A also present
un-7	IR	12:11D,19:7F,26:4H	
un-10	VIIR	10:12E,11:2D,16:5C,22:2B,23:1C	
vma-1	VR	3:2A, 5:8A, 6:3F, 6:12E, 8:7H, 10:9A, 12:2C, 14:4A, 18:2A, 20:2B, 22:9D, 22:11H, 23:11D, 24:2E, 25:3A, 25:10A, 27:5F, 29:4F, 30:5G, 31:8D Nearby cosmids:4:10G, 9:7B, 11:12F, 12:2A, 15:1B, 17:2A, 18:1B, 25:10E, 26:7D, 26:11C, 29:7E, 32:3H, 32:6A	
vma-2	IIR	21:10C	
vma-3		3:4A, 3:4G, 3:7H, 6:5C, 10:7C, 11:11D, 16:11D, 16:12C, 17:8G, 18:9A, 21:8G, 26:4E, 28:5F, 29:11G, 30:3B, 30:3H, 32:1F Nearby cosmids: 6:1G, 9:4E, 13:8E, 16:5H, 19:7G, 20:3A, 27:3H, 29:10B	
vma-4	IL	14:5H, 15:5C, 21:7E, 29:3H	
DNA polymerase		32:8C	

The following clones contain rDNA segments (linkage group VL)

1:6D, 1:7D, 1:8D2:1D, 2:3G, 5:1A, 5:2H, 5:3E, 5:3F, 5:10D, 6:7G, 6:7H, 7:3B, 7:5F, 7:8A, 7:10B, 8:3F, 8:6D, 8:8D, 9:3D, 10:3D, 10:8E, 10:11G, 11:1F, 11:2H, 11:11H, 11:12B, 12:5G, 13:5E, 13:6B, 13:10G, 14:3D, 14:4E, 15:2B, 15:5F, 16:7E, 18:2E, 18:4A, 18:6B, 18:11G, 19:6A, 19:9H, 20:1D, 20:1H, 20:3F, 20:9D, 20:10H, 20:11G, 21:9B, 22:8B, 22:9G, 22:10G, 23:3G, 23:10B, 23:10D, 23:11F, 24:4H, 24:12E, 26:6C, 29:1E, 29:3B, 29:4B, 29:C1, 9:4F, 13:A4

Cosmids located close to a particular gene: some overlapping, some with similar RFLP patterns

arg-5	25:1D	nuc-1	10:6F
cyh-2	14:7G	pyr-1	27:1F
cyt-21	2:7H	vma-1	18:A10, 23:1A
lys-4	2:7C, 5:5H, 10:9D, 12:11F, 13:1E, 13:4C, 16:4F, 17:5B, 17:11G, 18:12A, 25:12D, 30:7E		

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.

Neurospora cDNA libraries

cDNA libraries constructed by Matthew Sachs

Two cDNA libraries, which represent mRNA from the *Neurospora crassa* wild type strain, 74-OR23-1 VA, 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 germinating library is estimated to contain 1×10^5 independent clones (80% recombinant phage in the primary phage pool which was amplified). The mycelial library is estimated to contain 3.25×10^5 independent clones (75% recombinant). The libraries are supplied as lambda phage in SM containing 7% DMSO.

Nitrogen induced cDNA libraries constructed by R.H. Garrett

One library (NO₃⁻ 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 Perithecial Library (FGSC 4347 was grown on crossing plates and fertilized with 74A. Perithecia 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®). Because of our agreement with 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 corresponding 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).

Interested individuals should contact the FGSC for more details.

Neurospora EST clone banks and Unigene sets

While we are maintaining the EST banks for the present, we are not distributing ESTs.

We have a non-redundant set of cDNA clones from the New Mexico group. Please contact the FGSC for details.

Fee List

Lambda J1: \$20, \$40 additional for FedEx

Lambda Bargem7: \$20, \$40 additional for FedEx

pcosAX: \$20, \$40 additional for FedEx

Orbach/Sachs pMOCosX cosmid: \$200 on agar, \$250 frozen

Chromosome specific sub-library: \$100 to \$200 on agar, \$150 to \$250 frozen

pSV50 cosmid: \$200 on agar, \$250 frozen

YAC: \$200 on agar, \$250 frozen

any cDNA or phage library \$20, \$40 additional for FedEx

2-hybrid libraries \$20, \$40 additional for FedEx

Fungal Strains

PART I. Single Mutant Stocks

(listed alphabetically by 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^{ml} 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 background,' are described at the end of part VIII.

Locus	Allele	FGSC number		Linkage Group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ACCELERATED GROWTH GALACTOSE <i>see agg</i>							
ACETYLAMINOFLUORENE							
<i>aaf</i>	no#(t)	632	633		M	S	PT
ABNORMAL <i>see [abn] -- Part IV</i>							
ACETATE							
<i>ace-1</i>	Y2492	107	205	IIR	SL	M	DDP
<i>ace-2</i>	37812	6014	6015	IIIR	SL	UV	DDP
<i>ace-2</i>	KG511		3469	IIIR	E	UV	HK
<i>ace-2</i>	KG526		3470	IIIR	E	UV	HK
<i>ace-3</i>	KG536	6629	3471	IR	M/E	UV	DDP/HK
<i>ace-4</i>	KG508	8212	3472	IVL	E	UV	FGSC/HK
<i>ace-4</i>	KG523		3473	IVL	E	UV	HK
<i>ace-5</i>	KG512	7557	3474	VR	E	UV	DDP/HK
<i>ace-5</i>	KG513		3475	VR	E	UV	HK
<i>ace-6</i>	<i>see suc</i>						
<i>ace-7</i>	KG539	8213	3476	IR	M	UV	FGSC/HK
<i>ace-7</i>	KG571		3476	IR		UV	HK
<i>ace-8</i>	KG570		4448	VIIC	E	UV	HK
<i>ace-9</i>	KG601	6952	6953	IIR	SL	UV	HK
ACONIDIAL							
<i>acon-2</i>	RS91(t)	3262	3263	IIIR	SL	EMS	DDP
<i>acon-3</i>	RS503	3286	5074	IVL	SL	EMS	DDP
ACETATE PERMEASE							
<i>acpⁱ</i>	FS800	3456	3457	--	SL	UV	AGD
ACRIFLAVINE RESISTANT							
<i>acr-1</i>	KH1(r)	876	875	IL	SL	S	KSH
<i>acr-2</i>	1001(r)	1060		IIIL	M	UV	HBH
<i>acr-2</i>	1002(r)	1059		IIIL	M	UV	HBH
<i>acr-2</i>	KH2(r)	878	877	IIIL	SL	S	KSH
<i>acr-2</i>	KH5(r)	4043	4044	IIIC	SL7	S	EK
<i>acr-2</i>	RC3(r)	2585		IIIL	SL	DS	DDP
<i>acr-3</i>	KH14(r)	1209	1215	IL	SL4	UV	DNP
<i>acr-4;shg</i>	KH16(r);KH160	2322		IL;IIIR	M	S	KSH
<i>acr-5</i>	JLC74	5077	5078	IIR	M	S	DDP
<i>acr-5;mo(KH161)</i>	KH27(r);KH161	2323	2324	IIR;--	M	G	KSH
<i>acr-6 shg</i>	KH19(r) KH160	2325	2326	IIIR R	M	S	KSH
<i>acr-7</i>	P1676(r)	2314	3841	IIIL	M	S	DDP

