Dr Kenneth E. Papa's Collection
c/o Chris Albertin (RSCH TECH II)
Dept of PLT PATH
UGA - Athens GA 30602

Tulane

Department of Biology
2000 Percival Stern Hall
Tulane University
New Orleans, Louisiana 70118
(504) 865-5546

August 3, 1986

Dear Chris:

I'm taking my kids on a vacation next week and am afraid this won't get off in the mail before I leave if I give the letter to a typist. So I'm typing it myself.

I'm enclosing copies of the various letters that have gone to All Concerned in the business of closing down Dr. Papa's Culture Collection. Also enclosed is a copy of the Bennett and Papa paper.

I have spent rather a lot of time trying to find out what strains need to go to ATCC. I have generated two lists: Aspergillus parasiticus and A. flavus. These give the mutants in the sequence they appear in Tables 2 and 3, respectively, of the Bennett and Papa chapters. For the A. parasiticus strains, I could not find several of the genotypes listed in the 1978 paper in the silica gel log. I list what I could find -- I looked pretty hard and don't think I missed anything, but you are more familiar with the collection than I, so you are welcome to double check.

The A. flavus list seems to be more complete. It lists the mutant gene symbols in alphabetic order (which is the sequence of Table 4, Bennett and Papa). I have checked the genotypes which are already at ATCC on the master list. Of the remainder, I have given the silica gel numbers for everything but afl-20, afl-22, arg-2, arom (on linkage group IV), ts, and ylo. Here I'm not as certain that I excluded everything as I was with the A. parasiticus stocks. I suspect you can find these somewhere. My big problem is that I'm not sure the various "ylo's" or "arom's" I see listed in many places are the same ones that Dr. Papa mapped.

In any event, the two lists I have prepared tell you what strains go to ATCC. The contact person there is:

Dr. S. C. Jong
American Type Culture Collection
12301 Parklawn Drive
Rockville, MD 20852 301/881-2600

Also need chloro to grow

SINCE 1925, AN INDEPENDENT, NON-PROFIT ORGANIZATION DEVOTED TO
THE PRESERVATION AND DISTRIBUTION OF REFERENCE CULTURES

American
Type Culture
Collection

12301 PARKLAWN DRIVE · ROCKVILLE, MARYLAND 20852-1776 USA · (301) 881-2600 · TELEX: ATCCROVE 908-768

December 15, 1986

~~Dr.~~ J.C. Albertin RSCH TECH III
(Dr. K.E. Papa's Lab)
Department of Plant Pathology
University of Georgia
Athens, GA 30602

Dear ~~Dr.~~ Albertin:

The cultures which you kindly deposited have been assigned the following ATCC accession numbers:

Aspergillus flavus	71-31a-10	ATCC 62627
Aspergillus flavus	88-A14-1	ATCC 62628
Aspergillus flavus	100 5t-8	ATCC 62629
Aspergillus flavus	170 5t-8	ATCC 62630
Aspergillus flavus	241 T37-10	ATCC 62631
Aspergillus flavus	244 T37-17	ATCC 62632
Aspergillus flavus	650 5T-18-6	ATCC 62633
Aspergillus flavus	651 5T-18-7	ATCC 62634
Aspergillus flavus	653 16-7-8	ATCC 62635
Aspergillus flavus	654 A17-19	ATCC 62636
Aspergillus flavus	655 A14-1-3	ATCC 62637
Aspergillus flavus	656 A14-1-4	ATCC 62638
Aspergillus flavus	657 A14-1-5	ATCC 62639
Aspergillus flavus	658 9-2	ATCC 62640
Aspergillus flavus	659 9-6	ATCC 62641
Aspergillus flavus	660 9-7	ATCC 62642
Aspergillus flavus	1020 (19-8+579)-16	ATCC 62643
Aspergillus flavus	1025 (T44-7+592)-20	ATCC 62644
Aspergillus flavus	1028 (31a-18-1+579)-33	ATCC 62645
Aspergillus flavus	1060 81-46-193	ATCC 62646
Aspergillus flavus	1063 81-6-160	ATCC 62647
Aspergillus parasiticus	617 B43-23	ATCC 62648
Aspergillus parasiticus	619 B144-17	ATCC 62649
Aspergillus parasiticus	621 A43-7	ATCC 62650
Aspergillus parasiticus	624 B144-26	ATCC 62651

We also received a tube of Aspergillus flavus strain 652 16-7-4 labelled "will not grow" on it. Would it be possible for us to receive a replacement culture?

Thank you very much for your assistance.

Sincerely,

S. C. Jong, Ph.D.
Head, Mycology & Botany Department

SCJ/psk

Dr. Maren Klich of the Southern Regional Research Labs has agreed to curate the remainder of the collection, as described in the various letters enclosed. I think she should also have reference stocks of what goes to ATCC. Her address and phone:

Dr. Maren Klich
Southern Regional Research Center
P. O. Box 19687
New Orleans, LA 70179 504/589-7597

Since ATCC will be lyophilizing their stocks, they should be sent some living material. Dr. Klich will just keep the silica gel stocks as is.

I'll be out of town Aug. 5-17th, but back here after that. Please write or call if you have any questions. I know this is super-tedious, but we are almost finished.

Finally, a very big personal thank you for all you have done. I don't think I could have made verymuch progress if you hadn't prepared the "Blue Book" with all the silica gel log information typed up.

I'm only going to send copies of this to Dick Hanlin and Louise Miller since they are the most concerned.

Best regards.

Sincerely,

J. W. Bennett
Professor

cc: R. Hanlin
M. Klich
L. Miller

DR DAVID WICKLOW
PHONE: 309/685-4011 Ext 384
NORTHERN RSCH CTR
1815 N UNIV ST
PEORIA, IL 61604

Dr K. E Kapa

LIST OF ATCC ACQUISITIONS

ATCC #	SILICA Gel #		DESCRIPTION
-	1		"PC-7" wild type
44617	(34-4)	234	t pdx bi B_2/B_1 > 1 (HB2)
44617		649	afl 1 leu t
44618		241	afl 4 pdx t
46107	(2)	470	pdx w (NG/UV)
- 08	(17)	460	pab w (NG)
- 09	(6)	804	his w (NG)
- 10	(32)	516	IV w (NG)
- 11	(31a-22)	83	pro w (NG)
- 12	(31a-6)	176	phe w
- 13	(31a-18)	79	ad w (NG)
- 14	(58)	434	met w (NG)
- 15	(31a-17)	78	thi w
- 16	(19)	271	pdx w B_2/B_1 > 1 (NG/UV/NG)
60040	(1-N)	827	nor lys w
- 1	(31a-25)	86	arg-7 w
- 2	(86-1)	796/797	afl 15 arg-7 w
- 3	(5t-18)	109	leu t
- 4	(118-1)	118 (T44)	afl 16 arg-2 t
- 5	(271-1)	774 (19-1)	afl 21 pdx w
- 6		491	leu pdx t
- 7		506	leu pdx w
- 8		579	t pro met pab his
- 9		592	w pro met pab his

- complete list —

Aspergillus flavus

The following genetic loci were cited in Table 3 of the Bennett and Papa paper. They exclude loci already represented in stocks at the ATCC.

In listing genotypes, I have placed the spore color mutant first.

Available on silica gel:

#650. 5T-18-6 t leu afl-2

#651. 5T-18-7 t leu afl-3

#241. T37-10 pdx afl-4 Ts-1

#244. T37-17 afl-5

#652. 16-7-4 ylo pab afl-6

#653. 16-7-8 lgt ylo pab afl-7

#655. A14-1-3 w met afl-8

#656. A14-1-4 w met afl-9

#657. A14-1-5 w met afl-10

#658. 9-2 w nic afl-11

#659. 9-6 w nic afl-12

#660. 9-7 w nic afl-13

#654. A17-19 fawn arom afl-14

#1028. (31a-18-1 + 579)-33 t met his afl-17

#1025. (T44-7 =592)-20 w his afl-19

#1020. (19-8 + 579)-16 t pab met his afl-25

#1034. 31-7 cnx

#170. 5T-f fwn

#100. 5t-8 lys (lys-3)

#88. A14-1 met (met-4)

Aspergillus parasiticus

Published strains available on silica gel:

#621. A43-7 or nic afla-1

#617. B43-23 ylo pro afla-1

#619. B144-17 gb lys-2 afla-2

#624. B144-26 w met afla-2

Citation: Papa, K. E. 1978.
The parasexual cycle in Aspergillus parasiticus.
Mycologia 70: 766-773.

