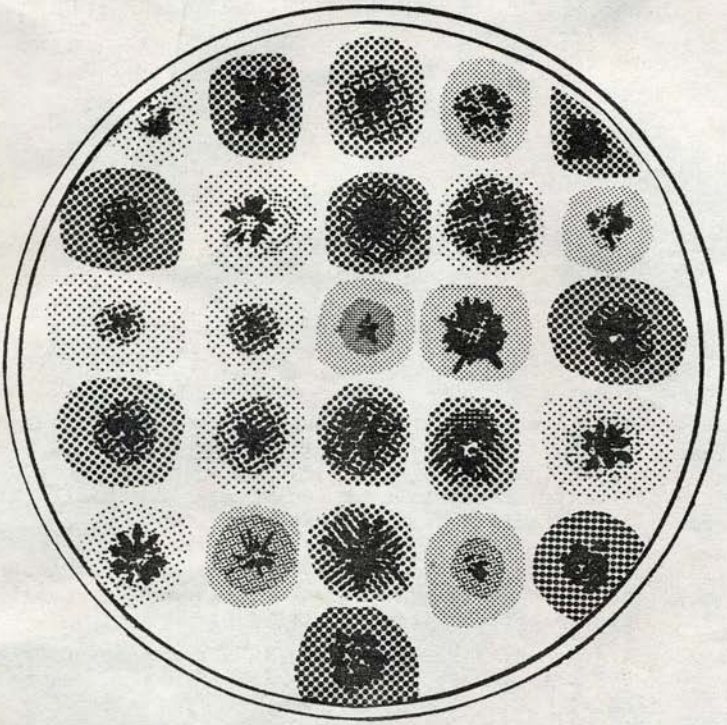
# ASPERGILLUS NEWS LETTER

summer 1975 number 13



# CONTENTS



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Dear Colleague

I again gratefully acknowledge the help of:

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I hope to compile ANL 14 in summer 1976 and will send requests for updating the mailing lists next spring. Material for ANL 14 is welcome any time.

John Clutterbuck

## ASPERGILLUS NIDULANS

### Bibliography supplement 2

An attempt at a complete bibliography of the genetics and biochemistry of A. nidulans was published in "Aspergillus nidulans" A.J. Clutterbuck 1974, in Handbook of Genetics I, pp. 447-510, ed. R.C. King, Plenum Press, New York. Supplement 1 was published in ANL 12. The editor will be grateful for all information of errors and omissions.

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## Related organisms

**Caten, C.E.1973: Genetic control of heterokaryon incompatibility and its effect on crossing and cytoplasmic exchange in Aspergillus amstelodami. Genetics 74: s40 (abstract).**

J.L.Azevedo, E.Pacheco Santana and R.Bonatelli Jr. Department of Genetics, ESALQ, University of São Paulo, 13.400 Piracicaba, São Paulo, Brazil.

## Effects of fungicides and ethidium bromide in a duplication strain of Aspergillus nidulans.

Strains of A.nidulans with a chromosome segment in duplicate are unstable at mitosis. They produce sectors of various kinds which can almost always be scored unequivocally by their characteristic morphology. The system was used successfully to test the effects of agents such as trypan blue to induce deletion in duplication strains (Cooke et al, Nature, 226: 276-277, 1970).

In order to test the effects of two fungicides, 1,4-dichloro-2,5-dimethoxibenzene (chloroneb) and 2,3-dihidro-5-carboxanilido-6-methil-2,4-oxatiin (vitavax) and of ethidium bromide (EB) on mitotic non-conformity, conidia of duplication strain A (Nga and Roper, Genetics 58:193-209, 1968) were inoculated at the centre of 10cm dishes of complete medium containing these agents. Sectors were scored after 7 days at 37°C. In the concentrations used there was only a slight reduction of the growth rate of the colonies. The results (Table 1) show that chloroneb increases the frequency of sectors; vitavax and ethidium bromide reduce instability.

Table 1: Sectors produced by control and treated colonies of strain B.

| Treatment | Nº of dishes | Mean nº of yellow sectors | Mean nº of green sectors | Mean nº of* other sectors | Total nº of sectors |
|---|---|---|---|---|---|
| Control | 29 | 2.48 | 0.76 | 0.10 | 3.34 |
| Chloroneb (5µg/ml) | 10 | 3.30 | 1.00 | 0.70 | 5.00 |
| Vitavax (5µg/ml) | 10 | 0.20 | 0.10 | 0.00 | 0.30 |
| EB (1.0µg/ml) | 39 | 0.33 | 0.08 | 0.15 | 0.56 |
| EB (1.5µg/ml) | 38 | 0.45 | 0.00 | 0.05 | 0.50 |

* - Includes heterokaryotic and deteriorated sectors.

Pacheco Santana (M.S. thesis, Univ. of São Paulo, 1974) did show that chloroneb increases the frequency of haploidization in diploid strains and that vitavax reduces the frequency of mitotic crossing-over and haploidization. Since the same tendency was show regarding instability in duplication strains it could be suggested that the mechanism which controls instability in duplication strains is related to that of mitotic crossing--over and haploidization. Ethidium bromide is known to affect extra--chromosomal elements in bacteria. In the present case it did not reduce the frequency of deteriorated sectors but did reduce the number of improved sectors, acting as a stabilysing agent for unstable duplication strains.

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The use of chloroneb to obtain haploid segregants from heterozygous diploids of Aspergillus nidulans.

Several agents including p-fluorophenylalanine, arsenate, benlate and acridine yellow are used in order to obtain haploid sectors from heterozygous diploids of A.nidulans (Clutterbuck, Handbook of Genetics 1: 447-510, 1974). We did find that other agent, the fungycide chloroneb (1,4-dichloro-2,5-dimethoxybenzene) have the same effect. Diploid conidia were stabed into complete medium plus 10µg/ml chloroneb and after 4-6 days incubation at 37°C many haploid sectors could be obtained and easily purified. Haploid sectors were very conspicuous and no inhibition of several auxotrophic and morphological markers use was observed.

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A temperature sensitive phenotype associated with the TVI-VII translocation

During a routine cross:-

1 pro A1 bi A1; gal E9 cnx H3 sC12; TIII-VIII (non-reciprocal) X y A1 ribo A1; nic B8 (translocation free)

it was found that the III-VIII duplication strains generated had a different morphology from the laboratory stock III-VIII duplication strain. This difference was only noticable after the strains had been grown on complete medium for seven days from a central inoculum. The two morphologies are:-

M1 - morphology of the III-VIII duplication strains from cross 1 - crinkled morphology (Bainbridge and Roper 1966) - produce few improved sectors.

M2 - morphology of the stock III-VIII duplication strain - again a crinkled morphology but many apparently improved sectors are produced. The majority of these sectors do not resemble those produced by the M1 morphology strains.

The strain with the M2 morphology was known to carry the TVI-VII reciprocal translocation often found in stock strains carrying the TIII-VIII (Käfer 1965). No TVI-VII was present in either of the strains used in cross 1. It was suspected that the morphologies M1 and M2 were determined by the absence or presence of the TVI-VII in the respective strains. Normal haploids with or without the TVI-VII show no morphological differences.

In a further cross:-

2 pyro B12 bi A1; wA3; TIII-VIII, TVI-VII X yA1; gal E9 cnx H3 sC12; nic B8; (translocation free)

of the six duplication strains isolated for further study three had the M1 morphology and three the M2 morphology. One of each morphological type was taken and analysed via the parasexual cycle. It was found that the morphologies corresponded with the presence of absence of the TVI-VII as above.

The III-VIII duplication strains carrying the TVI-VII produce many early sectors which show a slight reduction in conidiation and an apparent increase in growth rate as their only phenotypic change. When these sectors are subcultured via their conidia or leading hyphae the resulting colonies show the same phenotype as the parent duplication strain. That is, these 'sectors' are a feature of the colonial morphology and do not represent a class of sectors caused by deletion of duplicate material. (Bainbridge and Roper, 1966; Nga and Roper, 1968). The analysis shows this morphology to result from a combination of the III-VIII duplication with the TVI-VII or less likely, with a locus or loci linked to either or both breakpoints of the TVI-VII.

These pseudosectors are produced when the strains are grown at 37°C but not at 42°C. The morphology is more compact at 42°C but the complete lack of pseudosectors would seem to indicate a temperature sensitive phenotype. This phenotype was described by M.M. Lieber A.N.L. 12 26. However he interpreted the data to mean that there was an increase in chromosome instability with a reduction in temperature (36°C compared to 42°C). This new data may suggest an alternative interpretation.

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## Genetic imbalance and mitotic non-conformity in Aspergillus nidulans

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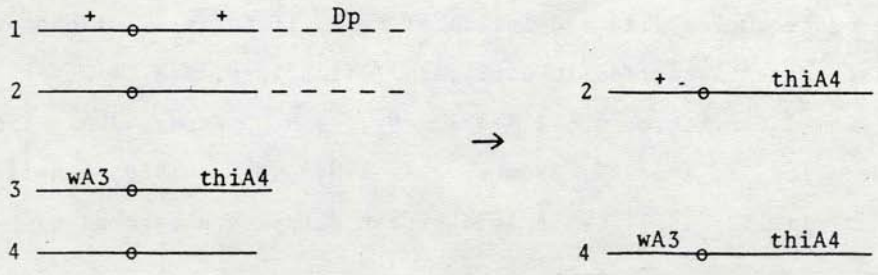
Strains of Aspergillus nidulans with a chromosome segment in duplicate (one in normal position and one translocated to another chromosome) show a characteristic instability at mitosis, and produce nuclei with a deletion of most, if not all, of one of the segments carried in duplicate (Bainbridge, B.W. & Roper, J.A., 1966, J.Gen.Micro. 42, 417-424; Nga, B.H. & Roper, J.A., 1968, Genetics 58, 193-209; Roper, J.A. & Nga, B.H., 1969, Genetical Res. 14, 127-136). A haploid strain carrying a segment of

chromosome I in duplicate has been studied extensively and shows deletions predominantly from the translocated segment and only rarely from the non-translocated segment. In studies of this duplication in a diploid, a considerably increased frequency of loss from the translocated segment was observed. Nga and Roper (1969, Genetical Res. 14, 63-70) suggested that this could be due to the genetic imbalance in these strains, although it is interesting to note that a duplication diploid is relatively less unbalanced than the corresponding duplication haploid.

The products of instability have now been examined from diploids carrying markers on the right arms of chromosomes II and VIII for the I-II and III-VIII duplications respectively. The I-II Dp diploid produced many diploid sectors which no longer carried the duplicate segment. These were assumed by Nga and Roper to arise from "simple" deletion. In fact, at least 50% arose by mitotic crossing-over, as shown by their homozygosity for thiA4 but not for other markers (Figure 1).

Figure 1



Mitotic crossing-over distal to thiA4 could also eliminate the duplicate segment but would have been indistinguishable from loss by deletion. Mitotic crossing-over was also involved in the instability of the III-VIII Dp diploid. These findings make it likely that the frequency of deletion of the translocated segment in diploids was little different from that seen in the duplication haploid. Deletions from the duplicate segments in normal position were also demonstrated and occurred at a frequency greater than that detected in the duplication haploid.

A diploid homozygous for the I-II duplication was synthesized and was shown to be very unstable although, in this strain, mitotic crossing-over could not eliminate either duplicate segment to yield products with a relative growth advantage. Analysis of a sample of sectors showed a) loss from either translocated duplicate segment, at a frequency similar to that which was occurring in the unbalanced haploid and b) frequent loss from both of the corresponding non-translocated segments. This pattern of instability was shown initially by the loss of appropriately arranged markers and confirmed by extensive genetic analysis.

The susceptibility of the translocated segment to deletion and its suggested increase in diploids must, in the light of these findings, be reassessed. The frequency of loss by deletion from the translocated segment appeared to be similar in the duplication haploid, the single duplication diploid and the double duplication diploid. However, the frequency

of loss from the non-translocated segments increased from the duplication haploid, through the single duplication diploid, to the double duplication diploid.

It is difficult, at this stage, to interpret these results in terms of a mechanism for deletion but clearly the different chromosomal positions of the duplicate segments affects their instability at different doses of the duplication. The translocated segments appeared to be unaffected by dosage whereas the non-translocated regions were greatly influenced by the dosage of the segments concerned.

## Possible revision of the right arm of linkage group II of *Aspergillus nidulans*

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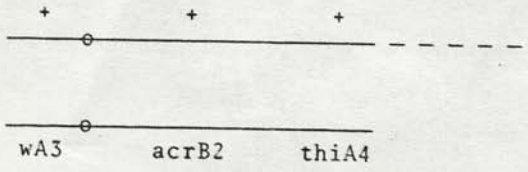
As reported elsewhere in this issue, it is easy to detect mitotic crossing-over in diploids which carry an extra chromosome segment in translocated position. Crossing-over between the centromere and the point of attachment of the duplication can yield a balanced diploid with a growth advantage over its unbalanced parent. This selective technique has been used to study gene order on II R.

Sectors were taken from a diploid heterozygous for wA3, acrB2, thiA4 and the terminally attached I-II Dp. Of 184 sectors which had lost the terminal duplication, 100 definitely arose by mitotic crossing-over. All 100 were homozygous for thiA4 and 67 were homozygous also for acrB2. The remaining 84 sectors arose either by "simple" deletion or mitotic crossing-over between the most distal marker and the point of attachment of the duplication. The presence of wA3 allowed distinction between mitotic crossing-over and non-disjunction as a cause of elimination of the duplicate segment. These findings are best explained by the gene order shown in Figure 1.

Figure 1




| | | | |
|---|---|---|---|
| no. of events | 67 | 33 | 84 |

The linkage relationships of mutant alleles between thiA4 and acrB2 are extensively reported (Dorn, G.L., 1967, Genetics 56, 619-631) but there is no good evidence for meiotic linkage of this region to any centromere linked genes. The order of these markers relative to the centromere had been determined by selection for either acriflavine resistance, (Käfer, E., 1958, Adv. in Genetics 9, 105-145) or yellow-green conidia

(Clutterbuck, A.J., 1970, Aspergillus Newsletter 11, 2-3) on the assumption that the selected marker was, in each case, the most distal. In fact, earlier results are compatible with the presently suggested order if allowance is made for double crossover events. Conversely the duplication diploid data, in terms of the accepted order of markers, would have required exceptionally improbable multiple events.