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ACETATE NON-UTILIZER							
<i>acu-1</i>	J148		4080	V	SL6	NG	EK
<i>acu-1 inl</i>	J148 R233	1731		VR R	M	NG	RBF
<i>acu-3</i>	J138	1732		VR	SL	NG	RBF
<i>acu-5</i>	J118	4032	4033	II(R)	SL7	UV	EK
<i>acu-6</i>	J131	1734		VIL	SL	NG	RBF
<i>acu-7</i>	J136	1735	3264	IIR	M	NG	RBF/DDP
<i>acu-8</i>	T37-3	7125	7126	IIR	SL	RIP	JRF
<i>acu-9 am</i>	T11-1 <i>am</i> ₁₃₂	7326		VII	SL	RIP	IFC
<i>acu-10</i>	S10-3	8214	7327	--	SL	NG	FGSC/IFC
<i>acu-11</i>	S30-12	8215	7328	VII	SL	NG	FGSC/IFC
<i>acu-12</i>	S10-4	7329	8216	IIR	SL	NG	IFC
<i>acu-13</i>	S10-2	7330		IIR	SL	NG	IFC
<i>acu-13</i>	S10-8	7331		IIR	SL	NG	IFC
<i>acu-13</i>	S10-15		7332	IIR	SL	NG	IFC
<i>acu-13</i>	S30-2	7333		IIR	SL	NG	IFC
<i>acu-13</i>	S30-9		7334	IIR	SL	NG	IFC
ADENINE							
<i>ad-1</i>	Y234M419	672		VIL	SL	UV	MEC Contains <i>T(I;VI)Y234M419</i>
<i>ad-1</i>	3254	2281	410	VIL	M	X	DDP
<i>ad-2</i>	20705	8081	397	IIR	M	X	MBM
<i>ad-2</i>	27663	8082	516	IIR	M	UV	RWB
<i>ad-2</i>	70004(t)	380	8077	IIR	M	UV	MBM
<i>ad-2</i>	STL2	26	8075	IIR	M	S	DDP
<i>ad-2</i>	Y175M256		673	IIR	SL	X	MEC
<i>ad-2;al(Y234M468)</i>	Y175M256;Y234M468	956		IIR;IR	SL	X	AMK
<i>ad-2</i>	Y83M32	674	8085	IIR	SL	X	MEC
<i>ad-2;inl</i>	1-175-256;JH319	5042	5046	IIR;VR	SL		FJD
<i>ad-3A</i>	1-68-13	5041		IR	SL	X	FJD
<i>ad-3A</i>	1-112-13	6655	6656	IR	SL	X	DDP
<i>ad-3A</i>	1-230-49		5485	IR	SL		FJD
<i>ad-3A</i>	2-17-52	886		IR	SL	NA	FJD
<i>ad-3A</i>	2-17-814	2458		IR	SL	NA	FJD
<i>ad-3A</i>	2-17-825	5038	5636	IR	SL	NA	FJD
<i>ad-3A</i>	2-31-2		5628	IR	SL		FJD
<i>ad-3A</i>	2-32-10		5637	IR	SL		FJD
<i>ad-3A</i>	2-33-3		5634	IR	SL		FJD
<i>ad-3A</i>	2-33-22		5630	IR	SL		FJD
<i>ad-3A</i>	2-33-34		5629	IR	SL		FJD
<i>ad-3A</i>	5-5-23		5632	IR	SL		FJD
<i>ad-3A</i>	5-5-47		5631	IR	SL		FJD
<i>ad-3A</i>	5-5-52		5635	IR	SL		FJD
<i>ad-3A</i>	5-5-74		5633	IR	SL		FJD
<i>ad-3A</i>	38701	5519	5518	IR	M	UV	MBM
<i>ad-3A</i>	38709	5521	5522	IR	M	UV	MBM
<i>ad-3A</i>	68306	5044	5043	IR	SL	UV	FJD
<i>ad-3A</i>	68306		5452*	IR	SL		FJD
<i>ad-3A</i>	IS11-10	4764		IR	SL		FJD
<i>ad-3A al-2;cot-1;</i> <i>pan-2</i>	N23 Y112M38;C102(t); Y387-15.7	3331		IR R; IVR;VIR	M	4-NQO	TMO
<i>ad-3A al-2 nic-2</i> <i>un-3;tol</i>	2-17-814 Y112M38 43002 55701(t);N83	3820†		IR R R L;IVR	M	NA	AJG
<i>T(I;II;III)Y155M64</i>	<i>ad-3A</i> Y155M64	3037	3038	I;II;III			DDP
<i>T(I-IV)Y112M15</i>	<i>ad-3A</i> Y112M15	2957		IR;IV			AJG
<i>ad-3A</i>	Y175M167		661	IR	SL	X	MEC
<i>ad-3A^{IR}</i>	12-5-194	5028		IR	SL	X	FJD
<i>ad-3A^{IR}</i>	12-7-215	5029		IR	SL	X	FJD