Other strains listed in this paper could not be located in Dr. Papa's silica gel log.

A. flavus con't

#1063. 81-6-160 nia NO_3 hc group 3 tester

#71. 31a-10 nic

#1060. 81-46-193 nii NO_2 hc group 3 tester

I used it to construct ... the genes which are already in stocks at ATCC. The list I sent Chris Mateson consists of those strains not already represented at ATCC.

Genetic Loci of Aspergillus flavus

"MASTER LIST"

Gene symbol	Linkage group	Properties	References
✓ ad ATCC 46613	II	adenine req.	2, 4, 10
✓ afl-1 ATCC 44617	VII	aflatoxin⁻, dominant (dominance expressed in diploids but not in heterokaryons)	9, 10, 13
✓ afl-4 ATCC 44618	II	aflatoxin⁻, recessive	9, 10
afl-2 afl-3 afl-5 afl-6 afl-7 afl-8 afl-9 afl-10 afl-11 afl-12 afl-13 afl-14	?	aflatoxin⁻, recessive, and all appear to be nonallelic	9
✓ afl-15	VII	aflatoxin⁻, recessive	13
✓ afl-16	VII	aflatoxin⁻, recessive	13
afl-17	VII	aflatoxin⁻, recessive	13
afl-19	VII	aflatoxin⁻, recessive	13
afl-20	VII	aflatoxin⁻, recessive	13
✓ afl-21 B2	VII	aflatoxin⁻, recessive	13
afl-22	VII	aflatoxin⁻, recessive (allelic to afl-20)	13
afl-25	VII	aflatoxin⁻, recessive	13
✓ afl-B2 ATCC 34081	VIII	higher B_2 than B_1 accumulation, recessive (originally referred to as HB2)	5, 6, 7, 10
✓ arg-2	II	arginine req.	2, 4
arg-4	IV	arginine req.	4
✓ arg-7	VII	arginine req.	13
arom	IV	aromatic metabolites req.	4
✓ bi	III	biotin req.	4

Genetic Loci of *Aspergillus flavus* (Continued)

Gene symbol	Linkage group	Properties	References
cnx	?	nitrate and hypoxanthine non-utilizing	14
fwn	II	fawn conidia	4
✓ his	VIII	histidine req.	7, 10
✓ iv	VII	isoleucine/valine req.	4, 10
✓ leu	VII	leucine req.	2, 4
lys-3	III	lysine req.	4
✓ lys-4	IV	lysine req.	4
✓ met-3	III	methionine req.	2, 4, 10
met-4	IV	methionine req.	4
nia	II	nitrate non-ut.	14
nic	IV	nicotinic acid req.	4
nii	VI	nitrate non-ut.	14
✓ nor	VII	norsolorinic acid accumulation	12, 13
✓ pab	V	p-aminobenzoic acid req.	4, 10
✓ pdx	VI	pyridoxin req.	2, 4, 10
✓ phe	III	phenylalanine req.	10
✓ pro	I	proline req.	2, 4, 10
✓ t	IV	tan conidia	1, 2, 4
✓ thi	I	thiamine req.	4, 10
ts (see #241-pg2)	VIII	temperature sensitive	
✓ w	II	white conidia	1, 2, 4
ylo (see #152)	III	yellow conidia	4

1. Leaich, Laurie and K. E. Papa. 1974. Aflatoxins in mutants of Aspergillus flavus. Mycopathologia et Mycologia Applicata 52: 223-229.

2. Papa, K. E. 1973. The parasexual cycle in Aspergillus flavus. Mycologia 65: 1201-1205.

3. Leaich, Laurie L. and K. E. Papa. 1975. Identification of Diploids of Aspergillus flavus by the nuclear condition of conidia. Mycologia 67: 674-678.

4. Papa, K. E. 1976. Linkage groups in Aspergillus flavus. Mycologia 68: 159-165.

5. Papa, K. E. 1977. A mutant of Aspergillus flavus producing more aflatoxin B_2 than B_1. Applied and Environmental Microbiology 33: 206.

6. Papa, K. E. 1977. Genetic analysis of a mutant of Aspergillus flavus producing more aflatoxin B_2 than B_1. Mycologia 69: 556-562.

7. Papa, K. E. 1977. Genetics of aflatoxin production in Aspergillus flavus: Linkage between a gene for a high B_2:B_1 ratio and the histidine locus on linkage group VIII. Mycologia 69: 1185-1190.

8. Papa, K. E. 1978. The parasexual cycle in Aspergillus parasiticus. Mycologia 70: 766-773.

9. Papa, Kenneth E. 1979. Genetics of Aspergillus flavus: Complementation and mapping of aflatoxin mutants. Genetical Research 34: 1-9.

10. Papa, K. E. 1980. Dominant aflatoxin mutant of Aspergillus flavus. J. Gen. Microbiol 113: 279-282.

11. Foudin, L. L., K. E. Papa, and R. T. Hanlin. 1981. Nuclear behavior during conidiogenesis in Aspergillus flavus. Canadian Journal of Botany 59: 2116-2120.

12. Papa, K. E. 1982. Norsolorinic acid mutant of Aspergillus flavus. J. Gen. Microbiol. 128: 1345-1348.

13. Papa, K. E. 1984. Genetics of Aspergillus flavus: Linkage of aflatoxin mutants. Can. J. Microbiol. 30: 67-73.

14. Papa, K. E. 1986. Heterokaryon incompatibility in Aspergillus flavus. Mycologia 78: in press.

For: Genetics of Pathogenic Fungi

(G. S. Sidhu, ed). Vol. 6

Advances in Plant Pathology

Genetics of Aflatoxigenic Aspergillus species

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I. INTRODUCTION

The genus Aspergillus is both common and cosmopolitan. The many known species are classified within eighteen "Groups" by Raper and Fennell (1965) in the major taxonomic treatment of the genus. The "A. flavus Group" consists of a number of closely related yellow-green molds; the precise number of distinguishable species is a matter of dispute among taxonomists.

Economically the four most important species within the "A. flavus group" are A. flavus, A. parasiticus, A. oryzae and A. sojae. A. oryzae and A. sojae are "good" species. Sometimes known as the "koji molds" these fungi are used in the preparation of Oriental condiments and drinks such as soy sauce, saké and miso. A. oryzae is on the GRAS list ("Generally Regarded as Safe") of the U. S. Food and Drug Administration. Several major industrial amylases and proteases are isolated from A. oryzae fermentations (Bennett, 1985 a,b).

A. flavus and A. parasiticus are "bad" species. They produce aflatoxins, a group of pharmacologically active secondary metabolites which are highly toxic, carcinogenic, and mutagenic. → Chemically the aflatoxins are substituted coumarins containing the reactive difuran moiety. The major aflatoxins are called B_1, B_2, G_1, and G_2 based on their respective blue and green fluorescence under long wave ultraviolet light and their relative chromatographic mobilities. Typically, aflatoxin B_1 is the major metabolite produced

by aflatoxigenic strains, and most studies concerning the biological activity of aflatoxin have concentrated on this metabolite. The early history of aflatoxin research is thoroughly reviewed in Goldblatt (1969).