Investigation of this phenomenon is continuing using additional markers but selection of mitotic crossing-over by the elimination of terminally attached duplications clearly offers an excellent method for mitotic mapping.

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Ascospore maturation and germination.

Inconsistent germination frequncies of stored ascospores led to the following investigation. Cleistothecia of the cross adF17 pabaA1 yA2 X proA1 biA1;acrA1; pyroA4 (cross d, experiment 36 of Pritchard in "Experiments in microbial Genetics" ed. Clowes and Hayes, Blackwell 1968) were harvested at intervals after inoculation of the cross plates. Ascospore suspensions were made in the usual way, counted with a haemocytometer and stored at 4°. They were then sampled periodically by plating on CM + adenine + sodium deoxycholate. The original cross was set up by mixing conidia of the parent strains on a small area at the centre of a thick MM plate and germination was started by the addition of a drop of liquid CM. The cross plate was sealed with cellulose tape and incubated at 37°.

The results in the table show that while very young ascospores have poor germination rates and these decline on storage, germination rates of ascospores harvested at 2-3 weeks improve on storage. This confirms the suspicions which led to these experiments.

Percentage germination of ascospores

| Days after cross set up | Cleistothecium a | b | c | d | e | f | g | h | i | j | k | l | m |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 7 | 1 | 2 | | | | | | | | | | | |
| 9 | - | - | 5 | 11 | | | | | | | | | |
| 11 | 10 | 3 | 4 | 7 | 4 | | | | | | | | |
| 14 | 1 | 7 | 2 | 4 | 2 | 5 | 10 | | | | | | |
| 18 | - | - | 1 | 3 | 4 | 7 | 11 | 13 | 39 | | | | |
| 22 | - | - | - | 2 | 26 | 3 | 8 | 39 | 37 | 22 | 44 | | |
| 33 | - | - | - | - | - | 25 | 28 | 43 | 44 | 45 | 60 | 100 | 77 |
| 37 | 0 | 0 | 1 | 0 | 11 | 54 | 63 | 44 | 52 | 44 | 78 | 100 | 77 |

The underlined figure indicates the plating made the day the cleistothecium was harvested from the cross plate.

A proportion of the ascospores examined at 7 and 9 days were not pigmented, but all older ascospores were the normal dark red. Germination of ascospores from cleistothecia harvested at 7 and 9 days was spread over five or more days, even with the stored ascospores, but ascospores from the cleistothecia harvested later appeared to germinate in two days or not at all. All cleistothecia were hybrid and the products apparently normal, although the cross was not analysed in detail.

It can be concluded that ascospores go through a definite maturation process, some steps of which can be completed in stored suspensions at 4°. Plating, however must interrupt this process and lead to death since delayed germination of immature ascospores was not observed.

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## Spontaneous mapping of Aspergillus terreus and Aspergillus nidulans.

It is now well documented both from academic and industrial circles that the mutagenic treatments used for the recovery of gene mutations can lead to chromosome damage. Provided there are adequate systems for the recognition

of such aberrations the problems are not insurmountable. However, imperfect fungi are limited in these systems resulting in the difficulties experienced in many laboratories when attempting to recombine highly mutagenised strains. Over the last few years powerful new selective techniques have emerged which enable the researcher to select spontaneous gene mutations and hence in theory at least allow the construction of a basic genetic map before mutagenic treatments are employed. The results to date of such an empirical approach to A.terreus and A.nidulans are presented below and we believe illustrate the suitability of the method to other organisms.

Aspergillus terreus.

This fungus was chosen for the following reasons

a) Its' growth morphology and nutritional requirements are extremely similar to those of A.nidulans so that no new techniques or media were required.

b) The vegetative cycles are identical with the production of uninucleate conidia.

c) It has a commercial value being used in the production of itaconic acid.

d) Nothing is published concerning the genetics of the organism.

The following classes of mutation have been recovered:-

(1) Spore colour These were easily obtained by microscopical screening of a dense plating followed by selecting the deviant colour from the brown background. Two such mutants have been isolated and designated whiA1 and creA1 (white and cream respectively). These are complementary, a heterozygous diploid having wild-type spore colour, albeit somewhat lighter brown than the wild-type haploid.

(2) Auxotrophs

a) Easily recovered were auxotrophs for sulphate metabolism isolated as resistors to selenate (Arst 1968). Two complementation groups have been identified, one of which is additionally resistant to chromate. As per A.nidulans this mutation has been designated sB, the nonchromate resistor sC.

b) Similarly, chlorate selection (Arst and Cove 1973) has yielded a spectrum of auxotrophs for nitrogen metabolism. Initially these experiments were carried out using arginine as the sole nitrogen source. In A.nidulans this gives rise almost exclusively to niaD mutations (Arst pers comm). Similarly, in A.terreus the vast majority of mutants recovered are non-complementary and hence we have classified these as niaD mutations. Additionally we have recovered five other complementing groups of auxotrophs the nomenclature for which we have not yet finalised.

c) A problem with both the sulphate and nitrate auxotrophs is leakiness which creates difficulties when attempting to synthesise heterokaryons and the subsequent isolation of heterozygous diploids. To make such procedures easier non leaky auxotrophs were screened for, using the nystatin selective

technique of Ditchburn and MacDonald (1971). This was modified by incorporating sodium desoxycholate into the basal and overlaying agars and by the velvet replication of the resultant colonies directly on to minimal medium. Three clean auxotrophs have been isolated, one requiring adenine (adeA1) and two complementing methionine auxotrophs (metA1 and metB1).

(3) Drug resistors To date we have isolated spontaneous mutations resistant to acriflavine, 8-azaguanine, sulphanilamide, p-fluorophenylalanine and benlate. Detailed allelism analyses are in progress but of interest are those resistant to sulphanilamide. Three classes have been identified resistant to increasing levels of concentration. Those resistant to the highest level (7.5 mg/ml) are somatically unstable and have an abnormal morphology when grown on sulphanilamide free medium.

Genetic analysis.

Parasexual analysis was initially inhibited by the fungus showing tolerance to p-fluorophenylalanine which nullified attempts at haploidisation analysis. However this drug was eventually more than adequately substituted by benlate which has proved a highly efficient haploidising agent. Results to date have identified five freely recombining linkage groups with only two genes showing association namely adeA1 and acriflavine resistance. Other selective procedures have been a) the utilisation of acriflavine for somatic crossing over. Few haploids are isolated from heterozygous diploids grown on the drug. b) the utilisation of both selenate (for sB) and chlorate (for niaD) as agents for both haploid and diploid recovery.

Technical problems:- The first was the recognition of diploidy, especially following selection for white or cream spore colour. Measurement of conidia is neither convenient nor accurate since the conidial diameter is small (about half the size of those of A.nidulans). The problem has been overcome by utilising benlate whence haploid colonies prove stable and diploids show a sectoring growth pattern on medium containing the fungicide.

The second problem concerns the presence on the mycelium of large hyaline cells which are produced in abundance and which are capable of germinating to produce colonies hence problems in attempting to use conidial suspensions. We have solved this by passing spore suspensions through millipore filters before use.

For control and repeatability purposes we have followed the same basic procedure in A.nidulans and have isolated the following mutant strains.

Spore colour - yellow; white; pale green (this is probably an allele at the white locus since no recombinants have been recovered from over a thousand meiotic progeny)

Auxotrophs:- alleles of sC and sB via selenate toxicity. Alleles of niaD niiA nirA cnxE cnxG and strains which complement all three closely linked cnx A B and C loci, via chlorate toxicity. Additionally via the modified nystatin technique, an allele of the pabaA locus (linked by 10 meiotic units to the yellow mutation spontaneously isolated) one adenine requiring and one methionine requiring strain. Allelism tests for the two latter strains are not yet complete.

Resistors to acriflavine; actidione; p-fluorophenylalanine; 8-azaguanine; methylammonium and benlate.

In none of the strains so far tested has a translocation type aberration been detected.

References

Arst, H.N. 1968. Nature 219 p.268.

Arst, H.N. & Cove, D.J. 1973. Mol.Gen.Genet. 126 p.111.

Ditchburn, P. & McDonald, K.D. 197. J.Gen.Microbiol 67 p.299.

## "Fluffy" colonies obtained from Aspergillus conidia after ageing and other treatments

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The spontaneous appearance of "fluffy" mutants is a common finding in Aspergillus cultures. We have investigated some factors which we thought might affect the mutation rate. Fluffies were defined as all colonies with excessive aerial mycelium; most were not tested further.

1. Heat treatment. An experience of Dr. B.L. Cohen's in which large numbers of fluffies appeared in cultures from spores of some rather old stocks carried across the U.S.A. in the boot of a car in summer suggested that heat treatment may induce fluffies. Slants of the biA1 strain (G051) were heated at 51° or 60° for various times. Conidia from these slants were then plated out and incubated at 37°. At 51° the decline in viability in 24 hours was slight and therewere no fluffies in a total of $10^4$ colonies. At 60°, on the other hand, viability declined rapidly to $10^{-6}$ or $10^{-7}$ after 24 hours and only 66 colonies were recovered in all. None of them were fluffy. It may be significant however, that subculture of one of the normal colonies obtained from this treatment did yield a fluffy colony.

2. Ageing. Samples of conidia were plated from slants of various strains stored for up to 18 weeks at 4° or room temperature. During this period viability changed only slightly, apparently rising from 7% at 10 days to 23% and 19% at 55 and 127 days respectively. Samples of $10^4$ colonies per strain taken from 10, 16 and 65 day old slants gave only one fluffy in all. However, 622 fluffies were obtained from $2.17 \times 10^5$ colonies in platings from 113-127 day old slants. In each test, separate platings were made from seven slants of each strain; variation between these slants was very high, e.g. from 1 to 192 fluffies per $4.5 \times 10^4$ colonies in the most extreme case. This variation was sufficient to obscure differences between strains and storage temperatures. The strains used were: biA1 (G051), biA1; methG1 (G0110), biA1; yqA6 (G0247), MSD (G93) and MSE (G94). All these gave rise to at least some fluffies (contrary to Dorn, Martin & Purnell, Life Sciences 6;629-633).

The biA1; methG1 strain was used in control experiments in which spontaneous mutation frequency to meth reversion was tested in the 127 day old cultures. No revertants were obtained from $2 \times 10^6$ viable conidia plated on MM + biotin. Alderson & Clark (Nature 210;593) quote reversion frequencies of methG1 from 1 to $16 \times 10^{-6}$ so we have no evidence of a general rise in mutation frequencies due to ageing.

3. Heavy metals. Preliminary experiments had suggested that copper might induce fluffies, however, experiments in which fresh conidia of the biA1 strain were inoculated onto CM plates in which sterilized copper coins were embedded gave no fluffies. Since in the earlier experiments fluffies had invaded the inhibition ring around the coin, this suggests that heavy metals may select for pre-existing mutants rather than induce them.

4. UV irradiation. This is clearly an efficient agent for the induction of fluffies. A ten minute irradiation (survival $7.0 \times 10^{-3}$) gave 78 fluffies: a frequency of $3.9 \times 10^{-4}$ (biA1 strain).

In conclusion, it seems likely that much of the "fluffy menace" results from the subculturing of old stocks. Although we have not specifically tested this, it is not our experience that conidia stored on silica gel (Roberts ANL 10;29) produce fluffies in any numbers, so the value of this storage method is re-emphasised.

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## Effect of vegetative incompatibility on cytoplasmic infection in Aspergillus amstelodami

The infectious spread of the cytoplasmically inherited condition "ragged" from donor to recipient mycelia of A.amstelodami is restricted where donor and recipient are unable to form heterokaryons, i.e. they show vegetative/heterokaryon incompatibility. This restriction is complete where the incompatibility is determined by several genes as is the case between most independent wild isolates, but appeared only partial when a single heterokaryon incompatibility gene, hetA, was involved, suggesting a degree of additivity in the action of the genes (Caten, J.gen.Microbiol. 72, 221-229,1972). The effect of three other known incompatibility genes hetB,hetC and hetE has recently been investigated using the same experimental system (Table 1).

Table 1. Effect of differences at single heterokaryon incompatibility loci on the transfer of "ragged" from donor to recipient strains.

| Locus | Compatibility | Number of mixtures showing Transfer | No Transfer |
|---|---|---|---|
| hetA | compatible | 46 | 0 |
| | incompatible | 9 | 33 |
| hetB | compatible | 17 | 0 |
| | incompatible | 0 | 13 |
| hetC | compatible | 19 | 0 |
| | incompatible | 2 | 13 |
| hetE | compatible | 15 | 0 |
| | incompatible | 12 | 0 |

Compatible controls included in each experiment always showed transfer of the infectious cytoplasmic factor. The effect of the single incompatibility genes varied with the particular gene involved; hetB completely blocked transfer while hetE had no effect, transfer occurring in all cases as in the compatible controls. Genes hetA and hetC were intermediate, showing a marked but not complete inhibition of transfer. Since a difference at a single heterokaryon incompatibility locus, hetB, completely blocks cytoplasmic infection, it is not necessary to invoke additivity of the het genes to account for the similar reaction observed between incompatible wild isolates. The differences in the strength of inhibition of

infection are correlated with the quantitative effects of the individual genes on heterokaryon formation and it seems likely that the occasional instances of incompatible transfer involving hetA and hetC reflect restricted heterokaryosis.

Although the available evidence suggests that the "ragged" determinant is not a mycovirus, it may be considered as a model of infectious, cytoplasmic genetic elements, as far as its transmission between mycelia is concerned, and it is suggested that the incompatibility genes studied would have similar effects on the transmission of mycoviruses.

## ISOLATION OF AMINOACYL ACCEPTOR-RNA FROM A WILD STRAIN OF *Aspergillus nidulans*

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A wild strain of *Aspergillus nidulans* (Green) was grown in minimal medium at 37°C (Pontecorvo *et al.* Advances in Genetics, 5, p.141, 1953). The mycelia obtained after 7 days' growth were washed with water, dried between folds of filter paper and then kept in cold room until it is worked out.