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ADENINE , continued from previous page							
<i>ad-3B</i>	1-112-2	677		IR	SL	X	MEC
<i>ad-3B</i>	1-112-2		4937	IR	SL		FJD
<i>ad-3B</i>	1-112-9	5447	5446	IR	SL		FJD
<i>ad-3B</i>	1-152-68		5483	IR	SL		FJD
<i>ad-3B</i>	1-155-55		5484	IR	SL		FJD
<i>ad-3B</i>	1-230-83		4928	IR	SL		FJD
<i>ad-3B</i>	1-234-148		5461	IR	SL		FJD
<i>ad-3B</i>	2-11-5		5462	IR	SL		FJD
<i>ad-3B</i>	2-11-6		5463	IR	SL		FJD
<i>ad-3B</i>	2-11-163		5464	IR	SL		FJD
<i>ad-3B</i>	2-15-72		5465	IR	SL		FJD
<i>ad-3B</i>	2-15-123	5051		IR	SL	DEB	FJD
<i>ad-3B</i>	2-15-146		5638	IR	SL		FJD
<i>ad-3B</i>	2-17-34	4004	4005	IL	SL5	NA	EK
<i>ad-3B</i>	2-17-34	883	4927	IR	SL	NA	FJD
<i>ad-3B</i>	2-17-55	884		IR	SL	NA	FJD
<i>ad-3B</i>	2-17-128	885	4765	IR	SL	NA	FJD
<i>ad-3B</i>	2-17-137	3259	3846	IR	SL/SL2	NA	FJD/DDP
<i>ad-3B</i>	2-31-8		4926	IR	SL	2-AP	FJD
<i>ad-3B</i>	2-32-3		4766	IR	SL	2-AP	FJD
<i>ad-3B</i>	2-32-5		4767	IR	SL	2-AP	FJD
<i>ad-3B</i>	3-10-16		5472	IR	SL		FJD
<i>ad-3B</i>	3-10-67		5473	IR	SL		FJD
<i>ad-3B</i>	3-10-70		5474	IR	SL		FJD
<i>ad-3B al-2</i>	3-10-109 1-112-38		5475	IR	SL		FJD
<i>ad-3B</i>	3-10-112		5476	IR	SL		FJD
<i>ad-3B</i>	3-10-114		5477	IR	SL		FJD
<i>ad-3B</i>	3-10-132		5478	IR	SL		FJD
<i>ad-3B al-2</i>	3-10-153 1-112-38		5479	IR	SL		FJD
<i>ad-3B al-2;pan-2</i>	3-10-384 1-112-38;1-153-96	5052		IR IR;VIR	SL		FJD
<i>ad-3B</i>	3-10-384		5047	IR	SL		FJD
<i>ad-3B</i>	3-10-446		5481	IR	SL		FJD
<i>ad-3B</i>	3-10-500		5482	IR	SL		FJD
<i>ad-3B</i>	35203	5517	244	IR	SL	UV	FJD/DDP
<i>ad-3B</i>	45601	5523		IR	SL		FJD
<i>ad-3B</i>	5-4-1	5050		IR	SL	S	FJD
<i>ad-3B</i>	5-4-5	5045		IR	SL	UV	FJD
<i>T(I-III)Y112M4i ad-3B</i>	Y112M4i	2637	2638	IR;IIIR			DDP
<i>ad-3</i>	Y175M155		675	IR	SL	X	MEC
<i>ad-4</i>	44206(t)	4045	4046	IIIR	SL6	UV	EK
<i>ad-4</i>	44415(t)	1106	8130	IIIR	M	UV	MEC
<i>ad-4</i>	Y112M16(F2)	442		IIIR	SL	X	MEC
<i>ad-4</i>	Y112M160(F4)	437		IIIR	SL	X	MEC
<i>ad-4</i>	Y155M13(F10)	445		IIIR	SL	S	MEC
<i>ad-4</i>	Y155M39(F12)	440		IIIR	SL	X	MEC
<i>ad-4</i>	Y193M1(F23)	438		IIIR	SL	S	MEC
<i>ad-4</i>	Y226M8(F31)	441		IIIR	SL	UV	MEC
<i>ad-4</i>	Y230M18(F39)	439		IIIR	SL	S	MEC
<i>ad-4</i>	Y234M63(F48)	444	443	IIIR	SL	UV	MEC
<i>ad-5</i>	71104	8129	15	IL	SL	UV	DDP
<i>ad-5</i>	Y152M40	3458	8193	IL	SL?		DDP
<i>ad-5</i>	Y175M253	8127	3459	IL	SL	X	DDP
<i>ad-6</i>	28610ad	65	628	IVR	L	UV	DDP
<i>ad-6</i>	35301	361	8076	IVR	L	UV	MBM
<i>ad-6</i>	Y175M30	664	8083	IVR	SL	X	MEC
<i>ad-6</i>	Y175M221		663	IVR	SL	X	MEC
<i>ad-6</i>	Y175M221	8206		IVR	SL		FGSC
<i>ad-7</i>	Y112M23		8207	VR	SL		FGSC

Locus	Allele	FGSC number		Linkage	Genetic	Muta-	Obtained
		mating type	A				
ADENINE , continued from previous page							
<i>ad-7; ylo-1</i>	44411; Y50539y	89		VR; VIL	M	UV	DDP
<i>ad-7</i>	44411	8084	517	VR	M	UV	RWB
<i>ad-7</i>	P73B171(t)	2619	2620	VR	SL	EMS	DDP
<i>ad-7</i>	Y112M23	666		VR	SL	X	MEC
<i>ad-7</i>	Y175M265	8132	665	VR	SL	X	MEC
<i>ad-8</i>	1-152-7(E6)	452	453	VIL	SL	X	TI
<i>ad-8</i>	1-175-1495 (E19)	3492		VIL	SL	S	TI
<i>ad-8</i>	1-182-20 (E27)	3493		VIL	SL	X	TI
<i>ad-8</i>	1-193-22(E32)	450		VIL	SL	UV	TI
<i>ad-8</i>	1-226-4 (E43)	3497		VIL	SL	S	TI
<i>ad-8</i>	1-226-21 (E51)	3498		VIL	SL	UV	TI
<i>ad-8</i>	1-226-41 (E70)	3499		VIL	SL	UV	TI
<i>ad-8</i>	1-261-12 (E200)	3507		VIL	SL	NA	TI
<i>ad-8</i>	1-262-3 (E206)	3508		VIL	SL	BUDR/FUDR	TI
<i>ad-9</i>	Y154M37	1984	952	IR	SL/M	X	BCT/DDP
<i>ad-9</i>	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

<i>adh</i>	NM227	1530	1531	VIII	E	UV	DDP
------------	-------	------	------	------	---	----	-----

ADENINE SENSITIVE

<i>ads</i>	<u>T</u> 51M1(s)(t)	3509		IV	SL	X	TI
<i>ads</i>	<u>T</u> 52M13(s)(t)	3512		IV	SL	S	TI
<i>ads</i>	<u>T</u> 52M15(s)(t)	3513		IV	SL	S	TI
<i>ads</i>	<u>T</u> 52M26(s)(t)	3514		IV	SL	S	TI
<i>ads</i>	<u>T</u> 52M6(s)(t)	3510		IV	SL	S	TI
<i>ads</i>	<u>T</u> 52M8(s)(t)	3511		IV	SL	S	TI