In the mycotoxin and plant pathology literature, the term "A. flavus group" has been used loosely in a collective sense for the various isolates and strains that are potentially aflatoxigenic, not to encompass the formal taxonomic unit delineated in Raper and Fennell (1965). Many researchers do not distinguish between A. flavus and A. parasiticus, choosing to call all aflatoxigenic molds "A. flavus". We will follow the practice of using "A. flavus group" in this limited sense, to describe strains and isolates of A. flavus and A. parasiticus.

II. AFLATOXIGENIC MOLDS AS PATHOGENS

The A. flavus group fungi are extremely common molds that can grow on a wide variety of substrates, under a wide range of conditions. In general, A. flavus group fungi are associated with damage to seed crops (grains, legumes, nuts) rather than with fruits and vegetables. The number of substrates from which the mold/and or aflatoxin has been isolated is long and impressive (Ciegler, 1977).

For convenience, the fungi that infest grains have been divided into: 1) field fungi, those which invade crops before harvest, and 2) storage fungi, those associated with post-harvest damage. The storage fungi are primarily saprophytes of the genera Aspergillus and Penicillium (Christensen and Kaufman, 1974). A. flavus

has been traditionally viewed as a storage fungus, and this categorization influenced the direction of much of the early research. As we have learned more and more about the A. flavus group it has become obvious that these molds can and do invade crops in the field, and that aflatoxins can accumulate prior to harvest, especially in peanuts (McDonald and Harkness, 1967; Hanlin, 1985; Hill et al., 1985), cottonseed (McMeans and Ashworth, 1966) and corn (Lillehoj et al., 1976; Payne, 1983). Such field invasion is frequently, but not always, associated with insect damage, drought or other environmental stress. Some evidence suggests that field contamination is more common in warm, wet climates, particularly in regions of subtropical and tropical agriculture (Williams and McDonald, 1983). Attempts to breed cultivars resistant to A. flavus invasion and aflatoxin damage have been made (Mixon and Rodgers, 1973; Mixon, 1981; Widstrom and Zuber, 1983).

One cannot help but respect the metabolic versatility and ecological adaptability of the A. flavus group. In addition to their nearly ubiquitous presence as saprophytes and their success as facultive plant pathogens, these molds are among the agents involved in aspergillosis, a frequently lethal opportunistic infection of Homo sapiens (Rippon, 1982) and are also aggressive insect pathogens (Steinhaus, 1949).

III. SOME TAXONOMIC AND PHYSIOLOGICAL CONSIDERATIONS

Not all wild type strains of A. flavus and A. parasiticus produce aflatoxins. In a literature survey of published studies encompassing 3343 isolates, a total of 1847 or 56% were aflatoxigenic (Bennett, 1982). The amount of aflatoxin produced by aflatoxigenic strains also varies widely. In general, isolates of A. parasiticus are highly toxigenic and produce both B and G aflatoxins, while A. flavus isolates produce only B aflatoxins and contain a greater percentage of non-toxigenic strains (Klich and Pitt, 1985; Hesseltine et al., 1970). Some taxonomists recognize a third aflatoxigenic species, A. toxicarius (Murakami, 1971) but others subsume A . toxicarius within A. flavus or A. parasiticus (Klich and Pitt, 1985). The 16th Edition of the American Type Culture Collection Catalogue (Jong and Gantt 1984) no longer lists a separate heading for A. toxicarius. Early reports that other species of Aspergillus, or species of Penicillium and Mucor produce aflatoxin, have never been confirmed (Detroy et al., 1971).

Substrate influences the amount of aflatoxin produced by toxigenic isolates. Nearly all natural substrates tested allow some aflatoxin formation, with high carbohydrate substrates being the best. In natural habitats, moisture content is the most important limiting variable. A seed moisture content of 15-30% and a relative humidity of 85% or higher are required for aflatoxin production. Optimal temperature range for aflatoxin synthesis is narrower than that required for growth; highest levels of aflatoxin are produced between 25-30°C. See Diener

and Davis (1969) for a review of environmental parameters affecting aflatoxin production.

The Aspergilli are not particularly fastidious and are easy to handle in the laboratory. Members of the A. flavus group are no exception. Recipes for media, and descriptions for single spore isolations, transfer and storage methods, and other routine microbiological maneuvers for aspergilli are given in Raper and Fennell (1965). The most commonly employed minimal medium used in both taxonomic identification and in genetic studies is Czapek-Dox formulated as follows (per liter of water): $NaNO_3$, 3.0 g; K_2HPO_4, 1.0 g; $MgSO_4 \cdot 7H_2O$, 0.5 g; KCl, 0.5 g; $FeSO_4 \cdot 7H_2O$, 0.01 g; sucrose, 30.0 g; agar 20.0 g.

Most complete media devised for molds will support satisfactory growth of A. flavus and A. parasiticus. In our genetic studies, the complete medium used by Bennett is potato dextrose agar supplemented with 0.5% yeast extract. The complete medium used by Papa is Czapek-Dox supplemented with 0.75% malt extract and 0.25% yeast extract. Sodium desoxycholate (0.08-0.096%) may be added to complete medium to restrict colony size. p-Fluorophenylalanine (0.1%) or benlate (3.5-4.0 mg ml^{-1}) may be added to complete medium to induce haploidization in parasexual diploids.

Aspergillus nidulans is one of the best characterized model systems for eukaryotic genetic analysis. Experimental protocols for mutagenesis, enrichment, culture practices, and biochemical analyses developed for A. nidulans usually can be modified for use with species

of the A. flavus group. Strategies developed for studying genetic phenomena in A. nidulans are reviewed in Smith and P eman (1977). Several textbooks devoted to fungal genetics also provide relevant methodologies and references (Esser and Kuenen, 1967; Burnett, 1975; and Fincham et al., 1979).

Many media have been devised for the laboratory production of aflatoxins. Highest yields are obtained with natural substrates (peanuts, rice, wheat) or with complex liquid media containing supplements such as yeast extract or corn steep liquor. Because Czapek-Dox medium is a poor substrate for aflatoxin production, two defined media have been devised especially for this purpose. The medium developed by Adye and Mateles (1964) is formulated as follows (per liter of water): (do not leave space)

KH_2PO_4, 10.0 g; $MgSO_4.7H_2O$, 2.0 g; $Na_2B_4O_7 \cdot 10H_2O$, 0.7 mg; $(NH_4)_6 Mo_7O_{24} \cdot 4H_2O$, 0.5 mg; $Fe_2(SO_4)_3 \cdot 6H_2O$, 10.0 mg; $CuSO_4 \cdot 5H_2O$, 0.11; $ZnSO_4 \cdot 7H_2O$, 17.6 mg; and sucrose, 50.0 g; $(NH_4)_2SO_4$, 3.0 g.

The medium developed by Reddy et al., (1971) is formulated as follows (per liter of water): (do not leave space)

(NH_4SO_4), 3.5 g; KH_2PO_4, 0.75 g; $MgSO_4 \cdot 7H_2O$, 0.35 g; $CaCl_2 \cdot 2H_2O$, 0.75 g; $ZnSO_4 \cdot 7H_2O$, 10.0 mg; $MnCl_2 \cdot 4H_2O$, 5.0 mg; $(NH_4)_2\ Mo_7O_{24} \cdot 9H_2O$, 2.0 mg; $Na_2B_4O_7$, 2 mg; $FeSO_4 \cdot 7H_2O$, 2 mg; sucrose, 85.0 g; L-asparagine, 10.0 g.

Several "quick screening" media facilitate plate assays of putative aflatoxin - producing ability. These are reviewed in Bennett and Deutsch (1985). The most useful one for genetic studies is "Aflatoxin Producing Ability Medium" developed by Hara et al., (1974).