*A.nidulans* sRNA was prepared by the procedure of Elinor F.Brunngraber (Biochem. Biophys. Res.Commun. Vol.8, p. 1 - 3 ). About 30 gms of dry mycelium of *Aspergillus nidulans* were homogenized in a waring blender with 40 ml of phenol saturated with water (Mallinckrodt, Analytical Reagent) and 30 ml of 1.0 M

sodium chloride, 0.005 N EDTA in 0.1 M Tris-HCl buffer (pH 7.5) for 3 to 5 minutes. The homogenate was spun down in an International refrigerated centrifuge for 10 minutes at 4000 r.p.m. The supernatant was carefully decanted off. To the aqueous residual solution, 3 volumes of 95% ethanol were added and kept overnight in the cold room. The precipitate was removed by centrifugation and dissolved into solution using 100 ml of 0.1 M Tris-HCl buffer (pH 7.5). The solution was chromatographed on a column of DEAE cellulose (2 gms filled in a column of 2 x 10 cm) previously equilibrated with cold 0.1 M Tris-HCl buffer of pH 7.5. The column was washed with one litre of the same buffer and the aminoacyl acceptor RNA was eluted with 1.0 M sodium chloride in 0.1 M HCl buffer of pH 7.5. Sufficient efluent was collected until the optical density of the efluent was less than 260 nm. The solution was extracted with equal volume of phenol saturated with water and then twice with ether. To the aqueous solution containing the sRNA, 3 volumes of 95% ethanol were added and kept in the cold room. The precipitate of s sRNA was spun down and washed with 80% ethanol and then twice with 90% ethanol and dried in a vacuum.

The absorbancy at 260 nm of a 0.1 mg/ml of solution was 2.0, which corresponds to sRNA.

The phosphate was detected as follows:

Less than a mg of sRNA was kept in muffle furnace for 3 hours. The ashes were dissolved in 1N HCl. To this solution, molybdate and ANSA were added. After 10 minutes, a blue colour

was obtained. Thr riboside was tested as follows: The sRNA was dissolved in 0.5 ml of 5 mM NaOH. To this solution, 1 ml of (0.5 N) $HClO_4$ was added, and put in 70°C for 20 min. To this mixture, 5 ml ferric chloride and 1 ml resorcinol in alcohol were added and kept in water bath for 10 minutes and cooled in tap water. Green colour indicates the presence of ribose.

The nitrogenous bases were detected as follows: The sRNA was hydrolysed with 0.5 N HCl at 120°C for 2 hours or 110°C for 2 hours, and an aliquot was spotted on Whatman No.1 filter paper and chromatographed using butanol:water (7:1) as solvent. The bases were detected under UV light and identified using standards. All the bases were detected.

Further work on the molecular weight determination, activity of sRNA using radioactive amino acids and the amino-acyl RNA synthetase are in progress.

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# Aspergillus Stock List (1st Revision, July 1975)*

This listing supercedes the original listing in Genetics (1965) 52: 233-246 (Barratt, Johnson and Ogata) and the supplements in Genetics (1967) 56: 619-631 (Dorn) and in Aspergillus News Letter (1970) #11: 23-24 (Barratt) and represents a complete revision of the stocks and the listing.

The list consists of eight sections as follows:

| | |
|---|---|
| Section I. | Alphabetical Listing of Genetic Loci and Alleles |
| Section II. | Aberration Stocks |
| Section III. | Wild Type Stocks and Related Strains |
| Section IV. | Mitotic and Meiotic Mapping Strains |
| Section V. | Special Purpose Strains |
| Section VI. | Numerical Listing of Stocks |
| Section VII. | Nomenclature: uvs and lys Terminology |
| Section VIII. | Key to Symbols |

Gene symbols employed are those given in Clutterbuck, (1973) Genet. Res. 21: 291-296.

Stocks are available free of charge for research and teaching. A charge of $25.00 per culture plus $5.00 service fee is made to commercial concerns. Write directly to FGSC.

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## Section I. Alphabetical Listing of Genetic Loci and Alleles*

The term "no T" signifies tested in diploids; the term "no T?" signifies tested in crosses, or not tested but derived from translocation free descendents.

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | Fungal Genetics Stock Center numbers: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| ALLANTOIC ACID UTILIZATION | | | | | | | | | |
| aa | aaX1 | VI | yA2;pyroA4 | 220 | no T | | ? | 279 | none |
| ACRIFLAVINE RESISTANT | | | | | | | | | |
| Acr | AcrA1 | IIL | pabaA1 yA2;coA1 | -- | T1(VI;VII) | S | none | 36 | 204,205,221,222,360 |
| | AcrA3 | IIL | biA1;adC1;sC12; pyroA4 | 259 | no T | S | none? | 346 | none |
| | | | | | | | | 338 | none |
| acr | acrB2 | IIR | | | | | | | |
| ACTIDIONE RESISTANT | | | | | | | | | |
| Act | ActA1 | IIIL | riboA1 yA1;nicB8 | 122 | no T | UV | none | 231 | 412,511 |
| ADENINE REQUIRING | | | | | | | | | |
| ad | adA55 | IL | prototroph | -- | no T? | UV | ? | 216,218 | none |
| | adB57 | VIII | prototroph | -- | no T? | UV | ? | 217 | none |
| | adC1 | IIR | yA2 (veA+) | -- | T1(III;IV;VIII) | X | ? | -- | 259,319,344 |

*For loci not in FGSC collection see end of Section I

Section I. (continued)

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | Fungal Genetics Stock Center numbers: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| ADENINE REQUIRING (continued): | | | | | | | | | |
| ad | adD3 | IIR | | | | | | 268 | 254 |
| | adE8 | IR | biA1 | 26 | no T | UV | ? | 42 | none |
| | adE20 | IR | biA1 | 26 | no T | UV | T1(II;VII) + other T? | -- | 377,428,485,509 |
| | adF15 | IR | biA1 | 26 | no T | UV | | 46 | none |
| | adF17 | IR | | | | | | 273 | none |
| | adG14 | IL | biA1 | 26 | no T | UV | none | 37 | 17,18,184,189,192 |
| | adH23 | IIL | | 26 | no T | UV | none | -- | 239 |
| | adI50 | IIIL | biA1 | 26 | no T | UV | none | 285 | 496 |
| am | see nir | | | | | | | -- | none |
| ANEURIN REQUIRING | | | | | | | | | |
| an | anA1 | IL | biA1 | 26 | no T | UV | none | 31 | 201,202 |
| | anB2 | II(R?) | biA1;AcrA1;wA3 | 123 | no T | UV | Aberration? | 261,382 | |
| ARGININE REQUIRING | | | | | | | | | |
| arg | argA1 | VI | | | | | | 230 | none |
| | argB2 | III | biA1 | 26 | no T | UV | ? | 89 | none |
| | argC3 | VIIIR | | | | | | 256 | none |
| BIOTIN REQUIRING | | | | | | | | | |
| bi | biA1 (veA1) | IR | wild type ($veA^+$) | 4 | no T | X | none | 26 | 26,194,357,391,39. |
| BLUE ASCOSPORES | | | | | | | | | |
| bl | blA1 | IIR | | | | | | 269 | none |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| bge | see fawn (fw) | | | | | | | | |
| **BROWN CONIDIA** | | | | | | | | | |
| bw | bwA1 | VIR | [2n]proA1 yA2;wA3// adG14 pabaA1 biA1 | -- | {T1(III→VIII) {T1(VI;VII)? | S | none | lost,366 | 112,113,114,115,366 |
| **CHARTREUSE CONIDIA** | | | | | | | | | |
| cha | chaA1 | VIIIR | biA1;choA1 | 1 | T1(I;VII) | S | none | lost | 23,204,360,416 |
| | chaA2 | VIIIR | biA1;sA2 | 316 | T1(V;VIII) | S | none | 372 | none |
| **CHOLINE REQUIRING** | | | | | | | | | |
| cho | choA1 | VII | biA1 | 26 | no T | UV | T1(I;VII) | 1 | 75,168,342,489,511 |
| **COLOURLESS ASCOSPORES** | | | | | | | | | |
| cl | clA6 | IL | | | | | | 280 | none |
| **NITRATE AND HYPOXANTHINE UTILIZATION** | | | | | | | | | |
| cnx | cnxB2* | VIIIR | AcrA1 wA3;nicB8 | -- | no T | ? | | -- | 449 |
| | cnxB50** | VIIIR | biA1 | 26 | no T | UV | none | 266 | |
| | cnxE16*** | IIR | biA1;wA3 | -- | {T1(III→VIII) {T1(VI;VII) | UV | none? | -- | 337,462 |
| | cnxH3 | IIIL | | | | | | | 451,490 |
| **COMPACT MORPHOLOGY** | | | | | | | | | |
| co | coA1 | VIIIR | pabaA1;biA1 | | T1(VI;VII) | S | none | 29 | 120,449 |
| **DILUTE CONIDIAL COLOUR** | | | | | | | | | |
| dil | dilA1 | IIIL | yA2;pyroA4 | 220? | no T | UV | ? | -- | 489,503 |

* also called ni21/11
** also called ni50
***also called ni3

Section I. (continued)

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | Fungal Genetics Stock Center numbers: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| FLUOROACETATE RESISTANT ACETATE NON-UTILIZATION | | | | | | | | | |
| fac | facA303 | VR | wA3;pyroA4 | -- | T1(VI;VII) | S | ? | -- | 502 |
| | facB101 | VIIIR | wA3;pyroA4 | -- | T1(VI;VII) | S | ? | -- | 409,420 |
| | facC102 | VIIIR | wA3;pyroA4 | -- | T1(VI;VII) | S | ? | -- | 427 |
| FLUFFY MORPHOLOGY | | | | | | | | | |
| fl | flA1 | VII | biA1;methG1 | 219 | no T | | | 326 | none |
| FLUOROPHENYLALANINE RESISTANT (also called fp) | | | | | | | | | |
| fpa | fpaA1 | IL | | | | | | 275 | none |
| | fpaA91 | IL | proA11 yA2;pyroA4 | -- | T? | NG | ? | 387 | 390,439 |
| | fpaB37 | IL | riboA1 biA1 | 158 | no T | S | none | 422 | 507 |
| | fpaC43 | VIII | riboA1 biA1 | 158 | no T | S | none | 286 | |
| | fpaD11¢ | III | adF17 pabaA1 yA2 | -- | T? | S | ? | 273 | none |
| FRUCTOSE NON-UTILIZATION | | | | | | | | | |
| fr | frA1 | IVR | yA2;pyroA4 | 220 | no T | UV | T1(IV;VIII) | 470,276,435 | none |
| FAWN CONIDIA (also called bge) | | | | | | | | | |
| fw | fwA1 | VIIIR | biA1 | 26 | no T | S | none | 378 | 379 |
| | fwA2 | VIIIR | AcrA1;lysB5 | 205 | no T | S | none | 371 | 440,469,485 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **GALACTOSE NON-UTILIZATION** | | | | | | | | | |
| gal | galA1 | IIIL | biA1;wA3 | -- | T1(III → VIII) T1(VI;VII) | UV | ? | -- | 211 |
| | galB3 | II | biA1;wA3 | -- | T1(III → VIII) T1(VI;VII) | UV | ? | 215 | none |
| | galC4 | VIII | biA1;wA3 | -- | T1(III → VIII) T1(VI;VII) | UV | ? | 291 | none |
| | galD5 | IL | biA1;wA3 | | T1(III → VIII) T1(VI;VII) | UV | ? | -- | 494 |
| | galE9 | IIIL | biA1;wA3 | | T1(III → VIII) T1(VI;VII) | UV | ? | -- | 214 |
| **HISTIDINE REQUIRING** | | | | | | | | | |
| his | hisA10 | IV(R?) | yA2 biA1;AcrA1;riboB2 | -- | no T (?) | UV | ? | 277 | none |
| | hisC38 | VIIIR | biA1;AcrA1 wA3;nicB8 | -- | no T | UV | ? | 257 | none |
| | hisH13 | VIII | yA2;biA1;AcrA1;riboB2 | -- | no T | UV | ? | 278 | none |
| | his 122 | VII | biA1;sB3 | | no T(?) | NA | ? | 299 | none |
| **HYPOXANTHINE NON-UTILIZATION** | | | | | | | | | |
| hx | hxA1 | VR | biA1 | 26 | no T | DES | ? | -- | 258, 491 |
| **ISOLEUCINE REQUIRING** | | | | | | | | | |
| ile | ileA1 | IIR | biA1;sB3 | 41 | no T(?) | NA | none? | 295 | none |
| | ileA3 = ab1 | IIR | biA1 | 26 | no T | UV | ? | -- | 505 |
| **IODOACETATE RESISTANT** | | | | | | | | | |
| Iod | IodA1 | IIL | biA1;wA3;nicB8 | -- | T1(III → VIII) | S | none? | -- | 492 |
| **LACTOSE NON-UTILIZATION** | | | | | | | | | |
| lac | lacA1 | VIR | yA2;pyroA4 | 220 | no T | UV | none | -- | 349, 455 |
| | lacB3 | IIR | biA1;wA3 | -- | (T1(III → VIII) (T1(VI;VII) | UV | | 292 | none |
| **LEUCINE REQUIRING** | | | | | | | | | |
| lu | luA1 | IL | biA1 | 26 | no T | UV | none | 55 | 406 |

♀semi-dominant

Section I. (continued)