ARGINASE

<i>aga</i>	UM906	1698	1699	VIIIR	M	UV	RHD
------------	-------	------	------	-------	---	----	-----

AGEING OF CONIDIA

<i>age-2</i>	1	6757	6758	VIR	SL2	S	KDM
<i>age-3</i> (allelic <i>al-1</i>)		6759	6760				

ACCELERATED GROWTH GALACTOSE

<i>agg</i>	L-5	3270		--	M	UV	WKB
------------	-----	------	--	----	---	----	-----

ALTERED GLUCOSE REPRESSION

<i>agr-1; cot-1</i>	RDS8; C102(t)?	7021		--; IVR		UV	SJF
---------------------	----------------	------	--	---------	--	----	-----

ALBINO

<i>al-1</i> (= <i>age-3</i>)	32	6759	6760	IR	SL		KDM
<i>al-1</i>	80-96	901		IR	SL	X	AMK
<i>al-1</i> (= <i>aur</i>)	34508	3622	3623	IR	SL4	UV	DDP
<i>al-1</i>	ALS4	1526	2085	IR	M	UV	ALS/DDP
<i>al-1</i>	ALS19	2147		IR	M	UV	RES
<i>al-1</i>	ALS22	2148		IR	M	UV	RES
<i>al-1</i>	ALS23	2149		IR	M	UV	RES
<i>al-1</i>	ALS25	2150		IR	SL	UV	RES
<i>al-1</i>	car10	903		IR	M	UV	AMK
<i>al-1</i>	E54R11	899		IR	M	UV	AMK
<i>al-1</i>	JH216	3713	3714	IR	SL4	M	DDP
<i>al-1</i>	JP45-2		3858	IR	SL	NG	MLS

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
ALBINO , continued from previous page							
<i>al-1; eas</i>	JP45-2;UCLA191	4657	4658	IR;IIR			MLS
<i>al-1</i>	RES-25-4	2156	2157	IR			RES
<i>al-1</i>	RWT-ylo	3855	3856	IR	SL2	UV	MLS
<i>al-1</i>	Y234M471	898		IR	M	UV	AMK
<i>al-1</i>	Y246M2	902		IR	M	UV	AMK
<i>al-1</i>	Y246M3	906		IR	M	UV	AMK
<i>al-1; eas</i>	80-96;UCLA191	4665	4666	IR;IIR			MLS
<i>al-1</i>	al ^C		800	IR	M	X	DDP
<i>T(I;II)4637 al-1</i>	4637	253	252	IR;IIR			DDP
<i>al-2</i>	15300	4014	3448	IR	SL7	X	EK/DDP
<i>al-2</i>	car1	900		IR	M	UV	AMK
<i>al-2</i>	car7	910		IR	M	UV	AMK
<i>al-2</i>	MN58p	2666	2667	IR	M	UV	DDP
<i>al-2;cot-1;pan-2</i>	Y112M38;C102;Y387-15.7	2583		IR;IVR;VIR	SL		FJD
<i>al-2</i>	Y234M469	914		IR	M	UV	AMK
<i>al-2</i>	Y254M165	904		IR	SL	UV	AMK
<i>al-2</i>	Y256M204	896		IR	M	UV	AMK
<i>al-2</i>	Y256M220		911	IR	M	UV	AMK
<i>al-2</i>	Y256M221	913		IR	M	UV	AMK
<i>al-2</i>	Y256M222		907	IR	M	UV	AMK
<i>al-2</i>	Y256M232	897		IR	M	UV	AMK
<i>al-3</i>	RP100	2082	4073	VR	SL/SL6	UV	RLP/EK
<i>al-3; eas</i>	P7775;UCLA191	4661	4662	VR;IIR			MLS
<i>al-3^{ros}</i>	Y234M470	3581	3582	VR	SL4	UV	DDP
<i>al(85201)</i>	85201		381	IR	M	M	MBM
<i>al(7-32)</i>	7-32	912		IR	SL?	S	AMK
<i>al(1500-008)</i>	1500-008	1138		IR	M	EMS	PCH
<i>al(1500-009)</i>	1500-009	1139		IR	M	EMS	PCH
<i>al(1500-010)</i>	1500-010	1140		IR	M	EMS	PCH
<i>al(1500-011)</i>	1500-011	1141		IR	M	EMS	PCH
<i>al(1500-012)</i>	1500-012	1142		IR	M	EMS	PCH
<i>al(1500-013)</i>	1500-013	1143		IR	M	EMS	PCH
<i>al(B102)</i>	B102		799	IR	SL	UV	DDP
<i>al(CN1)</i>	CN1		1107		M	S	NFR
<i>al(JH9698)</i>	JH9698		801	IR	M		DDP
<i>al(RES6)</i>	RES6	2152	2153	IR	M	UV	RES
<i>al(RES100SUE)</i>	RES100SUE	2154	2155	IR	M	UV	RES
<i>al(Y256M231)</i>	Y256M231	909		IR	M	UV	AMK
<i>al(Y602)</i>	Y602		797	IR	M	M	DDP
<i>al(Y2170)</i>	Y2170		796	IR	M	M	DDP
<i>al(Y2171)</i>	Y2171		795	IR	M	M	DDP
<i>al(al^M)</i>	al ^M		798	IR	SL	UV	DDP
<i>al(al^S)</i>	al ^S	827		IR	M	X	DDP
<i>al(no#);rib-1</i>	no#;C107		1225	IR;VIR			WSM
ALCOY see part VII							
<i>alcoy</i>		997	998				
<i>alcoy;csp-2</i>		3661	3434				
ALKALINE PHOSPHATASE see <i>pho</i>							
ALLANTOICASE DEFECTIVE							
<i>alc-1</i>	WRR1		2699	II	SL	UV	GAM
<i>alc-1</i>	WRR5		2700	II	SL	UV	GAM
ALLANTOINASE DEFECTIVE							
<i>aln</i>	U3		2701	VII	SL	UV	GAM