It is a modified Czapek-Dox medium and contains (per liter of water): $(NH_4)H_2PO_4$, 10 g; K_2HPO_4, 1 g; $MgSo_4 \cdot 7H_2O$, 0.5 g ; KCl, 0.5 g; $FeSO_4 \cdot 7H_2O$, 0.01 g; sucrose, 30 g; corn steep liquor, 0.5 g; and $HgCl_2$, 5×10^{-4}M. Inverted Petri plates are viewed under long wave ultraviolet light after 2-10 days of growth. Blue fluorescence in the agar surrounding the colonies is a putative test for aflatoxin production, which is then confirmed by an official method using thin layer chromatography or high performance liquid chromatography, and authentic standards (Walker, 1983).

IV. GENETIC STUDIES

A. General considerations

Both A. flavus and A. parasiticus are imperfect (anamorphic) species with multinucleate conidiospores. As such, neither species offers an advantage over A. nidulans for basic research in fungal genetics. They are of interest because they produce aflatoxins.

The parasexual cycle has been elucidated in both A. flavus (Papa, 1973; Gussack et al., 1977) and A. parasiticus (Papa, 1978; Bennett, 1979), and the genetics of aflatoxigenic molds has been reviewed by Bennett (1982), Bu'Lock (1985) and Bennett and Deutsch (1985). Parasexual analysis has been hampered by the non-random recovery of certain genotypes among segregants from diploids, and by a uniform diameter of haploid and diploid conidiospores which makes classification of segregant ploidy difficult (Leaich and Papa, 1975; Bennett et al., 1980; Foudin et al., 1981). Both fluoro-phenyl alanine and benlate are successful haploidization agents.

B. Aspergillus parasiticus

Three major classes of mutants have been described in A. parasiticus: 1) anthraquinone-accumulating mutants blocked in the aflatoxin pathway, 2) spore color and auxotrophic mutants used as markers in elucidating the parasexual cycle and generating linkage maps and 3) two peculiar classes of variants with lost or attenuated aflatoxigenicity which have been dubbed fan and fluff.

1. Anthraquinone-accumulating mutants. These mutants are blocked in the aflatoxin pathway and accumulate anthraquinone intermediates (Table 1). They all have brightly colored mycelia which can be used as a visual screen in parasexual studies. These mutants have been exploited even more extensively in studies of aflatoxin biosynthesis (Steyn, 1980; Bennett and Christensen, 1983). Each of these anthraquinone-accumulating strains has been deposited in several culture collections, and each one has been designated by a series of slightly different gene symbols in the many published reports on aflatoxin biosynthesis. Bennett confesses to being one of the worst offenders in this proliferation of symbols, and by way of penance, has compiled a comprehensive summary of synonymy in Table 1.

2. Spore color and auxotrophic mutants. Published spore color and auxotrophic mutants of A. parasiticus are listed in Table 2. Mutants from Bennett's and Lennox's laboratories were isolated from different transfers of A. parasiticus SU-1 (ATCC 56775 and ATCC 56856) by ultraviolet light mutagenesis (Bennett, 1979; Lennox and Davis, 1983). Mutants from Papa's laboratory were isolated from a strain of

A. parasiticus found on Georgia pecans by NTG mutagenesis (Papa, 1978).

After parasexual analysis, Papa (1978) assigned seven loci to four linkage groups: I pro; II. nic; III. lys-1, afl-1; IV. gb, lys-2, afl-2. By similar parasexual methods, ten loci were assigned to six linkage groups by Bradshaw et al., (1983): I. yeA II. brA III. whA cysA IV. lysA lysB; V. norA verA; and VI. adeA metA pdxA. Lennox and Davis (1983) performed complementation tests between aflatoxin-deficient mutants and proposed seven complementation groups: adm-4,7; adm-5,8,9; adm-10; adm-11, bwn-1; ver-1; and nor-1. No attempt to cross mutants from Papa's strain of A. parasiticus with the mutants derived from SU-1 have been made, so the rudimentary linkage groups proposed in Papa (1978) and Bradshaw et al., (1983) must be viewed as independent entities.

Each laboratory has followed different nomenclatural conventions for gene symbols. In some cases, the gene symbols are unique, e. g. independently isolated white-spored mutants are designated, respectively, w, wh-1 and w-1 by Papa, Bennett, and Lennox. In other cases there is overlapping usage; e. g. both Papa and Bennett have named different lysine requiring auxotrophs "lys-1", and both Lennox and Bennett have named different adenine-requiring auxotrophs "ade-1".

According to the conventions for gene symbols in A . nidulans (Clutterbuck, 1973), an italicized three letter symbol is used to describe the specific locus that produces a phenotype (e. g., pdx for pyridoxine- requirement); hyphenated numbers designate unmapped mutants (pdx-1); a capital letter immediately following the three

letter symbols designates a mapped gene (e. g., pdxA); and unhyphenated numbers designate alleles (e. g., pdxA1). Bradshaw et al., (1983) modified some of the gene symbols of A. parasiticus to conform to the A. nidulans conventions. Because there are virtually no collections of multiple alleles and because there have been almost no collaborative studies between laboratories, we now feel that these modifications were premature. We recommend, for the present, retention of original gene symbols, or use of the conventions for unmapped genes. For example, we prefer the symbol ver-1 (Bennett, 1979) rather than verA1 (Bradshaw et al., 1983) for the versicolorin-accumulating mutant (see Table 1).

We recognize that a uniform system for nomenclature should be adopted at some point and hope that as more workers become interested in the genetics of aflatoxgenic molds, sufficient numbers of mutants and crossing data will be available to justify revision of published gene symbols. The system adopted for the yeast Saccharomyces cerevisae offers some advantages to the A. nidulans system and before a wholesale change of gene symbols is proposed this system should be considered. For those interested in the subtleties of genetic nomenclatural conventions [illegible] fungi, see Bennett and Lasure (1983) for a comparative summary.

3. Attenuated strains. Experimental induction of attenuated and aflatoxin-negative strains of A. flavus and A. parasiticus can be achieved by successive transfers of mycelial macerates in defined medium (Bennett, 1981; Bennett et al., 1981a, 1986). These peculiar

variants display altered morphology as well as lowered or lost aflatoxigenicity. The characteristic phenotypes are called fan and fluff. The pleiotropic fan or fluff phenotype can be introduced into wild type strains as well as into auxotrophs and marked diploids (Bennett et al., 1981b, 1986). We originally reported that both fan and fluff were non-aflatoxigenic (Bennett et al., 1981a,b; Bennett, 1982); more recent data indicate that the fluff isolates are unstable and revert to aflatoxigenicity (Bennett et al., 1986). The high frequency with which fan and fluff variants are isolated, the pleiotropic nature of their respective phenotypes, and the anomalous behavior of anthraquinone genes (nor-1 and ver-1) in crosses involving fan and fluff are consistent with a model involving genetic transpositions.

C. Aspergillus flavus

Three major classes of mutants have been described in A. flavus: 1) high aflatoxin-B_2 accumulating strains, 2) spore color and auxotrophic mutants used as markers in elucidating the parasexual cycle and generating linkage map data, and 3) aflatoxin-negative mutants. The formal genetics of A. flavus is more developed than that of A. parasiticu and over thirty genes have been mapped to eight linkage groups.

1. High aflatoxin B_2- accumulating strains.

A number of natural isolates of A. flavus accumulate an excess of aflatoxin B_2 over aflatoxin B_1. Van Walbeek et al., (1968) isolated six of these strains from commercial food products (ATCC strains 18166-18171). (do not leave space)

Schroeder and Carlton (1973) isolated a similar variant from black

pepper (ATCC 24109; SRRC 141; Papa 5642), and Gunasekaran (1981) reported a high aflatoxin B_2 strain from the facial scar of a leukemia patient. The strain isolated by Schroeder and Carlton (ATCC 24109) has been used to study the late stages of aflatoxin biosynthesis (Dutton et al., 1985).

Papa (1977a) induced a mutant with a high aflatoxin B_2/ B_1 ratio using nitrosoguanidine. This mutant (afl-B2, originally referred to as HB2) has been linked to the histidine locus on Linkage Group VIII (Papa, 1977a, b, c; 1980).