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center number: original strain or untested descendent | Fungal Genetics Stock Center number: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| **LYSINE REQUIRING** | | | | | | | | | |
| lys | lysA1 | VIR | wA1 (veA+) | -- | none | X | AbV1 | 38 | 350* |
| | lysB5 | V | biA1 | 26 | no T | UV | none | 66(smA1) | 205,360,365 |
| | lysD7 | VII | biA1;sB3 | 41 | no T(?) | NA | ? | 300 | none |
| | lysD18 | VII | biA1;sB3 | 41 | no T(?) | NA | ? | 294 | none |
| | lysD20 | VII | biA1;sB3 | 41 | no T(?) | UV | T1(III;VII) | 395,418 | none |
| | lysE13 | V | biA1;sB3 | 41 | no T(?) | NA | ? | 296 | none |
| | lysE14 | V | biA1;sB3 | 41 | no T(?) | NA | ? | 298 | none |
| | lysE231 | V | biA1;sB3 | 41 | no T(?) | NA | ? | 301 | none |
| | lysF51 | IR | biA1;sB3 | 41 | no T(?) | NA | ? | 297 | none |
| | lysF88 | IR | biA1;sB3 | 41 | no T(?) | NA | none? | 293 | 376 |
| **MALTOSE NON-UTILIZATION** | | | | | | | | | |
| mal | malA1 | VIIR | yA2;pyroA4 | 220 | no T | UV | ? | 57 | 437 |
| **METHYLAMMONIUM RESISTANT** | | | | | | | | | |
| mea$^R$ | meaB6 | IIIL | | | | | | -- | 451,496 |
| **MELANIN FORMATION** | | | | | | | | | |
| mel | mel | | | | | | | 332 | none |
| **METHIONINE REQUIRING** | | | | | | | | | |
| meth | methB3 | VI | yA2;pyroA4 | 220 | no T | UV | ? | 272 | none |
| | methG1 | IVL | biA1 | 26 | no T | UV | none | 219 | 486,500 |
| | methH2 | IIIL | biA1 | 26 | no T(likely) | UV | none(?) | 34 | 503 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| MORPHOLOGICALLY ABNORMAL | | | | | | | | | |
| mo | moC96 | III | | | | P | | 232 | none |
| NITRATE REDUCTASE (also called nia and nii) | | | | | | | | | |
| ni | ni3 | | see cnxE16 | | | | | -- | 337,462 |
| | ni21 | | see cnxB2 | | | | | -- | 449 |
| | ni50 | | see cnxB50 | | | | | 266 | none |
| | ni51 | | see nirA14 | | | | | 260 | 472 |
| NICOTINAMIDE REQUIRING | | | | | | | | | |
| nic | nicA2 | V | wild type (veA+) | 4 | | X | ? | -- | 437,495 |
| | nicB8 | VIIR | biA1 | 26 | no T | UV | ? | -- | 122 |
| | nicC10 | VI | biA1;AcrA1 wA3 | -- | no T | UV | ? | 11 | none |
| NITRATE PATHWAY REGULATOR | | | | | | | | | |
| nir | nirA14 | VIIIR | biA1;phenA3 | -- | T1(I;IV) | S | none | 260 | 472 |
| nr | see uvs | | | | | | | | |
| OLIGOMYCIN RESISTANT | | | | | | | | | |
| oli | oliA2 | VIIR | pabaA1 yA2 | 187 | no T | S | none? | 450 | 453 |
| ORNITHINE REQUIRING | | | | | | | | | |
| orn | ornA4 | IVR | biA1 | 26 | no T | UV | ? | 43,358 | none |
| | ornB7 | VIIIR | | | | | | -- | 379 |
| | ornB9 | VIIIR | | | | | | 353 | none |
| | ornB20 | VIIIR | biA1 | 26 | no T | UV | none | 263 | 263 |
| PALE CONIDIA | | | | | | | | | |
| p | pA2 | VR | adG14 biA1 | 37 | no T | S | none | 35 | 460 |

*contains "Ab VI" = Inversion?

Section I. (continued)

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | Fungal Genetics Stock Center numbers: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| P-AMINOBENZOIC ACID REQUIRING | | | | | | | | | |
| paba | pabaA1 | IR | biA1 | 26 | no T | X | T1(VI;VII) | -- | 85,126,187,408 |
| | pabaA6 | IR | biA1 | 26 | no T | UV | ? | 28 | none |
| | pabaB22 | IVR | biA1 | 26 | no T | UV | ? | -- | 426,493 |
| ACID PHOSPHATASE DEFICIENT | | | | | | | | | |
| pac | pacA1 | IV | rA1 biA1 | -- | no T | UV | ? | 241 | none |
| | pacC5 | VI | biA1 | 26 | no T | UV | none | 242 | none |
| ALKALINE PHOSPHATASE DEFICIENT | | | | | | | | | |
| pal | palA1 | IIIL | rA1 biA1 | -- | no T | UV | T? | 243 | none |
| | palB7 | VIIR | rA1 biA1 | -- | no T | UV | none ? | 244 | 381,401 |
| | palC4 | IVR | rA1 biA1 | -- | no T | UV | ? | -- | 497 |
| | palD8 | VII | rA1 biA1 | -- | | UV | ? | 245 | none |
| | palE11 | VIIIL | rA1 biA1 | -- | | UV | ? | 246 | none |
| | palF15 | VIIR | rA1 biA1 | -- | no T | UV | none? | 247 | 400 |
| ACID & ALKALINE PHOSPHATASE DEFICIENT | | | | | | | | | |
| palc | palcA1 | IIL | rA1 biA1 | -- | no T | UV | ? | 248 | none |
| PANTOTHENIC ACID REQUIRING | | | | | | | | | |
| panto | pantoA1 | III or VIII | yA2;thiA1 | -- | T1(III→ VIII;IV) | X | T(VII;III or VII;VIII) | 340 | none |
| | pantoB100 | VIIIR | | | | UV? | ? | 397 | 453 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| PHENYLALANINE REQUIRING | | | | | | | | | |
| phen | phenA2 | IIIR | biA1 | 26 | no T | UV | T1(I;VIII) | 304 | 150,173,180,461 |
| | phenA3 | IIIR | biA1 | 26 | no T | S | T1(I;IV) | 260 | 402 |
| | phenB6 | VIIR | biA1 | 26 | no T | UV | ? | 394 | 499 |
| PROLINE REQUIRING | | | | | | | | | |
| pro | pro-94 | IL | wild type (veA$^+$) | 4 | no T | UV | ? | 386 | 393 |
| | proA1 | I | biA1 | 26 | no T | UV | none | 32 | 85,343,367,411 |
| | proA2 | I | biA1 | 26 | no T | UV | T1(II;III) | 111 | 364,415 |
| | proA5 | I | biA1 | 26 | no T | UV | ? | 45 | none |
| PUTRESCINE REQUIRING | | | | | | | | | |
| pu | puA1 | IIR | biA1;wA3 | -- | T1(III→VIII); T1(VI;VII) | UV | T(I;III) or (I;VIII) | -- | 341 |
| PYRIDOXINE REQUIRING | | | | | | | | | |
| pyro | pyroA4 | IVR | biA1 | 26 | no T | UV | none | 33 | 220,426 |
| RIBOFLAVIN REQUIRING | | | | | | | | | |
| ribo | riboA1 | IL | biA1 | 26 | no T | UV | none | 158 | 188,356,361 |
| | riboB2 | VIIIR | biA1;AcrA1 wA3 | -- | no T | UV | ? | -- | 198,410 |
| | riboD5 | VR | biA1 | 26 | no T | UV | ? | -- | 258 |
| SULPHATE NON-UTILIZATION | | | | | | | | | |
| s | sA1 | IIIL | biA1 | 26 | no T | UV | T1(V;VI) | 40 | 417 |
| | sA2 | IIIL | biA1 | 26 | no T | UV | T1(V;VIII) | 316 | 368 |
| | sA4 | IIIL | biA1 | 26 | no T | UV | none? | 2 | 339 |
| | sA49 | IIIL | biA1 | 26 | no T | NG | none? | -- | 404 |
| | sA91 | IIIL | biA1 | 26 | no T | NG | none? | -- | 405 |
| | sB3 | VIR | biA1 | 26 | no T | UV | none? | 41 | 147,369 |
| | sB25 | VIR | riboA1;AcrA1, chaA1 | -- | no T | NG | ? | 383 | none |
| | sC12 (=s0) | IIIL | wild type (veA$^+$) | 4 | no T | NM | ? | 24 | 488 |
| | sC13 | III | biA1;wA3 | -- | T1(III→VIII) T1(VI;VII) | UV | ? | 15 | none |
| | sC22 | IIIL | riboA1 yA2 | -- | no T | NG | ? | 384 | none |

Section I. (continued)

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | strain of origin: FGSC# | strain of origin: translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | Fungal Genetics Stock Center numbers: best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| SULPHATE NON-UTILIZATION (continued) | | | | | | | | | |
| s | sD50 | VIIIR | biA1 | 26 | no T | UV | T2(I;VIII) | 398,431,434 | none |
| | sD85 | VIIIR | biA1 | 26 | no T | NG | none? | 419 | 421,469 |
| | sD157 | VIIIR | biA1 | 26 | no T | NG | ? | -- | 420 |
| | sE15 | VIIIR | biA1 | 26 | no T | NG | none? | 385 | 399 |
| | sF211 | VIIR | biA1;pyroA4 | 33 | no T | NG | none? | 388 | 403 |
| SORBITOL NON-UTILIZATION | | | | | | | | | |
| sb | sbA3 | VIR | biA1;wA3 | -- | T1(III→VIII) T1(VI;VII) | UV | T2(I;VII)? | -- | 500,510 |
| SMALL COLONIAL SIZE | | | | | | | | | |
| sm | smA1 | IIIL | biA1 | 26 | no T | UV | none | 66 (lysB5) | 436,501 |
| SUPPRESSOR | | | | | | | | | |
| suadE20 | suA1adE20 | IL | adE20;pyroA4 | 227 | T(?) | S | none | 47 | 71,75 |
| | suC11adE20 | IVR | pabaA1 yA2 adE20 AcrA1;cnxB2;coA1 | -- | no T | S | none | 443 | 486 |
| sumeth | see sup | | | | | | | -- | none |
| suornB9 | | | | | | | | -- | none |
| supabaB22 | | | | | | | | -- | none |
| supal | suA1palB7 | VIIIR | biA1;palB7 | 244 | no T(?) | S | none | 281 | none |
| | suB2palB7 | VI | biA1;palB7 | 244 | no T(?) | S | none | 284 | none |
| | suC6palF15 | V | biA1;palF15 | 247 | no T(?) | S | none | 282 | none |
| | suD2palA1 | I | biA1;palA1 | 243 | T(?) | S | none | 287 | none |
| supro | suB4pro | IIIR | proA5 biA1 | 45 | ? | S | none | -- | 423,454 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| SULPHANILAMIDE RESISTANT | | | | | | | | | |
| sul | sulA1 | IL | yA2;pyroA4 | 220 | no T | UV | ? | -- | 452,511 |
| THIAZOLE REQUIRING | | | | | | | | | |
| thi | thiA4 | IIR | biA1 | 26 | no T | UV | ? | 52 | 337 |
| TRYPTOPHAN REQUIRING | | | | | | | | | |
| tryp | trypA69 | II(R?) | pabaA1 yA2 | 234 | no T | UV | ? | 235 | none |
| | trypB403 | I(L?) | pabaA1 yA2 | 234 | no T | UV | ? | 236 | none |
| | trypC801 | VIII | pabaA1 yA2 | 234 | no T | UV | ? | 237 | none |
| | trypD432 | II(R?) | pabaA1 yA2 | 234 | no T | UV | ? | 238 | none |
| TEMPERATURE-SENSITIVE | | | | | | | | | |
| ts | tsD15 | VIII | | | | | | 269 | none |
| UREA NON-UTILIZATION | | | | | | | | | |
| u | uY5 | VII | biA1 | 26 | no T | DES | | 262 | none |
| URIC ACID NON-UTILIZATION | | | | | | | | | |
| ua | uaX10 | VI | biA1 | 26 | no T | DES | | 264 | none |
| ULTRAVIOLET SENSITIVE | | | | | | | | | |
| uvs | uvs-4 | | adE20,biA1,wA3, methG1,pyroA4 | -- | no T | UV | ? | 329 | none |
| | uvs-5 | | adE20,biA1,wA3, methG1,pyroA4 | -- | no T | UV | ? | 327 | none |
| | uvs-77 | | adE20,biA1,wA3, methG1,pyrcA4 | -- | no T | UV | ? | 330 | none |
| | uvsA1 | | | | | | | 328 | none |

| symbol | locus and allele | linkage group and arm | strain of origin: genotype | FGSC# | translocation | mode of origin | new or induced translocations | Fungal Genetics Stock Center numbers: original strain or untested descendent | best available strains likely translocation free |
|---|---|---|---|---|---|---|---|---|---|
| ULTRAVIOLET SENSITIVE (continued) | | | | | | | | | |
| uvs | uvsB110 | IV | pabaA108 biA1 | -- | | UV | ? | 333 | none |
| | uvsC114 | VIII | pabaA108 biA1 | -- | | UV | ? | 334 | none |
| | uvsD153 | V | proA1,pabaA125, biA1;pyroA4 | -- | | UV | ? | 335 | none |
| | uvsE182 | V | proA1,pabaA125, biA1;pyroA4 | -- | | UV | ? | 336 | none |
| | uvsF201 | IL | riboA1 yA2 | 361 | no T | UV | none | -- | 389 |
| VELVET MORPHOLOGY | | | | | | | | | |
| ve | veA1 | VIII | wild type (veA+) | -- | no T | X | none | 26(biA1) | all strains if not labelled (veA+) |
| WHITE CONIDIA | | | | | | | | | |
| w | wA1 | IIL | wild type of Yuill(1936) | -- | no T | S | none | 38 | none |
| | wA2 | IIL | yA2 (veA+) | -- | T1(III;IV;VIII) | X | none | -- | 75,344 |
| | wA3 | IIL | pabaA1,biA1 | -- | T1(VI;VII) | S | none | 27 | 72,78*,188,191,357, 359,408 |
| | wA4 | IIL | biA1;smA1;lysB5 | 66 | no T | S | none | 69 | 436 |
| WET WHITE CONIDIA | | | | | | | | | |
| wet | | | | | | | | -- | none |
| YELLOW CONIDIA | | | | | | | | | |
| y | yA2 | IR | wild type (veA+) | 4 | no T | X | T1(III;IV; VIII) | lost,23 | 71,83,187,194,361 |
| | yoA91 (olive) | IR | biA1;phenA2 | 498 | no T? | S | none | 425 | 445 |
| YELLOW-GREEN CONIDIA | | | | | | | | | |
| yg | ygA1 | IIR | biA1 | 26 | no T | S | | 270 | 270 |

## LOCI NOT AVAILABLE FROM FGSC:

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anth
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apl
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are
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azg
bga
ben
brl
cre
csu
drk
est
fan
flu
fmd
gam
gdh
glu
hxn
icl
ind
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m
mas
mau
mec
med
mg
mol
nia
nii
npe
ota
oxp
pcnb
pdh
pen
ppa
ppp
prn
pur
pyc
pyr
r
rin
sa
sgp
sor
stu
suc
sul-req
sup
tcnb (pcnb)
te
tel
ths
tyr
uap
uru
uvr
v
wet
xpr

*78 -- may carry suA1adE20, wA2 and/or chaA1.