Locus	Allele	FGSC number		Linkage group	Genetic back-ground	Muta-gen	Obtained from
		A	a				
AMINATION DEFICIENT (NADP-specific glutamate dehydrogenase)							
<i>am</i>	32213(am ₁)	521	1184	VR	M/SL6	UV	RWB/JRF
<i>am</i>	47305(am ₂)	519	1185	VR	M/SL6	UV	RWB/JRF
<i>am;al^S</i>	47305(pr)(am _{2a});al ^S		782	VR;IR	M	UV-am ₃	RWB
<i>am</i>	S2929(am ₃)	522	523	VR	M	MC	RWB
<i>am</i>	S2929(am ₃)		1186	VR	SL6	MC	JRF
<i>am</i>	S2929(partial revertant)(am _{3a})		783	VR	M	UV-am ₃	RWB
<i>am</i>	1381(am ₄)	525	1187	VR	M/SL6	UV	RWB/JRF
<i>am</i>	B501(am ₅)	4343	1188	VR	SL	UV	ELT/JRF
<i>am</i>	am ₆		7095	VR	SL6	UV	JRF
<i>am;al^S</i>	K314(am ₆);al ^S		786	VR;IR	M		RWB
<i>am</i>	B410(am ₇)		1189	VR	SL6	UV	JRF
<i>am</i>	am ₈		788	VR	M	UV	RWB
<i>am</i>	am ₈		7096	VR	SL6	UV	JRF
<i>am;al^S</i>	am ₉ ;al ^S		789	VR;IR	M	UV	RWB
<i>am;al-2</i>	am ₁₀ ;15300		1679	VR;IR	M	UV	JRS
<i>am</i>	am ₁₁		790	VR	M	UV	RWB
<i>am</i>	am ₁₄		1190	VR	SL6	NA	JRF
<i>am</i>	am ₁₅		1678	VR	SL6		JRS
<i>am</i>	am ₁₆		1677	VR	SL6		JRF
<i>am</i>	am ₁₇	1680	1684	VR	M	NA	TWS
<i>am</i>	am ₁₉	1960	1961	VR	E4/E2	NA	DS
<i>am</i>	am ₁	7097	7098	VR	SL	NA	JRF
<i>am;al-2</i>	RU1(am ₂₁);15300	1737	1738	VR;IR	SL	UV	KJM
<i>am</i>	am ₂₄		1853	VR	M	UV	TWS
<i>am;rec-3</i>	am ₁₁₁ ;no#	5881		VR;IL	M	UV	JAK
<i>am;rec-3</i>	am ₁₂₈ ;no#	5882		VR;IL	M	NA	JAK
<i>am</i>	am ₁₃₂	5883	5884	VR	SL10	NA	JAK
<i>am;rec-3</i>	UK23-44;no#	5874		VR;IL	M	DEO	JAK
<i>am;rec-3</i>	UK23-81;no#	5875		VR;IL	M	DEO	JAK
<i>am;rec-3</i>	UK23-82;no#	5876		VR;IL	M	DEO	JAK
<i>am;rec-3</i>	UK39-A4;no#	5877		VR;IL	M	DEO	JAK
<i>am;rec-3</i>	UK48-2;no#	5878		VR;IL	M	DEO	JAK
<i>am;rec-3</i>	UK73-SG2;no#	5879		VR;IL	M	S	JAK
<i>am;rec-3</i>	UK73-40;no#	5880		VR;IL	M	DEO	JAK
Second site revertants							
<i>am</i>	am ₂₁	7099	7100	VR	SL	UV	JRF
<i>am</i>	am _{3a}		7101	VR	SL	UV	JRF
<i>am;arg-10</i>	am _{3a} -B317		7102	VR	SL	UV	JRF
<i>am</i>	am _{3a-1}		7103	VR	SL	UV	JRF
<i>am</i>	am _{3b}		7104	VR	SL	UV	JRF
<i>am</i>	am _{3b-1}	7105		VR	SL	UV	JRF
<i>am</i>	am ₃₋₁₈	7106		VR	SL	UV	JRF
<i>am</i>	am ₅ -L7		4389	VR	SL7	UV	JRF
<i>am</i>	am ₅ -R3		4386	VR	SL7	UV	JRF
<i>am</i>	am ₅ -R'13	4390		VR	SL7	UV	JRF
<i>am</i>	am ₅ -R14		4393	VR	SL7	UV	JRF
<i>am</i>	am ₅ -R15		4385	VR	SL7	UV	JRF
<i>am</i>	am ₅ -R27	4394		VR	SL7	UV	JRF
<i>am</i>	am ₁₄ R1	7107		VR	SL	NA	JRF
<i>am</i>	am ₁₄ -R5		4392	VR	SL7	UV	JRF
<i>am</i>	am ₁₅ R11		7108	VR	SL	A	JRF
<i>am</i>	am ₁₅ R15		7109	VR	SL	A	JRF
<i>am</i>	am ₁₅ R16		7110	VR	SL	A	JRF
<i>am</i>	am ₁₉ R24	7111		VR	SL	NA	JRF
<i>am</i>	am ₁₉ R24(1639-56)	7112		VR	SL	NA	JRF
<i>am</i>	am ₁₉ R24-1		7113	VR	SL	NA	JRF
<i>am</i>	am ₁₉ R24-2	7114		VR	SL	NA	JRF

Section C. *Aspergillus*

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 requested are the same as for individual fungal strains: \$20.00 per clone to academic users, \$50.00 per clone for commercial concerns. **The fee cap applied to fungal strains does not apply to cloned genes**