2. Spore color, auxotrophic and aflatoxin negative mutants.

Published genetic loci of A. flavus, including known linkage assignments, are listed in Table 3. Because this work was all done in Papa's laboratory, there is less confusion with gene symbols than for A. parasiticus. Papa's conventions have been followed in both Tables 3 and 4.

In addition to the loci listed in Table 3 a series of aflatoxin negative mutants has been isolated and mapped. The mutants afl-2, afl-3, afl-5, afl-6, afl-7, afl-8, afl-9, afl-10, afl-11, afl-12, afl-13, and afl-14 are all recessive and non-allelic; no linkages have been determined for these markers (Papa, 1979). Another recessive aflatoxin-negative locus (afl-4) maps to Group II (Papa, 1979; 1980), while afl-15, afl-16, afl-17, afl-19, afl-20, afl-21, afl-22, and afl-25 are all recessive and on Group VII; of these, afl-20 and afl-22 are allelic (Papa, 1979). Finally, afl-1 also maps to Linkage Group VII.

This marker acts as a dominant in diploids, but the dominance is not expressed in heterokaryons (Papa, 1979; 1980; 1984). As noted above, the high aflatoxin-B_2 accumulating mutant, afl-B2, maps to Group VIII (Papa, 1977a, b, c; 1980).

The sequence of markers on Group II is: afl-4 w ad arg-2 (Papa, 1973, 1976, 1979). The sequence of markers on Group VII is: (nor afl-1) leu afl-15 arg-7 afl-17 centromere. It has not been possible to determine whether nor or afl-1 is the terminal locus (Papa, 1979; 1982; 1984). A collection of mutant strains containing mapped loci has been deposited with the American Type Culture Collection (Table 4).

D. Interstrain and Interspecific Crosses

Heterokaryon incompatibility is widespread in the Aspergilli and the A. flavus group. No successful interstrain or interspecific crosses have been reported. Successful heterokaryons are only formed among complementing auxotrophs derived from the same ancestral wild type strain.

One study has specifically addressed heterokaryon incompatibility. Papa (1986) sampled strains of A. flavus from corn collected in fifteen Georgia counties. Auxotrophs of each of 32 strains were used to test all possible pair-wise combinations; 22 different heterokaryon compatibility groups were detected. Strains within the same heterokaryon compatibility group were not restricted to the same geographical area.

In an earlier study, six combinations of auxotrophs from A. flavus PC-7 and A. flavus NRRL 5565 failed to grow, as did twelve interspecific mixtures of auxotrophs of A. flavus and A. parasiticus (Gussack et al,

1977). Protoplast fusions between A. flavus and A. parasiticus auxotrophs were also unsuccessful (Leong et al., 1981).

Workers interested in isolating new mutants of aflatoxigenic molds would do well to select Papa's strain of A. flavus (PC-7) or the SU-1 strain of A. parasiticus. This would help insure that new mutants can be crossed with existing stocks of genetically marked strains.

The American Type Culture Collection contains an extensive lyophilized collection of wild type and mutant A.. flavus and A. parasiticus strains; historical information on each strain is listed in the "Sixteenth Edition of the ATCC Catalogue of Fungi/Yeasts" (Jong and Gantt, 1984). All of these reference strains were recently tested on three different substrates for aflatoxin production: 41% of the A. flavus strains and 85% of the A. parasiticus strains were toxigenic (Wei and Jong, 1986). The variability in aflatoxin-producing potential from wild type isolates remains an important enigma. Our inability to cross different aflatoxigenic strains make it difficult to design experiments to probe the genetic basis of this phenomenon.

V. THE FUTURE

Given the relatively rudimentary level of classical genetic studies on A. flavus and A. parasiticus, it is not surprising that there have been few studies at the molecular level. In fact, the only published molecular studies conducted to date have been taxonomic in intent. Using DNA hybridization, Kurtzman (1985 a, b) reported 100% complementarity between A. flavus and A. oryzae, and 91% complementarity between A. sojae and A. parasiticus. The complementarity between A. flavus and A. parasiticus was 70%. More recently, Klich and Mullaney (1986) found that different restriction patterns were produced after digestion of total DNA from A. flavus and A. oryzae with SmaI. A. parasiticus was not tested.

Out of these taxonomic surveys have come rapid methods for the isolation of DNA from A. flavus-group molds, and it is hoped that these techniques will hasten molecular genetic studies. Several laboratories are attempting to develop transformation systems for A. flavus or A. parasiticus, but at the writing of this paper (July, 1986) no one has yet reported a success. Nevertheless, it is almost inevitable that the power of modern genetic analysis will soon be brought to bear on aflatoxigenic molds. We predict further clarification of the taxonomic relationship of the koji molds to the aflatoxigenic species, and the cloning of an aflatoxin pathway gene in the near future.

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Dr. Kenneth E. Papa died May 10, 1986, at the age of 54. Although he had prepared Tables 3 and 4 before his untimely death, he was unable to contribute to the final writing of the manuscript. Every effort has been made to give a complete and accurate rendition of his pioneering work on the genetics of aflatoxigenic molds, but there may be errors and omissions. For these I take sole responsibility.

Many people helped me go through Dr. Papa's culture collection and laboratory notes. Particular thanks go to Chris Albertin, Wiley Carrett, Richard Hanlin, Branch Howell, Louise Miller and Libby Papa. Arrangements have been made for Dr. Papa's culture collection, including strains not mentioned in this chapter or published elsewhere, to be deposited with the American Type Culture Collection, Rockville, Maryland, the Fungal Genetics Stock Center, University of Kansas Medical Center, Kansas City, Kansas, or The Southern Regional Research Laboratory, New Orleans, Louisiana.

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Table 1. Characterized Anthraquinone-Accumulating Mutants of *Aspergillus parasiticus* Blocked in Aflatoxin Production

Mutant Genotype	Description of mutant stock[a]	Published stock and culture collection numbers[b]
nor-1	Accumulates norsolorinic acid and low levels of aflatoxin. Isolated by UV treatment of brown spored mutant of SU-1 (Bennett and Goldblatt, 1973; Lee *et al.*, 1971)[c]	1-11-79 br-1 red-1; br-1 nor-1; nor-1; NOR-1, SRRC 162; NR A-17996; ATTC 24690
avr-1	Accumulates averufin and low levels of aflatoxin. Isolated by UV treatment of wild type ATTC 15517 (Donkersloot *et al.*, 1972; Lin and Hsieh, 1973)	W 49; *av-1*; *avr-1*; AVR-1; SRRC 165; ATCC 24551
ver-1	Accumulates versicolorin A, versicolorin C, and trace levels of aflatoxin. Isolated by UV treatment of a white spored mutant of SU-1 (Bennett and Goldblatt, 1973; Lee *et al.*, 1975, 1976)	1-11-105 wh-1; wh- wh-1 ver-1, ver-1; VER-1; SRRC 169; NR 16462; ATCC 36537
avn-1	Accumulates averantin and no detectable aflatoxin. Isolated by NTG treatment of 1-11-105 wh-1 (=ver-1) (Bennett *et al.*, (1980). This a "double mutant", with two distinct blocks in the aflatoxin pathway.	ver-mu-39; avn-1; SRRC 163; ATCC 567

[a] Mutagens were ultra-violet light (UV) or nitrosoguanidine (NTG)

[b] SRRC= Southern Regional Research Center; NRRL= Northern Regional Research Center; ATCC= American Type Culture Collection

[c] In addition, several norsolorinic acid-accumulating mutants designated NOR were isolat by Detroy *et al.*, (1973) by NTG treatment of NRRL 2999. A norsolorinic-acid accumulat mutant was also isolated from *A. flavus* (See Tables 3 and 4 this paper).