## Section II. Aberration Stocks

### Reciprocal Translocation Strains

| | | |
|---|---|---|
| T1(I;IV) | : | 260 |
| T1(I;VII) | : | 1,129,354,430,438 |
| T2(I;VII) | : | 355 |
| T1(I;VIII) | : | 125,304,352 |
| T2(I;VIII) | : | 398,431,434 |
| T1(II;III) | : | 111,414 |
| T1(II;IV) | : | 345 |
| T1(II;VII) | : | 429 |
| T1(III;VII) | : | 395,418,447 |
| T1(IV;VIII) | : | 250,276,435,470 |
| T1(V;VI) | : | 40,370,373,518,521,522 |
| T1(V;VIII) | : | 316,372,413 |
| T1(VI;VII) | : | 27,29,36,482,519,520 |

### Other Aberration Strains

| | | |
|---|---|---|
| T1(VI;VII) T1(III → VIII) -- strains (± UV treatment) | : | 15,215,291,292 |
| various intrachromosomal aberrations | : | 38,228,229,261,382 |
| T1(III → VIII;VII) | : | 340 |
| T(I;V;VII;VIII) possibly related to T2(I;VII) | : | 347 |

## Section III. Wild Types and Related Strains

| FGSC NO. | Origin | References |
|---|---|---|
| 4 | Glasgow wild type ($ve^+$) | Yuill (1939)<br>Yuill (1950) |
| 90 | Grindle wild isolate #2 | Grindle (1963) |
| 92 | Grindle wild isolate #26 | Grindle (1963) |
| 94 | Grindle wild isolate #36 | Grindle (1963) |
| 96 | Grindle wild isolate #44 | Grindle (1963) |
| 251 | Aspergillus heterothallicus A #WB5096 | Raper |
| 252 | Aspergillus heterothallicus a #WB5097 | Raper |

## Mitotic Mapping Strains

44 suA1adE20 adE20 biA1; AcrA1; phenA2; pyroA4; lysB5; sB3; choA1; coA1 chaA1
68 suA1adE20 yA2 dE20; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; riboB2 (=MSD*)
70 suA1adE20 adE20 biA1; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; chaA1
79 suA1adE20 pabaA1 yA2 adE20; cnxE16; sC12; pyroA4; nicA2; sB3; choA1; chaA1
104 yA2 adE20; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; coA1
105 biA1; AcrA1 wA3; phenA2; pyroA4; lysB5; sB3; nicB8; coA1
146 pabaA1; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; riboB2 chaA1
154 adE20 biA1; wA2 cnxE16; sC12; methG1; nicA2; lacA1; choA1; chaA1
155 suA1adE20 pabaA1 yA2 adE20; AcrA1; phenA2; pyroA4; lysB5; sB3; choA1; coA1 chaA1
159 suA1adE20 pabaA1 yA2 adE20; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; riboB2
163 suA1adE20 yA2 adE20; AcrA1; phenA2; pyroA4; lysB5; sB3; nicB8; coA1
283 suA1adE20 yA2 adE20; AcrA1; galA1; pyroA4; facA303; sB3; nicB8; riboB2 (=MSF*)
288 suA1adE20 yA2 adE20; wA3; galA1; pyroA4; facA303; sB3; nicB8; riboB2 (=MSE*)
374 suA1adE20 yA2 adE20; AcrA1; sA4; pyroA4; pA2; lacA1; nicB8; riboB2
375 suA1adE20 adE20 biA1; AcrA1; sA4; pyroA4; pA2; lacA1; nicB8; riboB2
407 adE20 biA1; AcrA1; phenA2; pyroA4; lysB5; lacA1; choA1; riboB2 chaA1
446 suA1adE20 yA2 adE20; AcrA1; galA1; pyroA4; facA303; lacA1 sB3; choA1 nicB8; riboB2 chaA1
465 sulA1; AcrA1; galA1; pyroA4; facA303; lacA1; choA1; chaA1
468 sulA1; AcrA1 wA3; galA1; pyroA4; facA303; lacA1 sB3; choA1; riboB2 chaA1
473 sulA1 adE20; AcrA1 wA3; ActA1; pyroA4; facA303; lacA1 sB3; oliA2 choA1; riboB2 chaA1
477 sulA1 adE20; AcrA1 wA3; ActA1; pyroA4; lysB5; sB3; choA1; chaA1

*= Glasgow Master strains.

Section IV. (continued)

Mitotic Mapping Strains (continued):

478 sulA1 adE20; AcrA1 wA3; ActA1; pyroA4; lysB5; sB3; choA1; riboB2 chaA1
480 proA1 y°A91; IodA1; phenA2; methG1; nicA2; sbA3; malA1; riboB2
487 sulA1; AcrA1; galA1; pyroA4; facA303; lacA1 sB3; choA1 nicB8; riboB2 chaA1
513 sulA1 adE20; AcrA1; ActA1; pyroA4; facA303; lacA1 sB3; choA1; chaA1

Meiotic Mapping Strains (usually 4 or more markers)

| | |
|---|---|
| Linkage Group I | 71, 87, 121, 193, 208, 275, 362, 363, 376,432, 439, 463, 466, 475, 479, 483, 494, 507, 515 |
| Linkage Group II | 239, 254, 268, 338, 505 |
| Linkage Group III | 423, 441, 448, 456, 457, 458, 471, 490, 496, 516 |
| Linkage Group IV | no T: 512, 517 [with T1 (IV;VIII): 250, 276, 435] |
| Linkage Group V | 258, 491, 495, 504, 508 |
| Linkage Group VI | 459, 464 |
| Linkage Group VII | 424, 444, 467, 481, 506 |
| Linkage Group VIII | 269, 380, 401, 442, 484, 516 |

Main Meiotic Standards: 187, 356, 360, 408

## Section V. Special Purpose Strains

1) Combinations of colour mutants; yA2, wA3, chaA1, bwA1 (prototroph, no T): #78, 84, 112,-118, 366 (set of 10 strains)

2) Pairs of strains for diploids with all homologues marked: 159/154 or 68/154 or 283/154 — 465/480 or 477/480 or 513/480

3) Strains for Teaching or "mutagenesis" diploids: 514/515; 475/477 or 475/513

4) Set of strains for control, T/+ and T/T strains:

| | | | | | |
|---|---|---|---|---|---|
| a) T1(I;VII) | : | 424 (no T) | 430 (T) | 438 (T) | 439 (no T) |
| b) T2(I;VIII) | : | 432 (no T) | 431 (T) | 434 (T) | 433 (no T) |

5) Strain for Triploid : 475//473/480

6) Strains for diploids to map centromeres:

| | | |
|---|---|---|
| Linkage Group I | : | 475/474 or 513 |
| | | 466/474 |
| | | 479/476 or 474 |
| | | 363/477 or 154 |
| Linkage Group II | : | 338/480 |
| Linkage Group III | : | 457/458 |
| Linkage Group IV | : | 517/476 |
| Linkage Group V, T1(V;VI)/T | : | 518/370 or 521 |
| Linkage Group VI | : | 464/377 |
| Linkage Group VII, T1(VI;VII)/T | : | 519/520 |

7) Strains for teaching meiotic recombination; w, cha and green strains ±AcrA1: 189, 205, 221, 222, 356, 359, 360, 452

8) Strains for mutant selection by biotin starvation with biA1: 26, 194, 357, 378, 391, 392

9) Back cross strains:

| | | | |
|---|---|---|---|
| a) ($veA^+$) | BC VIII | 17, 18, 83, 85, 126 | standard in Montreal |
| | BC IX | 343 | a) = back crosses of adG14 proA1 pabaA1 yA2; wA3 |
| b) (veA1) | BC V | 360, 365 | b) = back crosses of yA2; AcrA1; lysB5; chaA1 |
| (veA1) | BC IV | 204, 205 | |
| c) (wA3; ±chaA1) | BC V | 221, 222, 223 | c) = crosses between strains of a) and b) |

## Section VI. Numerical Listing of Stocks

This revised stock list was prepared in conjunction with FGSC by Dr. Etta Käfer-Boothroyd, McGill University, Montreal, as a revision from the original list by Barratt et al., 1965 (Genetics 52: 233-246 and [1] and [2] refer to Figures therein), the supplement thereto (Barratt, Aspergillus Newsletter 11: 23-24), and that of Dorn, 1967 (Genetics 56: 619-631) updating the cultures at the Fungal Genetics Stock Center, Humboldt State University Foundation, Arcata, CA 95521, U.S.A. Numbers in parentheses refer to Figures in Käfer, 1965 (Genetics 52: 217-232). Underline refers to the unique characteristic(s) of strain. Number sign (#) in origin column refers to FGSC stock number.

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 1 | biA1;choA1 | T1(I;VII) | UV of #26 | M 7 |
| 2 | biA1;sA4 | no T(?) | UV of #26 | M 27 |
| 4 | Glasgow wild type (veA+) | | Yuill, 1950 δ | M 139 |
| 11 | biA1;AcrA1 wA3;nicC10 | T(?) | UV of #123♠ | M 231 |
| 15 | bi1;wA3;sC13 = cys2 | (T1(III → VIII) (T1(VI;VII) | UV of #51♠ | M 422 |
| 17 | adG14; (veA+) | no T | BC VIII [1] | M 635 |
| 18 | adG14 yA2;(veA+) | no T | BC VIII [1] | M 640 |
| 23 | pabaA1 yA2;chaA1 | no T(?) | Cross 507 | M 755 |
| 24 | sC12;(veA+) | T(?) | NM of #4σ | M 801 |
| 26 | biA1 | no T | X of #4 | M 804 |
| 27 | pabaA1 biA1;wA3 | T1(VI;VII) | X of #26 and S | M 805 |
| 28 | pabaA6 biA1 | T(?) | UV of #26 | M 807 |
| 29 | pabaA1 biA1;coA1 | T1(VI;VII) | X of #26 and S | M 809 |
| 31 | anA1 biA1* | no T | UV of #26 | M 812 |
| 32 | proA1 biA1 | no T | UV of #26 | M 813 |
| 33 | biA1;pyroA4 | no T | UV of #26 | M 815 |
| 34 | biA1;methH2* | no T (likely) | UV of #26 | M 818 |
| 35 | adG14 biA1;pA2 | no T | S in #37 | M 820 |
| 36 | pabaA1 yA2;AcrA1;coA1 | T1(VI;VII) | S in pabaA1 yA2;coA1; T1(VI;VII) | M 822 |
| 37 | adG14 biA1 | no T | UV of #26 | M 823 |
| 38 | wA1;lysA1 (veA+) | Ab VI (T?) | X of wA1? | M 829 |

| | | | | |
|---|---|---|---|---|
| 40 | biA1;sA1 | T1(V;VI) | UV of #26 | M 837 |
| 41 | biA1;sB3 | no T(?) | UV of #26 | M 834 |
| 42 | adE8 biA1* | T(?) | UV of #26 | M 851 |
| 43 | biA1;ornA4 | T(?) | UV of #26 | M 232 |
| 44 | Mitotic Mapping Strain | no T | Cross 474 [2] | M 857 |
| 45 | proA5 biA1 | T(?) | UV of #26 | M 861 |
| 46 | adF15 biA1 | T(?) | UV of #26 | M 862 |
| 47 | suA1adE20 adE20;pyroA4 | T(?) | S in #227 | M 864 |
| 52 | biA1;thiA4 | T(?) | UV of #26 | M 882 |
| 55 | luA1 biA1 | no T | UV of #26 | M 892 |
| 57 | yA2 pyroA4;malA1 | no T | UV of #220 | M 895 |
| 66 | biA1;smA1;lysB5 | no T | UV of #26 | M 905 |
| 68 | Mitotic Mapping Strain | no T | Cross of Forbes: MSD | M 911 |
| 69 | biA1;wA4;smA1;lysB5 | no T | S in #66 | M 912 |
| 70 | Mitotic Mapping Strain | no T | C 434 [2] | M 915 |
| 71[Δ] | suA1adE20 riboA1 pabaA1 yA2 adE20;AcrA1 wA2 | no T | C KK (3) | M 59 |
| 72 | adG14 proA1 pabaA1 yA2;wA3 | no T | BC I [1] | M 140 |
| 75 | suA1adE20 adE20 biA1;wA2;choA1;chaA1 | no T | C 362 [2] | M 391 |
| 78[¢] | wA3 | no T | C 419 [1] | M 552 |
| 79 | Mitotic Mapping Strain | no T | C 400 (4) | M 626 |
| 83 | yA2;(veA$^+$) | no T | BC VIII [1] | M 643 |
| 84[Y] | yA2;chaA1 | no T | C 419 [1] | M 701 |
| 85 | adG14 proA1 pabaA1 yA2;wA3 (veA$^+$) | no T | BC VIII [1] | M 765 |
| 87[Δ] | riboA1 adG14 proA1 pabaA1 yA2 | no T | C X (2) | M 841 |
| 89 | biA1;argB2* | T(?) | UV of #26 | M 894 |
| 90 | Grindle wild isolate 2 | | | MG |
| 91 | white spores | | UV of #90 | MG |

[δ] See Pontecorvo et al., 1953 (Adv. Genetics 5: 141-238)

[Δ] Meiotic mapping strain (see Section IV)

[¢] May carry suA1adE20, yA2 and/or chaA1

[Y] May carry suA1adE20

* Poor strain, contains UV induced morphological mutants

[σ] Hockenhull

[†] Discarded from collection; replaced by standard strain #357

Section VI. (continued)