A. *nidulans* plasmids

<u>Cloned gene</u>	<u>Plasmid name</u>	<u>Reference</u>
AMA1	pRG-AMA1-NotI	Genetics 155:647-656
AMA1	pRG-AMA1-niiA	
AMA1	pRG-AMA1-niaD	
actin	pSF5	Fidel <i>et al.</i> 1988. Gene <u>70</u> :283-293
acuE (malate synthase)	pRAS12	Sandeman & Hynes 1989. MGG <u>218</u> :87-92
acvA (aminoadipyl-cys-val synthetase)	pSTA207	MacCabe <i>et al.</i> 1990. EMBO J. <u>9</u> :279-287
acvA (penicillin acyltransferase)	pSTA200	MacCabe <i>et al.</i> 1990. EMBO J. <u>9</u> :279-287
ade3	pLH107	Hamer, FGN 45: 13-14
alcA	pAST30	1994 Mol Cell Biol <u>14</u> :5333-5348
alcR (regulatory)	palcR (SalI- SalI)	Felenbok <i>et al.</i> , Gene 73:385-396
amdR (acetamidase regulation)	pALX-1	Andrianopoulos & Hynes 1988. Mol Cell Biol <u>8</u> :3532
amdS (acetamidase)	p3SR2	Hynes <i>et al.</i> , 1983. Mol. Cell. Biol. <u>3</u> :1430-1439
Aras	pAST33	1994 Mol Cell Biol <u>14</u> :5333-5348
Aras (cDNA under control of PalcA)	pAST40	1994 Mol Cell Biol <u>14</u> :5333-5348
areA	pAR4-322-1	Davis and Hynes, unpublished
argB (ornithine transcarbamylase)	pILJ16	Johnstone <i>et al.</i> 1985. EMBO J. <u>4</u> :1307
argB	pDC1	Aramayo <i>et al.</i> 1989. Genetics <u>122</u> :65-71
argB	pMS12	M. Stringer (unpubl)
benA (β -tubulin)	p β -5	May <i>et al.</i> 1987. Gene <u>55</u> :231-243
benA	pbenA3, pbenA7, pbenA10 pbenA13, pbenA715, pbenA16	Oakley Cell Motil Cytoskel <u>22</u> :170-174
bimC	pAEBamI	Enos & Morris 1990. Cell <u>60</u> :1019-1027
bimG (protein phosphatase)	pBG4	Doonan & Morris 1989. Cell <u>57</u> :987-996
calmodulin-dependent protein kinase	p4b-11	Kornstein <i>et al.</i> 1992 Gene <u>113</u> :75-82
crnA (nitrate transport)	pSTA4	Johnstone <i>et al.</i> 1990. Gene <u>90</u> :181-192
facA (acetyl-CoA synthetase)	pRAS7	Sandeman & Hynes 1989. MGG <u>218</u> :87-92
fadA ^{dr}	pSM8P2	Embo J. <u>15</u> :5184-5190
flbA (genomic)	pBN29	Mol Microbiol <u>14</u> :323-334
flbA (cDNA)	pBN30	<i>ibid.</i>
gdhA (glutamate dehydrogenase)	pSJG1	Gurr <i>et al.</i> 1986. Curr. Genet. <u>10</u> :761-766
hxA (xanthine dehydrogenase)	pBAN884	Glatigny and Scazzocchio, J Biol Chem <u>270</u> :3534-3550
ipnA (isopenicillin N synthetase)	pSTA204	MacCabe <i>et al.</i> 1990. EMBO J. <u>9</u> :279-287
lamA (lactamase)	pLAM7	Katz & Hynes 1989. Genetics <u>122</u> :331-339
leu-2	pLH105	Hamer, FGN 45:13-14
mipA (γ -tubulin)	pLO6[genomic]	Oakley & Oakley 1989. Nature <u>338</u> :662
mipA (γ -tubulin)	pTH2[cDNA]	<i>ibid.</i>
niaD (nitrate reductase)	pSTA8	Johnstone <i>et al.</i> 1990. Gene <u>90</u> :181-192
niiA (nitrite reductase)	pNIIA	Johnstone <i>et al.</i> 1990. Gene <u>90</u> :181-192
nimA (protein kinase)	pSAO1	Osmani <i>et al.</i> 1987. J. Cell Biol. <u>104</u> :1495-1504
nudC	pnudC/6.4	Osmani <i>et al.</i> 1990. J. Cell Biol. <u>111</u> :543-551
pyrG (orotidine 5'- monophosphate decarboxylase)	ppyrG pJR15	Oakley <i>et al.</i> 1987. Gene <u>61</u> :385-399
riboB	pLO1, pPL1	<i>ibid.</i>
rodA (condial rodlet layer)	pTA51	Oakley <i>et al.</i> 1987. Gene <u>53</u> :293-298
sp11	pLH112	Stringer <i>et al.</i> 1991. Genes & Devel <u>5</u> :1161-1171
trpC (trifunctional)	pHY201	Hamer, FGN 45: 13-14
tubA (α tubulin)	pDP485	Mullaney <i>et al.</i> 1985. MGG <u>199</u> :37-45
tubB (α tubulin)	pDP6031	Doshi <i>et al.</i> 1991. MGG <u>225</u> :129-141
		Doshi <i>et al.</i> 1991. MGG <u>225</u> :129-141

<u>Cloned gene</u>	<u>Plasmid name</u>	<u>Reference</u>
tubC (β -tubulin)	p β -14-2	May <i>et al.</i> 1987. <i>Gene</i> <u>55</u> :231-243
uaZ (urate oxidase)	bAN640	Oestreicher <i>et al.</i> , <i>Gene</i> <u>132</u> :185-192
wA (polyketide synthase?)	pNK3	Mayorga & Timberlake 1990. <i>Genetics</i> <u>126</u> :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:

<u>Gene</u>	<u>Positive cosmids that are unique to 1 chromosome</u>
abaA	L6:D12
alcC	L15:H7, L31:H2, L31:G9, W2:B9, W3:A3, W3:B11, W3:C5, W12:G2, W12:G9, W16:E11
alcA	L31:F11, L31:H2
aldA	L16:D5, L9:D1
amdS	L6:H3, L26:D7, L30:G5, L31:C5, L31:F3
areA	L20:H2
benA	L6:G2, L9:F8, L14:B12, L15:F8, L17:A11, L17:H1, L18:C12, L22:C2, W2:C8, W6:F8, W16:H11, W26:G6, W29:G10
bimB	L30G05
bimC	L9:D7, L9:E12, L22:B6, L26:B4, W24:F1
bimD	W24F12
bimE	L8:C12, L31:F12
bimG	W2:B4
catA	W7:E08, W2:C09, W22:C01
creA	W3:F8, W7:B12, W29:G8
cysC	W5:C10
br1A	W6:E8
facA	L4:C12, L15:G5, L22:D2
facB	L15:H10, L30:B1, L31:B5, L31:F4
figA	L15:G11, L21:G9, L29:G3
flbA	L5:F6, L23:G9, L28:D11, L28:D12
flbB	L6:H12, L25:B12, L25:C12
fluG(acoD)	L12:F7, L12:H9, L28:H7
gatA	L18:E2, L10:A7(?)

<u>Gene</u>	<u>Positive cosmids that are unique to 1 chromosome</u>
ivoB	W3:H11, W8:B9, W18:G4, W23:D6, W28:H4
k1pA	W5:B9
niaD	W2:C5, W4:H10, W12:F3, W30:C7
nimA	L4:F11, L21:E6 (Both unique to chr. #3)
nimE	W1:H8
nirA	W2:E2, W27:A6
nudC	L11:A11, W5:E3 (both unique to chr. #5)
pabaA	L11:C3, L22:B4, L29:B8, L30:G9
pyrG	L10:F9, L10:G9, L19:A12, L19:B11 (all unique to chr. #1)
pyroA	L24:D3, W2:E9, W27:E7, W29:A1, W30:A5, W30:C6(?)
qutE	L17:E5, L18:F1, W1:E5, W8:E12, W16:F12, W24:F10, W24:G7, W28:F2, W30:A8
riboB	W7:H5, W19:C1
rodA	W16:H5, W21:H6
sepB	L30:D12
spoC1	L10:C1 (unique to chr. #3)