p-24 (ATCC 56858)	y-11 glu-1 adm-7	yellow	glutamic acid	-	Lennox and Davis (1983)
p-25 (ATCC 56859)	w-1 ade-1 adm-8	white	adenine	-	Lennox and Davis (1983)
p-26 (Atcc 56860)	W-1 ade-1 adm-9	white	adenine	-	Lennox and Davis (1983)
p-27 (ATCC 56861)	w-1 ade-1 adm-10	white	adenine	-	Lennox and Davis (1983)
p-28 (ATCC 56862)	w-1 ade-1 adm-11	white	adenine	-	Lennox and Davis (1983)
-1	ye-1 lys-2 yeA1 lysA2[b]	yellow	lysine	Tr	Bradshaw et al., (1983)

+= producer, - = non-producer; Tr = trace

convention used in Bradshaw et al., (1983)

listed as br-1 red-1 ade-1 in Gussack et al., (1977)

listed as Ap-23 in ATCC update 1985

Table 2. Mutants of *Aspergillus parasiticus*

Strain number	Genotype	Phenotype			Citation
		Spore color	Nutritional requirement	Aflatoxin[a]	
A43-1	*or nic*	orange	nicotinic acid	+	Papa, 1978
A43-7	*or nic afla-1*	orange	nicotinic acid	-	Papa, 1978
B-11-2	*yg lys-1*	yellow green	lysine	+	Papa, 1978
B43-21	*ylo pro*	yellow	proline	+	Papa, 1978
B43-23	*ylo pro afla-1*	yellow	proline	-	Papa, 1978
B144-17	*gb lys-2 afla-2*	green buff	lysine	-	Papa, 1978
B-144-26	*w met afla-2*	white	methionine	-	Papa 1978
A44-16	*w pab*	white	paraminobenzoic acid	?	Leong *et al.*, 1981
y1-1	*ye-1*	yellow	none	+	Bennett (1979)
1-1-6	*ye-1 lys-1*	yellow	lysine	Tr	Bennett (1979) Bennett *et al.*, 1980b
2-1-6	*ye-1 lys-4*	yellow	lysine	Tr	Bennett 1979
w1-2	*wh-1*	white	none	+	Bennett 1979
1-13-18	*wh-1 met-1* = *whA1 metA1*[b]	white	methionine	+	Bennett (1979) Bennett *et al.*, 1980b
1-14-22	*wh-1 cys-1*	white	cysteine	+	Bennett (1979) Bennett *et al.*, (1980b)

14-24	wh-1 pdx-2 (=whA1 pdxA2)[b]	white	pyridoxine	+	Bennett (1979); Bennett et al., 1980
23-114	wh-1 ver-1 lys-7	white	lysine	-	Bennett (1979); Bennett et al., 1980
22-103	wh-1 ver-1 cys-5	white	cysteine	-	Bennett (1979); Bennett et al., 1980
23-110	wh-1 ver-1 arg-2	white	arginine	-	Bennett (1979); Bennett et al., 1980
22-102	wh-1 ver-1 ser-1	white	serine	-	Bennett (1979); Bennett et al., 1980
-2	br-1	brown	none	+	Bennett (1979); Bennett et al., 1980
11-7	br-1 pdx-1 (= brA1 pdxA1)[b]	brown	pyridoxine	+	Bennett (1979); Bennett et al., 1980
19-78	br-1 nor-1 lys-5	brown	lysine	Tr	Bennett (1979); Bennett et al., 1980
16-51	br-1 nor-1 ade-1[c] (= brA1 norA1 adeA1)[b]	brown	adenine	+	Bennett (1979); Bennett et al., 1980
19-80	br-1 red-1 arg-1	brown	arginine	+	Gussack et al., (1977)
22-100	wh-1 yel-1 lys-6 (= whA1 ver A1 lysB6)[b]	white	lysine	-	Gussack et al., (1977)
-14	y-11 glu-1	yellow	glutamic acid acid	+	Lennox and Davis (1983)
-16	w-1 ade-1	white	adenine	+	Lennox and Davis (1983)
-11	bwn-1	green	none	-	Lennox and Davis (1983)
-22 (ATCC 56857)[d]	y-11 glu-1 adm-4	yellow	glutamic acid	-	Lennox and Davis (1983)
-23	y-11 glu-1 adm-5	yellow	glutamic acid	-	Lennox and Davis (1983)

Table 3. Genetic Loci of *Aspergillus flavus*

Gene symbol	Linkage group	Phenotype	Citations
ad	II	adenine requirement	Papa (1973, 197 1980)
arg-2	II	arginine requirement	Papa (1973, 197
arg-4	IV	arginine requirement	Papa (1976)
arg-7	VII	arginine requirement	Papa (1984)
arom	IV	aromatic metabolites requirement	Papa (1976)
bi	III	biotin requirement	Papa (1976)
cnx	?	nitrate and hypoxanthine non-utilizing	Papa (1986)
fwn	II	fawn conidia	Papa (1976)
his	VIII	histidine requirement	Papa (1977c, 19
iv	VII	isoleucine/valine requirement	Papa (1976, 198
leu	VII	leucine requirement	Papa (1973, 197
lys-3	III	lysine requirement	Papa (1976)
lys-4	IV	lysine requirement	Papa (1976)
met-3	III	methionine requirement	Papa (1973, 197 1980)
met-4	IV	methionine requirement	Papa (1976)
nia	II	nitrate non-utilizing	Papa (1986)
nic	IV	nicotinic acid requirement	Papa (1976)
nii	VI	nitrate non-utilizing	Papa (1986)
nor	VII	norsolorinic acid accumulation	Papa (1982, 198
pab	V	P-aminobenzoic acid requirement	Papa (1976, 198
pdx	VI	pyridoxin requirement	Papa (1973, 197 1980)
phe	III	phenylalanine requirement	Papa (1980)

pro	I	proline requirement	Papa (1973, 1976, 1980)
t	IV	tan conidia	Leaich and Papa (1974) Papa (1973, 1976)
thi	I	thiamine requirement	Papa (1976, 1980)
ts	VIII	temperature sensitive	
w	II	white conidia	Leaich and Papa (1974) Papa (1973, 1976)
ylo	III	yellow conidia	Papa (1976)

Table 4. Mutant Strains of Aspergillus flavus Deposited with the American Type Culture Collection (ATCC)

ATCC number	Linkage group markers							
	I	II	III	IV	V	VI	VII	VIII
36081	-	bi	-	t	-	pdx	-	afl-B2
44617	-	-	-	t	-	-	afl-1 leu	-
44618	-	afl-4	-	t	-	pdx	-	-
46107	-	w	-	-	-	pdx	-	-
46108	-	w	-	-	pab	-	-	-
46109	-	w	-	-	-	-	-	his
46110	-	w	-	-	-	-	iv	-
46111	pro	w	-	-	-	-	-	-
46112	-	w	phe	-	-	-	-	-
46113	-	w ad	-	-	-	-	-	-
46114	-	w	met-3	-	-	-	-	-
46115	thi	w	-	-	-	-	-	-
46116	-	w	-	-	-	pdx	-	afl-B
60040	-	w	-	lys-4	-	-	nor	-
60041	-	w	-	-	-	-	arg-7	-
60042	-	w	-	-	-	-	arg-7 afl-15	-
60043	-	-	-	t	-	-	leu	-
60044	-	arg-2	-	t	-	-	afl-16	1
60045	-	w	-	-	-	pdx	afl-21	-
60046	-	-	-	t	-	pdx	leu	-
60047	-	w	-	-	-	pdx	leu	-
60048	pro	-	met-3	t	-	-	-	his
60049	pro	w	met-3	-	pab	-	-	his

JOURNAL ARTICLES - K. E. Papa

1. Papa, K. E., J. H. Williams, and D. G. Hanway. 1961. Effectiveness of selection for quantitative characters in the third generation following irradiation of soybean seeds with X-rays and thermal neutrons. Crop Science 1: 87-90.

   - no isolates identified.