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 92 | Grindle wild isolate 26 | | | MG |
| 93 | yellow spores | | UV of #92 | MG |
| 94 | Grindle wild isolate 36 | | | MG |
| 95 | white spores | | UV of #94 | MG |
| 96 | Grindle wild isolate 44 | | | MG |
| 97 | yellow spores | | UV of #96 | MG |
| 104 | Mitotic Mapping Strain | no T | C 282 (4) | M 301 |
| 105 | Mitotic Mapping Strain | no T | C 280 (4) | M 276 |
| 108 | adE20 biA1;wA2 cnxE16;sC12;methG1;nicA2;choA1;chaA1 | no T | C 349 | M 455 |
| 111 | proA2 biA1 | T1(II;III) | UV of #26 | M 233 |
| 112Y | yA2;bwA1 | no T | set of | M 545 |
| 113Y | bwA1 | no T | prototroph | M 546 |
| 114Y | bwA1;chaA1 | no T | (not veA+) | M 547 |
| 115♀ | wA3;bwA1 | no T | colour mutants | M 548 |
| 116Y | yA2 | no T | from C 419 | M 549 |
| 117Y | prototroph, wild type colour (no veA+) | no T | (includes #78, | M 550 |
| 118Y | chaA1 | no T | 84 and 366) | M 551 |
| 120 | pabaA1 yA2 adE20;AcrA1;coA1 | no T | C 281 (4) | M 286 |
| 121Δ | suA1adE20 riboA1 proA1 pabaA1 adE20;chaA1 | no T | C 300 (= cross d, Käfer 1962) | M 310 |
| 122 | riboA1 yA2;nicB8 | no T | C 4 | M 15 |
| 125 | riboA1 biA1;AcrA1;pyroA4;sB3;nicB8 | T1(I;VIII) | C 62 (6) | M 78 |
| 126 | pabaA1 yA2;wA3; (veA+) | no T | BC VIII [1] | M 740 |
| 129 | pabaA1 yA2 adE20;choA1 | T1(I;VII) | C 103 (= b1, Käfer 1962) | M 96 |
| 146 | Mitotic Mapping Strain | no T | C 434 [2] | M 927 |
| 147 | AcrA1;lysB5;sB3;chaA1 | no T | C 434 [2] | M 940 |
| 148 | suA1adE20 pabaA1 yA2 adE20; lysB5 | no T | C 461 [2] | M 951 |
| 150 | suA1adE20 adE20 biA1;phenA2;sB3;nicB8 | no T | C 434 [2] | M 955 |
| 154 | Mitotic Mapping Strain | no T | C 500 | M 1043 |

| | | | | |
|---|---|---|---|---|
| 155 | Mitotic Mapping Strain | | | |
| 158 | riboA1 biA1 | no T | C 474 [2] | M 1056 |
| 159 | Mitotic Mapping Strain | no T | UV of #26 | M 827 |
| 163 | Mitotic Mapping Strain | no T | C 283 (4) | M 1295 |
| 168 | suA1adE20 adE20 biA1;sB3;choA1;chaA1 | no T | C 282 (4) | M 300 |
| 173 | suA1adE20 pabaA1 yA2 adE20;phenA2;nicB8 | no T | C 474 [2] | M 878 |
| 180 | adE20 biA1;phenA2;sB3;chaA1 | no T | C 461 [2] | M 947 |
| 183 | riboA1 pabaA1 yA2;wA3 | no T | C 434 [2] | M 1061 |
| 184 | adG14 yA2 | no T | C 630 [1] | M 1072 |
| 186 | riboA1 pabaA1 biA1 | no T | C 630 [1] | M 1073 |
| 187 | pabaA1 yA2 (Meiotic Standard Strain) | no T | C 630 [1] | M 1078 |
| 188 | riboA1;wA3 | no T | C 630 [1] | M 1079 |
| 189 | adG14;wA3 | no T | C 640 [1] | M 1085 |
| 191 | wA3 | no T | C 640 [1] | M 1086 |
| 192 | adG14 | no T | C 640 [1] | M 1088 |
| 193Δ | riboA1 adG14 pabaA1 yA2;wA3 | no T | C 639 [1] | M 1090 |
| 194 | yA2 biA1 | no T | C 637 [1] | M 1202 |
| 198 | adE20 biA1;sB3;nicB8;riboB2 | no T | C 638 [1] | M 1205 |
| 201 | anA1 | no T | C 434 [2] | M 935 |
| 202 | riboA1 anA1 | no T | C 758 [1] | M 1243 |
| 204 | AcrA1;chaA1 | no T | C 758 [1] | M 1244 |
| 205 | AcrA1;lysB5 | no T | C 751 [1] | M 1240 |
| 206 | riboA1 adG14 yA2 | no T | C 751 [1] | M 1241 |
| 208Δ | suA1adE20 riboA1 proA1 pabaA1 adE20;choA1;chaA1 | no T | C 758 [1] | M 1250 |
| 211 | biA1;wA3;galA1 | no T | C 300 | M 279 |
| 214 | biA1;wA3;galE9 | no T | Cross of Roberts | CFR |
| 215 | biA1;wA3 galB3 | no T | Cross of Roberts | CFR |
| | | T1(III → VIII) T1(VI;VII | UV of #51† | CFR |
| 216 | adA55 | | | |
| 217 | adB57 | T(?) T(?) | UV of green prototroph from cross #82++ x #34 (no T) | JMF JMF |

ΥMay carry suA1adE20
ÇMay carry suA1adE20, yA2 and/or chaA1
ΔMeiotic mapping strain (see Section IV)
†Discarded from collection; replaced by standard strain #357
++Discarded from collection; see Barratt et al. Genetics 1965 for genotype

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 218 | adA55 yA2 biA1;AcrA1;riboB2 | T(?) | cross of #216 x yA2 biA1;AcrA1;riboB2 | JMF |
| 219 | biA1;methG1 | no T | UV of #26 | M 800 |
| 220 | yA2;pyroA4 | no T | yA2;sC12 x #33 | M 1105 |
| 221 | adG14;AcrA1 wA3 } For teaching: crosses | no T | Cross 753 (no T) | M 1248 |
| 222 | AcrA1 wA3;lysB5;chaA1 } w x cha | no T | Cross 762 (no T) | M 1251 |
| 223 | wA3;lysB5;chaA1 } or w cha x ++ | no T | Cross 762 (no T) | M 1252 |
| 227 | adE20;pyroA4 | T(?) | Cross AAA | RHP |
| 228 | yA2;dp(adE20 biA1);pyroA4 | duplication strains | | RHP |
| 229 | adE20 biA1;dp(adE20 biA1) | T(?) | Cross of #344 x biA1;argA1 (T?) | BWB |
| 230 | yA2;wA2;argA1;(veA+) | | | |
| 231 | riboA1 yA2;ActA1;nicB8 | no T | UV of #122 | BWB |
| 232 | yA2;adD3;sA1 moC96 | T(?) | P | BWB |
| 234 | pabaA1 yA2 | no T | from cross of JMF | CFR |
| 235 | pabaA1 yA2;trypA69 | T(?) | | CFR (M 1722) |
| 236 | trypB403 pabaA1 yA2 | T(?) | UV of #234 | CFR |
| 237 | pabaA1 yA2;trypC801 | T(?) | | CFR (M 1716) |
| 238 | pabaA1 yA2;trypD432 | T(?) | | CFR |
| 239Δ | biA1;adH23 AcrA1 wA3;nicB8 | no T | Cross 59 | M 6 |
| 241 | biA1;pacA1 | T(?) | recomb. as #243 | GD |
| 242 | biA1;pacC5 | no T | UV of #26 | GD (M 1541) |
| 243 | biA1;palA1 | T(?) | | GD (M 1484) |
| 244 | biA1;palB7 | T(?) | | GD (M 1654) |
| 245 | biA1;palD8 | T(?) | *UV induced in rA1 biA1 | GD (M 1286) |
| 246 | biA1;palE11 | T(?) | | GD (M 1653) |
| 247 | biA1;palF15 | T(?) | | GD (M 1287) |
| 248 | biA1;palcA1 | T(?) | | GD |
| 250Δ | yA2;frA1 T1(IV;VIII) palC4 pabaB22 pyroA4 | T1(IV;VIII) | from cross | GD |
| 251 | Aspergillus heterothallicus (see Section III) | | | |
| 252 | Aspergillus heterothallicus (see Section III) | | | |
| 254Δ | biA1;AcrA1 wA3 ileA3 (= ab1) cnxE16 (=ni3) adD3 | no T(?) | Cross of E. Forbes | GD |

| | | | | |
|---|---|---|---|---|
| 256 | pabaA1;wA3;argC3 facB101 riboB2 | T(?) | Cross of E. Forbes | GD |
| 257 | biA1;AcrA1 wA3;nicB8;hisC38 | T(?) | UV of no T strain of J. Foley | MB |
| 258Δ | nicA2 hxA1 (not facA303) riboD5 | no T | Cross of Darlington | GD (M 21[illegible]3) |
| 259 | biA1;adC1;sC12;pyroA4 | no T | Cross R (2) | GD |
| 260 | biA1;phenA3;nirA14 (=ni51) | T1(I;IV) | S in biA1;phenA3; T1(I;IV) | GD (M 1579) |
| 261 | biA1;AcrA1 wA3 anB2 | no T, other aberration? | UV of #123† | GD (M 1384) |
| 262 | biA1;uY5 | T(?) | DES of #26 Darlington | GD |
| 263 | biA1;ornB20 | no T | UV of #26 | GD (M 1378) |
| 264 | biA1;uaX10 | T(?) | DES of #26 Darlington | GD |
| 266 | biA1;cnxB50 (= ni50) | no T | UV of #26 | GD |
| 268Δ | yA2;wA2 thiA4 cnxE16 (=ni3) adD3 blA1 | T(?) | Cross of Apirion | GD |
| 269Δ | pabaA1;tsD15 fwA2 facB101 riboB2 | T(?) | Cross of Forbes | GD (M 1871) |
| 270 | biA1;ygA1 | no T | S of #26 | GD (M 1386) |
| 272 | yA2;pyroA4;methB3 | T(?) | UV of #220 mutant of Roberts | GD |
| 273 | adF17 pabaA1 yA2;fpaD11 | T(?) | mutant of Sinha | GD |
| 275Δ | faA1 adG14 pabaA1 yA2 | T(?) | from cross of McCully | GD |
| 276Δ | yA2;frA1 T1(IV;VIII) pabaB22 pyroA4 | T1(IV;VIII) | Cross of Siddiqi | GD |
| 277 | yA2 biA1;AcrA1;hisA10;riboB2 | T(?) | his UV ind. by Berlyn in strain (no T) of JMF | GD |
| 278 | yA2 biA1;AcrA1;riboB2 hisH13 | T(?) | | GD |
| 279 | yA2;pyroA4;aaX1 | T(?) | induced in #220 (?) | GD |
| 280 | clA6 proA1 pabaA1 yA2;palB7 | T(?) | from cross of Apirion | GD |
| 281 | biA1;suA1palB7;palB7 | T(?) | S in #244 | GD |

ΔMeiotic mapping strain (see Section IV)

*Crossed to a variety of strains to separate from rA1 (e.g. x yA2;methH2 argB2 galA1 smA1 phenA2)

†Discarded from collection; replaced by standard strain #357

Section VI. (continued)

| FGSC# | genotypes | | translocaitons | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|---|
| 282 | biA1;suC6palF15;palF15 | | T(?) | S in #247 | GD |
| 283 | Mitotic Mapping Strain | | no T | MSF of McCully | GD (M 1655) |
| 284 | biA1;su82palB7;palB7 | | T(?) | S in #244 | GD |
| 285 | biA1;adI50** | | no T | UV of #26 | GD |
| 286 | riboA1 biA1;fpaC43 | | T(?) | S in #158 | GD |
| 287 | biA1;suD2palA1;palA1 | | T(?) | S in #243 | GD |
| 288 | Mitotic Mapping Strain | | no T | MSE of McCully | GD |
| 291 | biA1;wA3;galC4 | both with | T1(III → VIII) | UV in #51* | CFR |
| 292 | biA1;wA3 lacB3 | both with | T1(VI;VII) | | CFR |
| 293 | lysF88 biA1;sB3 | | no T(?) | NA of #41, Pees | GD (M 1305) |
| 294 | biA1;sB3;lysD18 (BL*) | | T(?) | NA of #41, Pees | GD |
| 295 | biA1;ileA1;sB3 | | no T(?) | NA of #41 | EP |
| 296 | biA1;lysE13 (EL* on V);sB3 | | T(?) | NA of #41 | EP |
| 297 | lysF51 biA1;sB3 | | T(?) | NA of #41 | EP |
| 298 | biA1;lysE14 (EL* on V);sB3 | | T(?) | NA of #41 | EP |
| 299 | biA1;sB3 his-7122 (EL*) | | T(?) | NA of #41 | EP |
| 300 | biA1;sB3;lysD7 (BL* onVII) | | T(?) | NA of #41 | EP |
| 301 | biA1;lysE231 (EL* on V);sB3 | | T(?) | NA of #41 | EP |
| 303 | proA1 yA2;AcrA1 | | T(III → VIII)? | Cross 38 (3) | RHP |
| 304 | proA1 pabaA1 yA2;phenA2 | | T1(I;VIII) | Cross 2 (6) | RHP (M 1156) |
| 305 | proA2 pabaA18 biA1;phenA2;lysB5 | Teaching strains (Clowes and Hayes 1968) | T(?) | Cross of RHP | RHP |
| 306 | adF17 pabaA1 yA2 | | T(?) | Cross of RHP? | RHP |
| 307 | proA1 pabaA1;nicB8 | | T(?) | Cross of RHP? | RHP |
| 308 | pabaA18 biA1 | | T(?) | UV of #26? | RHP |
| 309 | proA2 pabaA18 yA2 | | T(?) | Cross of ? | RHP |
| 310 | proA1 biA1;AcrA1;pyroA4 | | T(III → VIII)? | Cross 38 (3) | RHP (M 1148) |
| 311 | adE20 biA1;wA2;nicA2 riboD3 | | T(?) | Cross of RHP | RHP |
| 312 | suA1adE20 yA2 adE20;AcrA1;phenA2;lysB5 | | T(?) | Cross of RHP? | RHP |
| 314 | proA1 pabaA1 yA2;wA3 adC1 (veA+) | | no T | Cross of Forbes, #13 x adC1 (veA+) strain, T(III → VIII) | M 821 |