Gene Positive cosmids that are unique to 1 chromosome, continued

ST cluster L11:C9, L19:F12, L24:B3, L31:H10, W7:H3, W27:H5
stuA L9:G2, L23:B12
sudD L26D03

Gene Positive cosmids that are unique to 1 chromosome

trpC L9:F12, L12:A10, L30:F9, W2:B5, W17:F7, W22:A8, W23:E5, W28:E2
tubA L15:H12, W19:B2, W19:F8, W27:F3
tubB W30:D2, W31:B1, W31:F4 (all are unique to chr. #4)
tubC W6:C10 (unique to chr. #1)
uaY L4:F5, L7:H11, L11:F7, L17:E1, L17:F1, W8:D4, W11:C10, W17:G9, W19:C3
wA W18:G2(?)
wetA L6:D8, L7:C3, L20:F11, L32:D8
yA L11:C4, L14:D10, L18:E5, L26:C8, L9:C12

Gene More cosmids with possible chromosome identity

actin L11:C3, L12:A3, L29:B8, L30:G9 (all unique to chr. #1)
pCAN26 W10:E10, W13:G1, W13:H1, W22:E12, W5:F4 (all unique to chr. #7)
pCAN67 L6:D12 (unique to chr. #8)
calmodulin L9:F4 (unique to chr. #7)
histone H3 L9:A9, L9:B6, W11:F3, W12:C2, W23:C5 (all unique to chr. #8)
histone H4 W2:G1, W3:C7 (both unique to chr. #8)

Gene Cosmids with no specific chromosome identity

penN L24:F3, L31:D4, L32:C2
pelA L30:C5, L4:E4, L5:C7
phytochrome L6:F8, L12:C5, L14:B10, L14:C1, L21:A11, L26:B11, L27:G5
histone H2A L22:H1

Ribosomal RNA positive clones (all in pWE15 set):

2:C7, 2:F6, 4:A9, 4:B10, 4:E9, 5:B10, 6:C1, 6:C7, 6:D2, 6:D11, 6:G12, 7:A4, 7:D2, 7:G1, 8:C9, 8:D1, 8:D9, 8:F5, 8:F11, 9:B5, 9:C11, 9:C12, 9:F2, 9:F10, 10:B5, 10:C11, 10:C12, 10:F2, 11:A6, 11:A8, 11:C3, 11:D5, 11:E11, 11:G10, 12:H4, 13:F5, 13:F6, 14:D3, 15:C9, 15:D11, 15:E9, 15:F1, 15:H4, 15:H5, 16:H9, 17:B5, 17:C2, 17:C4, 17:G2, 18:A4, 18:A10, 19:E2, 19:G7, 19:H2, 21:E12, 22:B4, 22:B7, 22:E8, 22:H10, 23:G2, 24:C11, 24:F7, 24:H7, 25:D2, 25:D7, 27:F9, 28:B6, 28:F10, 28:H1, 29:C4, 29:D5, 30:D6, 30:G3, 31:A2, 31:E8

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: Osharov and May. Genetics, 155:647-656 and Osharov, 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 as suggested by Maniatis. 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.

Fee list

pWE15 and pLORIST2 cosmid \$200 on agar, \$250 frozen
Ordered chromosome specific library \$200 on agar, \$250 frozen
Compressed minimal library \$150 on agar, \$200 frozen
Individual chromosomes from the chromosome specific library \$75
24 Hr cDNA library \$20, \$40 additional for FedEx
Unizap or Lambda GT10 cDNA library \$20, \$40 additional for FedEx
AMA1 genomic libraries \$20, \$40 additional for FedEx

+ 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.

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	I	Used by G.A. Marzluf
AB	Used by Thomas E. Johnson	j	Used by I.B. Barthelmess
ALS	Alice L. Schroeder	JBM	Joyce B. Maxwell
ANTAS	Used by John H. Chalmers, Jr.	JC	J.B. Courtright
AR	Alan Radford	JFL	J.F. Lehman--used by R.L. Metzberg
B	Brookhaven National Laboratory--used by Val Woodward; also by M.E. Case <u>et al.</u> to refer to <u>pan-2</u> alleles	JH	Johns Hopkins Univ.--used by W.D. McElroy
BAT	Used by J.L. Reissig	JI	John Innes (Inst.)--used by J.R. Fincham
BC	Used by R.L. Metzberg	JL	John Leslie
BE	Bruce Eberhart	JP	Used by M.L. Sargent
BS	B.R. Smith	K	Used by D.G. Catcheside; also by K.C. Atwood for K22 (<i>amyc</i>)
BVS	B.V. Smith	KG	Kwansei Gakuin--used by H. Kuwana
C	California Institute of Technology	KGP	K.G. Perrine - Used by G. Marzluf
C-	Cornell University	KH	K.S. Hsu
CA	Canberra--used by D. Smyth	KO	Used by A. Radford
car	Used by A.M. Kapular	KS	Kansas State--used by V. Woodward
CD	Used by R.H. Davis	L	C.C. Lindegren
CJS	Carol J. Smarr--used by D.D. Perkins	L	L. Livingston
CL	Used by A.S. Sussman	LD	Lori Dunn
CM	Used by A.M. Eberhart	LLM	Laura Livingston Mays
CN	Used by N.F. Robertson	LO	Lori Olson
CR	Used by W.M. Thwaites to denote citrulline resistant	LP	Lakshmi Pendyala
CR-	Used by H. Bertrand	LW	Lloyd Wolfenbarger
CU	Columbia University	M	B.D. Maling
D	Duke University--used by S.R. Gross	MB	Monica Bjorkman
D	Used by G.A. Marzluf	MD	Michael C. Deeley
DBL	D.B. Lee	MEP	Used by R.H. Davis
DFC	D.F. Caroline	MK	Used by V.E.A. Russo
DH	Dorothy Halsall	MKG	Used by R.L. Metzberg
DJ	David Jacobson	MN	Mutant Neurospora--used by D.E.A. Catcheside
DK	Used by S.R. Gross	MW	Used by A.S. Sussman
DL	A.M. DeLange--used by N.B. Raju	N	Dorothy Newmeyer
DS	David Stadler	NAN	Used by Morris Grindle
DW	Dow Woodward	NM	Noreen Murray
E	Emerson--used by Sterling Emerson; also used by T. Ishikawa to refer to <i>ad-8</i> mutants	NMR	Used by G.A. Marzluf
ER	Used by V.E.A. Russo	NS	W.N. Strickland
F	Used by D. Woodward, <u>et al.</u> to refer to <i>ad-4</i> mutants	OP	Used by G.J. Sorger
FB	Frank Buxton	ORS	Used by O. Mylyk
FK	Fraser and Käfer	OY	O.C. Yoder
FLR	Used by S.R. Gross	P	Perkins--used by D.D. Perkins; also by N.E. Murray nee Parker
FS	Florida State--used by DeBusk/Selitrennikoff	PB	Used by Thomas E. Johnson
G	B. Gowdridge--used by M.J. Mayo	PD	Peter Dodd
GH	George Hoffmann	PJR	Peter J. Russell
GN	Used by G.W. Charlang	PR	Designates partial reversion
GNB	George N. Bistis	R	Rockefeller--used by E.L. Tatum
H	Hungate--used by Frank Hungate	RC	Reed College
HC	Ho Coy Choke	RES	R.E. Subden
HK	Homare Kuwana	RLM	R.L. Metzberg
HS	Hugh Sweeney	RLP	R. LePage
HY	Used by Julian Hartley	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	UK	Univ. of Kansas--used by J.A. Kinsey
S	Stanford--used by E.L. Tatum	UM	Univ. of Michigan--used by R.H. Davis
SAT	Sharon A. Thomas	UT	Univ. of Texas
SC	South Carolina--used by Mishra & DeLange	UV	Used by M. Grindle
SDS	San Diego State	UVC	Used by M. Grindle
SF	Used by H.G. Gratzner	UW	Univ. of Wisconsin--used by R.L. Metzenberg
SG	Sam Gross--used by D.D. Perkins	UWO	Univ. of Western Ontario--used by W.L. Greer
STL	St. Lawrence	V	N.V. Vigfusson
SUE	Used by R.E. Subden	<u>V</u>	Virginia--used by R.H. Garrett
SV	S.J. Vollmer	WRN	Used by T.W. Seale to designate reversion by nitrous acid.
T	Texas--used by R.P. Wagner	WRR	Used by G.A. Marzluf
<u>T</u>	Tokyo--used by T. Ishikawa	WRU	Used by T.W. Seale to designate reversion by ultraviolet
TB	Thomas Baker	Y	Yale--used by E.L. Tatum (1945-49);
TJS	T.J. Schmidhauser	X	Used by B.M. Eberhart, also N.H. Giles (to 1973)
TL	T. Legerton	Z	H. Zalkin
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		