2. Papa, K. E., A. M. Srb and W. T. Federer. 1966. Selection for increased growth rate in inter- and intra-strain crosses of Neurospora. Heredity 21: 595-613.

St. Louis Strains 74A & 77a	D Bonner, Yale
Honduras Strains HON 3A	RN Storer, Hondures
HON IA	SR Freiberg, Hondures
Philippines Strains 3-723-3A	FT Orillo & HR Everett, Phili.
3-723-5a	

3. Papa, K. E., A. M. Srb and W. T. Federer. 1967. Inheritance of growth rate in Neurospora crassa: Reverse selection in an improved strain. Heredity 22: 285-296.

   Hon 3A and 77a

4. Papa, K. E., W. A. Campbell and F. F. Hendrix, Jr. 1967. Sexuality in Pythium sylvaticum: Heterothallism. Mycologia 59: 589-595.

Isolates:	1063-7	
	1063-8	
	1063-10	from Tennessee
	1063-11	
	56	from Mississippi

5. Papa, K. E. 1969. Auxotrophic mutants of Cochliobolus carbonum. Mycologia 61: 799-807.

   4 strains from Nelson at NC State University not identified

6. Papa, K. E. 1970. Inheritance of growth rate in Neurospora crassa-crosses between previously selected lines. Canadian Journal of Genetics and Cytology 12 (1): 1-9.

Honduras	1) HON3A	2) Hon 1a
St Lawrence	1) 74A	2) 77a

7. Papa, K. E. 1971. Growth rate in Neurospora crassa: Linkage of polygenes. Genetica 42: 181-186.

   Used line from cross of HON 3a X 77a

8. Papa, K. E. 1971. Continuous selection of linear growth rate on Neurospora crassa. Journal of Heredity 62: 87-89.

   Crosses: HON 1a/HON3a
   77a/74a
   HON3A/77a

- cont -

9. Leaich, Laurie and K. E. Papa. 1974. Aflatoxins in mutants of Aspergillus flavus. Mycopathogia et Mycologia Applicata 52: 223-229.

Stock culture: PC7
produced 183 morphological + 33 auxotrophic mutants by UV.

10. Papa, K. E. 1973. The parasexual cycle in Aspergillus flavus. Mycologia 65: 1201-1205.

Probably PC7 stock: white & tan mutants (UV)
Diploids identified: arg + t + / + ad + w
met = t + / + ad + w
met + t + / + prol + w
leu + T + / + pdx + w

11. Leaich, Laurie L. and K. E. Papa. 1975. Identification of Diploids of Aspergillus flavus by the nuclear condition of conidia. Mycologia 67: 674-678.

Wild type PC7 from pecans - R. T. Hanlin
developed 7 haploid mutants identified by white 1-4 and tan 1-4.

12. Papa, K. E. 1976. Linkage groups in Aspergillus flavus. Mycologia 68: 159-165.

Stock culture PC 7 (R. T. Hanlin: UGA) 16 different auxotrophs not identified (UV).

13. Papa, K. E. 1977. A mutant of Aspergillus flavus producing more aflatoxin B_2 then B_1. Applied and Environmental Microbiology 33: 206.

Original stock: PC7
tan bi pdx $\xrightarrow{NG}$ HB2: B_2/B_1 = 7.1
ATCC #36081:234 (34-4)

14. Hendrix, F. F., Jr. and K. E. Papa. 1974. Taxonomy and Genetics of the Genus Pythium. Proc. Amer. Phytopath. Soc. 1: 200-207.

no isolates identified

15. Papa, K. E. 1977. Genetic analysis of a mutant of Aspergillus flavus producing more aflatoxin B_2 than B_1. Mycologia 69: 556-562.

used: pdx bi t HB2 ATCC 36081: 234 (34-4)
crosses: a) nic w #264
b) pab w
c) pro w
d) leu w #205
e) pab ylo #777

16. Papa, K. E. 1977. Genetics of aflatoxin production in Aspergillus flavus: Linkage between a gene for a high B_2: B_1 ratio and the histidine locus on linkage group VIII. Mycologia 69: 1185-1190.

- cont -

See Bk III p5 6/18/79 (HB2 = Hi B2 Afl production)

1) pro w met pob
2) w pdx leu (#271?)
3) t his (#116:T38)
4) tHB2 (36081:234) X w pdx (46107:470)→ w pdx HB2 (46116:271)

17. Papa, K. E. 1978. The parasexual cycle in Aspergillus parasiticus. Mycologia 70: 766-773.

"A" and "B": original stock cultures of Pecan Group. Isolates - mutants per NG

orange	nic	+	A43-1	fr 5325-43
or	nic	Afl-1	A43-7	#621 –
ylo gr	lys-1	+	B11-2	fr 5319-11
ylo	pro	+	B43-21	fr 5319-43
ylo	pro	Afl-1	B43-23	#617 –
gr buff	lys-2	Afl-2	B144-17	#619 –
w	met	Afl-2	B144-27	fr ~~5319-144~~ #624

Diploids (#610): A43-7/B144-17; B43-23/B144-17; B43-23/B144-26; A43-7/B43-23; B11-2/B42-23; B43-23/B144-26 (#609); B43-1/B43-21

18. Papa, Kenneth E. 1979. Genetics of Aspergillus flavus: Complementation and mapping of aflatoxin mutants. Genetical Research 34: 1-9.

Testers: #700 pro w met t pab his

w t leu

#827 ATCC 60040 nor lys w

Parents: t leu 60043:109 (5T-18); t pdx 241 (T37-10); ylo pab 177 (16-7); w met 88 (A-14-1); w nic 425 (~~w nic~~ 5); fwn arom 178 (a-17)

Mutants:

t leu afl 1 #649	t pdx afl 4 #241	w met afl 8 #655	w nic afl 11 658
t leu afl 2 650	t pdx afla 5 244	w met afl 9 656	w nic afl 12 659
t leu afl 3 651	ylo pab afl 6 652	w met afl 10 657	afl 1 44617:649
fwn arom afl 14 654	ylo pab afl 7 653		afl 4 44618:241

19. Papa, K. E. 1980. Dominant aflatoxin mutant of Aspergillus flavus. J. Gen. Microbiol. 118: 279-282.

Mutants produced by NG

afl 1	leu	t	ATCC 44617:649	IV	w	ATCC 46110:516
afl 4	pdx	t	44618:241	pro	w	46111:83
afl B2	pdx	w	46116:271	phe	w	46112:176
	pdx	w	46107:470	ad	w	46113:79
	pab	w	46108:460	met	w	46114:434
	his	w	46108:804	thi	w	46115:78

- cont -

20. Foundin, L. L., K. E. Papa, and R. T. Hanlin. 1981. Nuclear behavior during conidiogenesis in Aspergillus flavus. Canadian Journal of Botany 59: 2116-2120.

Continued PC7 and white and tan mutants.

21. E. J. Mullaney and K. E. Papa. 1982. Heterokaryons among strains of Neurospora crassa with different linear growth rates. The Journal of Heredity 73: 245-245.