| | | | | |
|---|---|---|---|---|
| 315 | adG14 pabaA1 yA2 | no T | Cross V (2) of G. Pontecorvo #37 x pabaA1 yA2;coA1 T1(VI;VII) | M 825 |
| 316 | biA1;sA2 | T1(V;VIII) | UV of #26 | M 845 |
| 319 | anA1 yA2;wA3 adC1;sC12 | no T | Cross n, EKB | M 1128 |
| 320 | suA1adE20 riboA1 proA1 adE20 biA1;pyroA4 | T(?) | Cross g, EKB | GD (M 1100) |
| 326 | biA1;methG1;flA1 | T(?) | mutant in #219? | JLA |
| 327σ | adE20 biA1;wA3;methG1 pyroA4;uvs-5 | T(?) | UV of #139++ | RWT |
| 328σ | biA1 ad-20;met-3;uvsA1 (probably allele of methG) | T(?) | strain of Lanier | RWT |
| 329σ | adE20 biA1;wA3;methG1 pyroA4;uvs-4 | T(?) | UV of #139++ | RWT |
| 330σ | adE20 biA1;wA3;methG1 pyroA4;uvs-77 | T(?) | UV of #139++ | RWT |
| 332σ | mel (different wild type, from Birmingham)] 8-azaguanine | | AZA | ? |
| 333σ | pabaA108 biA1;uvsB110 | T(?) | UV of pabaA108 biA1 | GJOJ |
| 334σ | pabaA108 biA1;uvsC114 | T(?) | UV of pabaA108 biA1 | GJOJ |
| 335 | proA1 pabaA125 biA1;pyroA4;uvsD153 | T(?) | UV of proA1 | GJOJ |
| 336 | proA1 pabaA125 biA1;pyroA4;uvsE182 | T(?) | pabaA125 biA1;pyroA4 | GJOJ |
| 337 | riboA1 biA1;wA3 thiA4 cnxE16 (= ni3) | no T | C 50 | M 23 |
| 338Δ | yA2;wA3 puA1 cnxE16 adC1 acrB2 | T(?) | C 85 | M 94 |
| 339 | suA1adE20 pabaA1 yA2 adE20;sA4 | no T | C 136 | M 146 |
| 340 | proA1 biA1;phenA2;pantoA1 | T1(III→VIII;VII) | C 243 | M 347 |
| 341 | suA1adE20 proA1 pabaA1 yA2 adE20;AcrA1 puA1;choA1 nicB8;chaA1 | no T | C 347 | M 426 |
| 342 | suA1adE20 adE20 biA1;AcrA1;choA1;chaA1 | no T | C 365 | M 771 |
| 343 | adG14 proA1 pabaA1 yA2;wA3; (ve+) | no T | C 1620(= BCIX) | M 799 |
| 344 | yA2;wA2 adC1;sC12;(ve+) | no T | C J (2) | M 814 |
| 345 | biA1;sC12;pyroA4 | T1(II;IV) | C s (2) | M 854 |
| 346 | biA1;AcrA3 adC1;sC12;pyroA4 | no T(?) | S in #259 | M 875 |
| 347 | anA1 adE20 biA1;wA2;lysB5 | T1(I;V;VII;VIII) | S in #348 | M 900 |
| 348 | anA1 adE20 biA1;wA2;lysB5 [from cross of dupl. T1(III→VIII)] | no T | C 512 | M 921 |
| 349 | adE20 biA1;lacA1;choA1;chaA1 | no T | C 496 | M 917 |
| 350 | biA1 phenA2;lysA1 sB3 | "Ab VI"=Inversion? | C 346 | M 918 |

ΔMeiotic mapping strain (see Section IV)

σSee uvs -- terminology (Section VII)

*Leiden, terminology of E. Pees

**adI50 strains do not respond well on acetate

†Discarded from collection; replaced by standard strain #357

++Discarded from collection; genotype adE20 biA1; wA3; methG1 pyroA4

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 352 | riboA1 adG14 yA2;phenA2 | T1(I;VIII) | C 2 (6) | M 962 |
| 353 | biA1;ornB9 riboB2 | T(?) | C 494 | M 966 |
| 354 | AcrA1;lysB5 | T1(I;VII) | C 515 | M 1014 |
| 355 | anA1 adE20 biA1;wA2;lysB5 | T2(I;VII) | C 542b | M 1054 |
| 356 | riboA1 biA1 (Meiotic standard strain) | no T | C 630 [1] | M 1076 |
| 357 | biA1;wA3 (replaces #51) | no T | C 640 [1] | M 1089 |
| 358 | riboA1 adG14 proA1 yA2;ornA4 | T(?) | C 3 | M 1101 |
| 359 | pabaA1;wA3 | no T | C 639 [1] | M 1231 |
| 360 | AcrA1;lysB5;chaA1 (Meiotic Standard Strain [5th BC]) | no T | C 752 | M 1239 |
| 361 | riboA1 yA2 | no T | C 630 [1] | M 1265 |
| 362Δ | riboA1 anA1 adG14 proA1 pabaA1 yA2 | no T | C 773 | M 1267 |
| 363Δ | suA1adE20 riboA1 anA1 luA1 pabaA1 yA2 adE20 biA1;AcrA1 | no T | C 792 | M 1274 |
| 364 | suA1adE20 proA2 yA2 adE20;AcrA1 wA2 | no T | Dipl. 629 | M 1277 |
| 365 | yA2;AcrA1;lysB5;chaA1 (5th BC) | no T | C 752 | M 1279 |
| 366 | yA2;chaA1;bwA1 | no T(?) | C 789 | M 1282 |
| 367 | suA1adE20 proA1 yA2 adE20;AcrA1 wA2 | no T | Dipl. 628 | M 1285 |
| 368 | riboA1 yA2;sA2 | no T | C 785 | M 1301 |
| 369 | pabaA1 biA1;sB3 | no T | C 788 | M 1303 |
| 370 | adG14;sA1;pyroA4;chaA1 | T1(V;VI) | C 838 | M 1309 |
| 371 | AcrA1;lysB5;fwA2 | no T | S in M 1241 | M 1318 |
| 372 | biA1;sA2;chaA2 | T1(V;VIII) | S in #316 | M 1319 |
| 373 | anA1;sA1;lysB5;chaA1 | T1(V;VI) | C 838 | M 1324 |
| 374 | Mitotic Mapping Strain | no T | C 569 | M 1335 |
| 375 | Mitotic Mapping Strain | no T | C 569 | M 1343 |
| 376Δ | suA1adE20 lysF88 pabaA1 yA2 adE20 | no T(?) | C 841 | M 1346 |
| 377 | riboA1 yA2 adE20 | no T | C 847 | M 1368 |
| 378 | biA1;fwA1 | no T | S in #26 | M 1370 |
| 379 | ornB7 fwA1 (veA+) | no T(?) | cross of AJC | M 1371 |
| 380Δ | lysB5;fwA2 cnxB2 facB101 palB7 chaA1 | no T | C 804 | M 1373 |
| 381 | cnxB2 (=ni21/11) palB7 | no T(?) | C 804 | M 1376 |
| 382 | yA2;adH23 AcrA1 wA3 anB2 | no T, other aberr.? | Cross of AJC | M 1383 |

| | | | | |
|---|---|---|---|---|
| 383 | riboA1;AcrA1;sB25;chaA1 | T(?) | NG of M 1421 (lost) | M 1398 |
| 384 | riboA1 yA2;sC22 | T(?) | NG of M 1420 (lost) | M 1400 |
| 385 | biA1;sE15 | no T(?) | NG of #26 | M 1402 |
| 386 | pro-94;(veA$^+$) | T(?) | UV of #4 | M 1414 |
| 387 | fpaA91 proA11 yA2;pyroA4 | T(?) | NG of orig. proA11 strain | M 1415 |
| 388 | biA1;pyroA4;sF211 | no T(?) | NG of #33 | M 1433 |
| 389 | uvsF201 pabaA1 | no T(?) | C 915 | M 1444 |
| 390 | fpaA91 pabaA1 biA1;pyroA4 | no T(?) | C 883 | M 1447 |
| 391 | biA1;chaA1 | no T | C 843 | M 1466 |
| 392 | yA2 biA1;chaA1 | no T | C 843 | M 1469 |
| 393 | suA1adE20 pro-94 yA2 adE20;AcrA1 wA3 | no T(?) | Dipl. 860 | M 1474 |
| 394 | biA1;phenB6 | T(?) | UV of #26 | GD (M 1490) |
| 395 | biA1;sB3;lysD20 T1(III;VII) | T1(III;VII) | UV of #41 | EP (M 1493) |
| 397 | pantoB100 | no T(?) | UV?(BMR) | M 1498 |
| 398 | biA1;lysB5;sD50 T2(I;VIII) | T2(I;VIII) | C 980 | M 1500 |
| 399 | facB101 riboB2 sE15 | no T | C 898 | M 1503 |
| 400 | yA2 adE20;AcrA1;sF211 palF15 choA1 | no T(?) | C 2116 | M 2281 |
| 401$^\Delta$ | facB101 riboB2 palB7 chaA1 sE15 | no T | C 1932 | M 1581b |
| 402 | phenA3;palB7 chaA1 (ni51) = nirA14 | no T(?) | C 1045 | M 1626 |
| 403 | pabaA1;wA3;pyroA4;sF211 | no T(?) | C 966 | M 1631 |
| 404 | biA1;AcrA1 wA3;sA49;lysB5 | no T(?) | C 1164 | M 1641 |
| 405 | pabaA1 yA2;sA91 | no T(?) | C 1166 | M 1643 |
| 406 | luA1 yA2 | no T | C 1605 | M 1824 |
| 407 | Mitotic Mapping Strain | no T | C 1608 | M 1832 |
| 408 | pabaA1 yA2;wA3 (Meiotic Standard Strain) | no T | C 1621 | M 1849 |
| 409 | pabaA1;facB101 chaA1 | no T(?) | C 1701 | M 1854 |
| 410 | pabaA1 biA1;riboB2 chaA1 | no T | C 434 | M 1869 |
| 411 | proA1 pabaA1 yA2 | no T | C 1709 | M 1885 |
| 412 | pabaA1 yA2;ActA1 | no T | C 1649 | M 1897 |
| 413 | pabaA1;sA2;chaA2 | T1(V;VIII) | C 1708 | M 1907 |
| 414 | riboA1 proA2 yA2;ActA1 | T1(II;III) | C 1760 | M 1937 |
| 415 | riboA1 proA2 biA1;ActA1 | no T | C 1760 | M 1940 |
| 416 | riboA1;chaA1 | no T | C 1754 | M 1941 |

$^\Delta$Meiotic mapping strain (see Section IV)

Section VI. (continued)

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 417 | pabaA1;sA1;chaA1 | no T | C 1754 | M 1942 |
| 418 | pabaA1 yA2;lysD20 T1(III;VII) | T1(III;VII) | C 1732 | M 1944 |
| 419 | biA1;sD85 | no T(?) | NG of #26 | M 1951 |
| 420 | pabaA1;sD157 facB101 | no T | C 1801 | M 1986 |
| 421 | riboA1;sD85 | no T | C 1794 | M 1987 |
| 422 | fpaB37 riboA1 biA1 | no T | S in #158 | AJC (M 1990) |
| 423Δ | riboA1 proA1 yA2;sC12 phenA2 suB4pro | no T | C 1846 | M 1998 |
| 424Δ | suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;AcrA1;pyroA4;phenB6 sF211 malA1 nicB8;chaA1 | no T | C 1530 | M 2006 |
| 425 | $y^{o}$A91 biA1;phenA2 | no T(?) | S in #498 | M 2012 |
| 426 | yA2;pabaB22 pyroA4 | no T | C 1783 | M 2023 |
| 427 | pabaA1;AcrA1;sD85 facC102 | no T | C 1802 | M 2027 |
| 428 | pabaA1 adE20 biA1 | no T | C 1716 | M 2032 |
| 429 | pabaA1 adE20 biA1 | T1(II;VII) | C 1716 | M 2033 |
| 430 | suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;pyroA4;phenB6 sF211 malA1;chaA1 | T1(I;VII) | C 1530 | M 2039 |
| 431 | galD5 suA1adE20 riboA1 adE20 biA1;sD50 T2(I;VIII) fwA2 facC102 | T2(I;VIII) | C1808 | M 2054 |
| 432 | galD5 suA1adE20 riboA1 adE20 biA1;fwA2 facB101 | no T | C 1809 | M 2055 |
| 433 | fpaB37 sulA1 anA1 pabaA1 yA2 adE20;pyroA4;cnxB2 chaA1 | [±T1(VI;VII)] | C 1822 | M 2056 |
| 434 | fpaB37 anA1 pabaA1 yA2 adE20;sD50 T2(I;VIII) cnxB2 chaA1 | T2(I;VIII)[as #433] | C 1822 | M 2057 |
| 435Δ | frA1 T1(IV;VIII) palC4 pabaB22 pyroA4;chaA1 | T1(IV;VIII) | C 1911 | M 2070 |
| 436 | adE20 biA1;wA4;smA1;lysB5 | no T | C 1914 | M 2071 |
| 437 | proA1;wA3;nicA2;malA1 | no T | C 1923 | M 2072 |
| 438 | fpaA91 anA1 adE20 biA1;wA2;lysB5;choA1 | T1(I;VII) | C 1519 | M 2074 |
| 439Δ | fpaA91 anA1 adE20 biA1;AcrA1 wA4;ActA1;choA1 | no T | C 1518 | M 2076 |
| 440 | riboA1 yA2;AcrA1;fwA2 | no T | C 1844 | M 2102 |
| 441Δ | riboA1 proA1 biA1;wA3;sC12 galA1 ActA1 phenA2 suB4pro | no T | C 1838 | M 2108 |
| 442Δ | facB101 riboB2 chaA1 sE15 nirA14 (=ni51) | no T | C 1932 | M 2113 |
| 443 | pabaA1 yA2 adE20;AcrA1;suC11adE20;coA1 cnxB2 (=ni21/11) | no T | S in rec. from 1799 | M 2131 |
| 444Δ | suA1adE20 yA2 adE20;AcrA1;phenB6 sF211 malA1 choA1 nicB8 | no T | C 1942 | M 2132 |