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		

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

FJL	Franz J. Leinweber	KF	Kouhei Furuya	RBF	Richard B. Flavel
FPB	Frank P. Buxton	KJM	K.J. McDougall	RDG	Roger D. Goos
GAM	George A. Marzluf	KKJ	Krishna K. Jha	REB	R.E. Beever
GAS	G.A. Scarborough	KN	Kazuo Nakamura	REN	Robert E. Nelson
GM	Gregory May	KSH	K.S. Hsu	RES	Ronald E. Subden
GRH	George R. Hoffman	LB	Leon Belcour	RF	Robert Fuerst
GS	George Sorger	LG	Laura Garnjobst	RH	Ruth Halaban
GYC	Giisela W. Charlang	LGW	Larry G. Williams	RHD	Rowland H. Davis
GWG	G.W. Grigg	LLM	Laura L. Mays	RHG	R.H. Garrett
HA	Harold Aurich	LRL	Laura R. Livingston	RKL	R.K. Littlewood
HB	Helmut Bertrand	LTC	Lung-Ting Chang	RLM	R.L. Metzenberg
HBH	H. Branch Howe	LW	Lloyd Wolfinbarger	RLP	R.L. Phillips
HCC	Ho Coy Choke	MA	Majeed Ahmad	RM	Ramesh Maheshwari
HDB	H.D. Braymer	MB	Monika Björkman	RMD	Ruth M. DeBusk
HDV	Hans de Vries	MBM	Mary B. Mitchell	RPW	Robert P. Wagner
HFT	Hector F. Terenzi	MEC	Mary E. Case	RRB	R.R. Burk
HGG	Howard G. Gratzner	MF	Mark Farman	RTP	Robert T. Pollock
HGK	H.G. Kølmark	MG	Morris Grindle	RWB	Raymond W. Barratt
HI	Hirokazu Inoue	MGS	Michael G. Schechtman	RWH	Roy W. Harding
HK	Homare Kuwana	MJM	M. Jean Mayo	RWT	Robert W. Tuveson
HWS	H. Wayne Shew	ML	Melanie Loo	SB	Stuart Brody
HVE	Hans VanEtten	MLP	Martin L. Pall	SD	Steve Dennison
IBB	I.B. Barthelmess	MLS	Malcom L. Sargent	SE	Sterling Emerson
JAD	John A. DeMoss	MS	Marie Shields	SEG	S.E. Gochenaur
JAK	John A. Kinsey	MU	Martin Urban	SRG	Samson R. Gross
JBC	J.B. Courtright	NBR	N.B. Raju	SRS	S.R. Suskind
JBM	Joyce B. Maxwell	NCM	N.C. Mishra	SW	Susan Wellman
JCK	John C. Krug	NEM	Noreen E. Murray	TEJ	Thomas E. Johnson
JCM	J.C. Murray	NFR	N.F. Robertson	THP	T.H. Pittenger
JFF	Jerry F. Feldman	NGB	Neil G. Brink	TI	Tatsuo Ishikawa
JFL	John F. Leslie	NK	Nancy Keller	TM	Tadako Muryama
JFW	J.F. Wilson	NHH	N.H. Horowitz	TMO	Tong-Man Ong
JH	J. Hartley	NJW	N.J. Weston	TWS	Thomas W. Seale
JHC	J.H. Chalmers, Jr.	NRRL	Northern Regional Research Laboratory	VEAR	V.E.A. Russo
JJL	Jennifer J. Loros	OCY	Olen C. Yoder	VWW	Val W. Woodward
JLR	Jose L. Reissig	OMM	Orest M. Mylyk	WK	W. Klingmuller
JM	Jaime Mora	PCH	P.C. Huang	WKB	William K. Bates
JRF	J.R. Fincham	PJR	Peter J. Russell	WLG	W.L. Greer
JW	Jan Weijer	PMM	P.M. Mohan	WMT	William M. Thwaites
JWT	John W. Taylor	PSL	P. St. Lawrence	WNS	W.N. Strickland
KAZ	Kurt Zeller	PT	Phillips Thayer	WSM	Walter S. McNutt
KEA	Kenneth E. Allen	RBC	R.B. Cain	YK	Yoshiaki Kitani
KDM	Kenneth D. Munkres				