| | | | | |
|---|---|---|---|---|
| 445 | riboA1 y°A91 | no T | C 1903 | M 2136 |
| 446 | Mitotic Mapping Strain | no T | C 1924 | M 2139 |
| 447 | anA1 yA2;wA3;adI50** galA1 ActA1;sF211 lysD20 T1(III;VII) choA1;nicB8 | T1(III;VII) | C 1736 | M 2150 |
| 448Δ | proA1;AcrA1;galE9 sA1 adI50** ActA1;chaA1 | no T | C 1868 | M 2151 |
| 449 | AcrA1;lysB5;coA1 cnxB2 | no T(?) | C 1799 | M 2152 |
| 450 | pabaA1 yA2;oliA2 | no T(?) | S in #187 | RTR |
| 451 | pabaA1;meaB6 cnxH3 sC12 | no T(?) | C 332 | 332.1 of Arst |
| 452 | sulA1 anA1 pabaA1;wA3;chaA1 | no T | C 1950 | M 2162 |
| 453 | oliA2 pantoB100 | no T | C 1945 | M 2165 |
| 454 | riboA1 proA1 yA2;ActA1 suB4pro | no T | C 1846 | M 2167 |
| 455 | sulA1;AcrA1 wA3;lacA1 sB3;choA1;chaA1 | no T | C 1988 | M 2175 |
| 456Δ | proA1 yA2;galE9 adI50** methH2 dilA1 | no T | C 1969 | M 2176 |
| 457Δ | proA1 biA1;galE9 sC12 dilA1 phenA2;choA1 | no T | C 1973 | M 2186 |
| 458Δ | riboA1 proA1 yA2;AcrA1;adI50** methH2 galA1 ActA1 suB4pro | no T | C 1972 | M 2187 |
| 459Δ | suA1adE20 pabaA1 yA2 adE20;AcrA1;lacA1 bwA1 sbA3;sF211 | no T | C 1952 | M 2198 |
| 460 | AcrA1;lysB5 pA2 | no T | C 2128 | M 2200 |
| 461 | proA1 biA1;phenA2;malA1;riboB2 | no T | C 1975 | M 2204 |
| 462 | pabaA1 y°A91;iodA1 cnxE16 | no T(?) | C 1976 | M 2205 |
| 463Δ | suA1adE20 pro-94 lysF88 pabaA1 yA2 adE20;wA2 | no T | C 1985 | M 2207 |
| 464Δ | suA1adE20 pabaA1 yA2 adE20;AcrA1;lacA1 bwA1 sB3 sbA3 | no T | C 1952 | M 2209 |
| 465 | Mitotic Mapping Strain | no T | C 1987 | M 2212 |
| 466Δ | galD5 suA1adE20 riboA1 anA1 pro-94 lysF88 pabaA1 yA2 adE20 | no T | C 2113 | M 2213 |
| 467Δ | yA2 adE20;lacA1;phenB6 oliA2 sF211 palF15 malA1 choA1 nicB8 | no T(?) | C 2116 | M 2214 |
| 468 | Mitotic Mapping Strain | no T | C 1987 | M 2216 |
| 469 | AcrA1;lysB5;sD85 fwA2 | no T | C 1983 | M 2218 |
| 470 | proA1 biA1;methG1 frA1 T1(IV;VIII);chaA1 | T1(IV;VIII) | C 1929 | M 2219 |
| 471Δ | proA1 yA2;meaB6 sC12 methH2 dilA1 | no T(?) | C 2108 | M 2220 |
| 472 | riboB2 nirA14 | no T | C 1932 | M 2221 |
| 473 | Mitotic Mapping Strain | no T | C 2125 | M 2233 |
| 474 | sulA1 adE20;AcrA1;ActA1;choA1;chaA1 | no T | C 2112 | M 2234 |
| 475Δ | fpaB37 galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1;sD85 fwA2 | no T | Dipl. 2195 | M 2235 |

ΔMeiotic mapping strain (see Section IV)
**adI50 strains do not respond well on acetate

Section VI. (continued)

| FGSC# | genotypes | translocations | origin or Montreal cross nos. | Montreal stock number or depositor |
|---|---|---|---|---|
| 476 | sulA1 adE20;AcrA1 wA3;ActA1;lysB5;choA1; (chaA1?) | no T | C 2112 | M 2239 |
| 477 | Mitotic Mapping Strain | no T | C 2125 | M 2240 |
| 478 | Mitotic Mapping Strain | no T | C 2125 | M 2242 |
| 479Δ | galD5 suA1adE20 riboA1 anA1 pabaA1 yA2 adE20 biA1 | no T | C 1523 | M 2243 |
| 480 | Mitotic Mapping Strain | | C 1974 | M 2246 |
| 481Δ | yA2 adE20;AcrA1;phenB6 oliA2 sF211 malA1 choA1 nicB8 | no T | C 2120 | M 2247 |
| 482 | bwA1 sbA3;phenB6 oliA2;riboB2 | T1(VI;VII) | C 2121 | M 2248 |
| 483Δ | fpaB37 galD5 suA1adE20 sulA1 riboA1 anA1 pabaA1 yA2 adE20 biA1 | no T | C 1523 | M 2255 |
| 484Δ | AcrA1;lysB5;sD85 fwA2 facC102 | no T | C 1983 | M 2256 |
| 485 | riboA1 adE20;fwA2 | no T | C 2105 | M 2259 |
| 486 | riboA1 yA2 adE20;methG1 suC11adE20 | no T | C 2134 | M 2303 |
| 487 | Mitotic Mapping Strain | no T | C 1987 | M 2269 |
| 488 | pabaA1 yA2;sC12 | no T | C 1762 | M 2270 |
| 489 | riboA1 biA1;dilA1;choA1 | no T | C 1967 | M 2271 |
| 490Δ | proA1;meaB6 cnxH3 adI50** dilA1 | no T(?) | C 2108 | M 2272 |
| 491Δ | AcrA1;lysB5 pA2 facA303 hxA1 riboD5 | no T | C 2133 | M 2309 |
| 492 | pabaA1 y°A91;IodA1 | no T | C 1978 | M 2274 |
| 493 | pabaB22 | no T(?) | C 1907 | M 2276 |
| 494Δ | galD5 suA1adE20 riboA1 yA2 adE20;AcrA1 | no T | C 1951 | M 2277 |
| 495Δ | lysB5 nicA2 pA2 | no T | C 2127 | M 2278 |
| 496Δ | pabaA1 yA2;meaB6 adI50** dilA1 | no T(?) | C 2108 | M 2279 |
| 497 | AcrA1;palC4 pabaB22;chaA1 | no T | C 1911 | M 2280 |
| 498 | biA1;phenA2 | T(?) | C 1632 | M 2013 |
| 499 | suA1adE20 pabaA1 yA2 adE20;phenB6 sF211 | no T | C 1951 | M 2282 |
| 500 | biA1;methG1;nicA2;sbA3;malA1 | no T | C 1977 | M 2283 |
| 501 | adE20 biA1;smA1 ActA1 | no T | C 1935 | M 2284 |
| 502 | sulA1;AcrA1;facA303 lysB5;sB3;chaA1 | no T | C 2125 | M 2285 |
| 503 | proA1 yA2;methH2 dilA1 | no T | C 1969 | M 2286 |
| 504Δ | AcrA1;lysB5 pA2 riboD5 | no T(?) | C 2127 | M 2287 |

| | | | | |
|---|---|---|---|---|
| 505Δ | pabaA1 (yA2?);AcrA1 wA3 ileA3 | no T(?) | C 1642 | M 2288 |
| 506Δ | AcrA1;phenB6 oliA2 sF211 malA1 choA1 nicB8 | no T | C 2120 | M 2289 |
| 507Δ | fpaB37 sulA1 anA1 pabaA1 | no T | C 1950 | M 2295 |
| 508Δ | AcrA1;nicA2 facA303;hxA1 riboD5;sB3;chaA1 | no T | C 2133 | M 2309 |
| 509 | riboA1 adE20 | no T | C 2110 | M 2203 |
| 510 | pabaA1 yA2 adE20;AcrA1;nicA2;sbA3 | no T | C 1955 | M 2298 |
| 511 | sulA1;ActA1;choA1;chaA1 | no T | C 2107 | M 2325 |
| 512Δ | AcrA1;palC4 pabaB22 pyroA4;chaA1 | no T(?) | C 1911 | M 2307 |
| 513 | Mitotic Mapping Strain | no T | C 2125 | M 2308 |
| 514 | anA1 adE20 biA1;AcrA1;ActA1;sB3;fwA2 | no T | C 2216 | M 2312 |
| 515Δ | fpaB37 galD5 suA1adE20 riboA1 yA2 adE20;pyroA4;facA303;chaA1 | no T | C 2217 | M 2313 |
| 516 | galE9 meaB6 adI50** ActA1;chaA1 sE15 nirA14 (= ni51) | no T? | C 2124 | M 2328 |
| 517Δ | riboA1 yA2 adE20;methG1 suC11adE20 palC4 pabaB22 pyroA4 | no T | C 2135 | M 2316 |
| 518 | AcrA1;lysB5 facA303 hxA1;lacA1 sB3 sbA3 | T1(V;VI) | C 2131 | M 2318 |
| 519 | suA1adE20 riboA1 proA1 pabaA1 yA2 adE20;wA2;oliA2 malA1 choA1 nicB8 | T1(VI;VII) | Dipl. 1995 | M 2319 |
| 520 | pabaA1;AcrA1;sB3 sbA3;phenB6;riboB2 | T1(VI;VII) | Dipl. 1998 | M 2320 |
| 521 | suA1adE20;AcrA1;galA1;pyroA4;pA2 facA303 riboD5;sbA3 | T1(V;VI) | C 2131 | M 2321 |
| 522 | pabaA1 yA2 adE20;AcrA1;facA303;lacA1 sB3 | T1(V;VI) | C 2131 | M 2322 |

ΔMeiotic mapping strain (see Section IV)

**adI50 strains do not respond well on acetate

## Section VII. Nomenclature: uvs and lys Terminology

1) uvs of Tuveson

| | FGSC# | Residual Genotype |
|---|---|---|
| uvs-1 | 328 | bi1 ad20; met-3 (met-3 probably allelic to meth1, induced by Lanier). |

Origin: cross of Glasgow strains with new mutants induced in these by Lanier (Bot. Gazette, 128, p.16, 1976).

Caution: ad20 according to Lanier gives 3-8% recombination with y.

| | | Strain of origin |
|---|---|---|
| uvs-4 | 329 | FGSC #139: adE20 biA1; wA3; methG1 pyroA4 |
| vus-5 | 327 | |
| uvs-77 | 330 | |

2) uvs - mutants -change of isolation numbers (Kafer, Jansen and Pateman)

| Utrecht Jansen | FGSC# | Strain of origin | Linkage Group |
|---|---|---|---|
| uvsA101 | | UT408 = pabaA108 biA1 | IR |
| B110 | 333 | " | IV |
| C114 | 334 | " | VIII |
| D153 | 335 | UT439 = proA1 pabaA125 biA1;pyroA4 | V |
| E157 | | " | V |
| E180 | | " | V |
| E182 | 336 | " | V |
| C190 | | " | VIII |
| B191 | | " | IV |
| C194 | | " | VIII |

unmapped mutants

uvs-111 and uvs-115 in UT408

28 mutants from uvs-116 to uvs-195 in UT439

3) Montreal

| | FGSC# | Strain of origin | Linkage Group |
|---|---|---|---|
| uvsF201 | 389 ($F_1$) | M 1265 (riboA1 yA2) | IL |
| F202 | | | |
| uvsG211 | | M 1421 (riboA1; AcrA1; chaA1) | VIII with T (III;IV?) |

unmapped:

3 uvs mutants
(uvs-208, -209 and -228) all in M 1423 (pabaA1 yA2; AcrA1)

4) Pateman (Wright and P., Mut. Res. 9, 579, 1970) has agreed to add 300 to all isolation numbers. Resulting published mutants:

uvs-304, -311 and -313 on IV,
uvs-308 on V,
uvs-302 on VII

unmapped -- uvs-303, uvs-307, uvs-309

## Section VII. (continued)

5) lys-gene terminology (lysC and D recombine freely, also lysB and E)

| Glasgow old | Glasgow new* | Linkage Group | Leiden -- (internal designations, used by Pees) |
|---|---|---|---|
| lys1 | lysA | VI | lysAL |
| lys5 | lysB | V | lysCL |
| | lysC | VII | lysDL (alleles 6, 15) |
| | lysD | VII | lysBL " 18 = FGSC #294 (?) |
| | | | " 7 = FGSC #300) |
| | | T(III;VII) | " 20 = FGSC #395) |
| | lysE | V | lysEL (alleles 13 = FGSC #296 |
| | | | " 14 = FGSC #298 |
| | | | " 231 = FGSC #301) |
| | lysF | IR | lysFL (alleles 51 = FGSC #297) |

*To be used for publications (according to Millington-Ward).

## Section VIII. Key to Symbols

1) Symbols used are as follows:

| | | | |
|---|---|---|---|
| Ab | Aberration | MSE | master strain E; excellent tester strain |
| BC | back cross | MSF | master strain F; excellent tester strain |
| C | cross | T | translocation (reciprocal or other Aberration strains) |
| MSD | master strain D | | |

2) Symbols used to indicate Montreal numbers or depositor are as follows:

| | | | | | |
|---|---|---|---|---|---|
| AJC | A.J. Clutterbuck | GD | Gordon Dorn | MB | M. Berlyn |
| BMR | B.M. Revers | GJOJ | G.J.O. Jansen | MG | M. Grindle |
| BWB | B.W. Bainbridge | JLA | J.L. de Azevedo | RHP | R.H. Pritchard |
| CFR | C.F. Roberts | JMF | J.M. Foley | RTR | R.T. Rowlands |
| EP | E. Pees | M | Montreal | RWT | R.W. Tuveson |

3) Symbols used in mode of orgin are as follows:

| | | | |
|---|---|---|---|
| AZA | azaguanine | P | β-propiolactone |
| DES | diethyl sulfate | S | spontaneous |
| NA | nitrous acid | UV | ultraviolet light |
| NG | nitrosoguanidine | X | x-rays |
| NM | nitrogen mustard | | |