Isolates from these crosses: HON 1a/HON3A
77a/74a
HON 3a/77a

22. Papa, K. E. 1982. Norsolorinic acid mutant of Aspergillus flavus. J. Gen. Microbiol. 128: 1345-1348.

Strains used:

		NG	
1)	w lys → 1 N (w lys nor)		ATCC 60040: 827
Diploids:	2)	t pdx leu	60046:491
	3)	t leu	60043:109 (5t-18)
	4)	t leu afl-1	44617:649 (5T-18-2)
	5)	t arg	118 (T44)

23. Papa, K. E. 1984. Genetics of Aspergillus flavus: Linkage of aflatoxin mutants. Can. J. Microbiol. 30: 68-73.

Testers:

pro w met pab his	60049: 592
pro met t pab his	60048: 579
w pdx leu	60047: 506
t pdx leu	60046: 491
t leu	60043: 109 (5T-18)
w arg-7	60041: 86 (31a-25)
w lys nor	60040: 827 (1-N:31a-6-2)
t leu afl 1	44617: 649 (5T-18-2)

Aflatoxin Mutants:

w arg-7 afl 15	60042: 86-1
t arg-2	60044: 118-1 (T44)
w ad	~~60044~~: 79-1 (31a-18)
t arg-2	~~60044~~: 118-2 (T44-7) [log bk I 10.22.70]
w ad	~~60044~~: 79-4 (31a-18) ?
w pdx	60045: 271-1
w ad	~~60045~~: 79-3 (31a-18) ?
w pdx	~~60045~~: 271-2 (#19 from 34-4 + 16-7)

Haploid Segregants:

lys t nor	1017:(1N/109)-22	pro t	(79-2/579)-20
w pab his	1025:(118-1/592)-20	pro t	1020:(271-1/579)-3
met t	1028:(79-1/579)-33	met t pab his	(271-2/579)-16
w his	1029:(118-2/592)-10		

24. Papa, K. E. 1986. Heterokaryon incompatibility in Aspergillus flavus. Mycologia 78: 98-101.

No isolates identified.

= END =

TABLE OF CONTENTS - SILICA GEL LOG

- cont -

# 841-892	In container	XXVIII	Selections
# 893-940		XXIX	Selections
# 941-986		XXX	Selections
# 987-1029		XXXI	Selections
# 1030-1056		32	Selections
# 1057-1085		33	Selections
# 1086-1149		34	Selections
# 1150-1204		35	Selections
# 1205-1262		36	Selections
# 1263-		37	Selections

- end -

Nutritional requirements - vitamins or amino acids

pdx - pyroxidine

ribo - ribonucleic acid

cys - cystine

met - methionine

ser - serine

paba - para-amino benzoic acid

arg - arginine

lys - lysine

bi - biotin

ad - adenine

his - histidine

leu - leucine

nic - nicitinamide

Hx - hypoxanthine

pan - pantothenate

prol - proline

cit - L citrulline

arom - aromatics

tryp - tryptophane

glu - glucose

thi - thiamine

iv - isoleucine/valine

anthr - anthranilic acid

tyr - tyrosine

orn - ornithine

comp - complete media

I-l - Isoleucine

Øal or phe - phenalalanine

- cont -

Colors

Lg - lg light green

t - tan

ylo - yellow

ylo-or - yellow orange

A - albino

W - white

fwn-f -fawn

gt - golden tan

or - orange

Rf - running front of spot on TLC plates

nor - norsolorinic acid

NG - nitrosaguanidine

(np) NP - non producer of aflatoxin

su - suppressor mutant - possibly prevented aflatoxin production - blocked pathway?

afl 1-4 - aflatoxin 1 etc. 2, 3, 4

- end -

1-208 all derived from PC-7

1-60 in container I (silica gel 11/16/71)

* 1.	PC-7	original isolates from pecans (R. T. Hanlin)	
2.	PC3-76	cys$^-$ met$^-$	green
3.	PC3-234	ser$^-$	g
4.	PC3-241	paba$^-$	g
5.	PC3-264	arg$^-$	g
6.	Lg-80	Lg = light green prototroph	
7.	Lg-81	lys$^-$	
8.	Lg-82	arg$^-$	
9.	Lg-83	cys-hist?	
	Lg-84	cys + met	
10.	Lg-85	cys + met	
11.	Lg-86	leu	
12.	Lg-87	met	
13.	Lg-88	met	
14.	Lg-89	met	
15.	Lg-90	Lys	
16.	Lg-91	bi leaky	
17.	Lg-91-1	multiple requirements	
18.	Lg-91-2	bi	
19.	Lg-91-3	casein	
20.	Lg 91-4	bi	
21.	Lg 91-5	bi	
22.	Lg 91-6	met	
23.	Lg 92	cys + met	
24.	Lg 93	lys	
25.	Lg 94	ad	
26.	Lg 96	ad	

27.	Lg 97	?
28.	Lg 98	ser leaky
29.	Lg 99	?
30.	Lg 100	?
31.	Lg 101	leu
32.	Lg 102	ribo
33.	Lg 103	ad leaky
34.	3-255	light green prototroph
35.	3-255-1	nic
36.	3-255-2	?
37.	3-255-3	paba (green)
38.	3-255-4	multiple requirements
39.	3-255-5	lys (very leaky)
40.	3-255-6	paba
41.	3-255-7	lys albino (fluffy)
42.	3-255-8	paba, green leaky
43.	3-255-9	?
44.	3-255-13	paba green
45.	3-255-14	paba green
46.	3-255-15	nic very leaky
47.	3-255-16	cys-met
48.	3-255-17	paba g
49.	3-255-18	paba g
50.	3-255-19	paba g
51.	3-255-20	bi g leaky
52.	3-255-21	paba g
53.	3-255-22	paba g
54.	3-255-23	paba g

55. 3-255-24 paba t
56. 3-255-25 bi, g, leaky
57. 3-255-26 paba, g
58. 3-255-27 paba g
59. 3-255-28 paba g
60. 3-255-29 paba g
61. 31a albino prototroph
62. 31a-1 met-cys
63. 31a-2 met
64. 31a-3 multiple requirements
65. 31a-4 pdx
66. 31a-5 met (leaky)
67. 31a-6 lys (lys-4)
68. 31a-7 ad
69. 31a-8 ad
70. 31a-9 multiple requirements
71. 31a-10 nic
72. 31a-11 pan leaky
73. 31a-12 bi leaky
74. 31a-13 paba
75. 31a-14 paba
76. 31a-15 nic
77. 31a-16 nic
78. 31a-17 thi
79. 31a-18 ad
80. 31a-19 bi
81. 31a-20 ?
82. 31a-21 met

83. 31a-22 prol (slight growth on arg)

84. 31a-23 prol (slight growth on arg)

85. 31a-24 lys

86. 31a-25 (arg-7) arg (no compl with #18) on VII # 18 = arg-7
grows on orn, cit, + arg

87. A29-10 met A = albino

88. A14-1 met (met-4)

89. ~~A19-3 met~~ LOST

90. A30-6 cys-met met-2

91. A7-2 ?

92. A13-3 arg (arg-4)

93. ~~5t tan prototroph~~ LOST

94. 5t-1 met (met-3)

95. 5t-2 bi

96. 5t-3 ad

97. 5t-4 met

98. 5t-5 ad

99. 5t-7 pdx

100. 5t-8 lys (lys-3)

101. 5t-9 asparagine (slight on glu-may be inhibited on comp.)

102. 5t-10 uracil leaky

103. 5t-12 ?

104. 5t-13 nic

105. 5t-14 ad

106. 5t-15 ad

107. 5t-16 nic

108. 5t-17 paba

109. 5t-18 leu

110.	5t-19	ad	
111.	T41	bi?	T = tan
112.	T37	pdx	
113.	T39	ad?	
114.	T53	?	
115.	T40	lys	
116.	T38	hist	
117.	T45	?	
118.	T44	arg (arg-2) grows on orn, cit, and arg	
119.	Lg-71	morphological mutants 119-139 all Lg	
120.	-64		
121.	-32		
122.	-62		
123.	-65		
124.	-22		
125.	-46		
126.	-43		
127.	-42		
128.	-68		
129.	-61		
130.	-27		
131.	-70		
132.	-39		
133.	-44		
134.	-38		
135.	-20		
136.	-58		
137.	-17		
138.	-41		
139.	-51		

140 PC 26-1 140-147 all PC

141. 3-125

142. 58-2

143. 67-8

144. 5b

145. 23-4

146. 210-42

147. 3-216

148. 21-3 albino

149. 26-4 albino

150. 11-3 albino

151. 28-7 albino

152. T54 tan

153. T19

154. T-6

155. T-5

156. T-24

157. T-13

158. T-48

159. T-51

160. 31a M_1

161. M_2

162. M_3

163. M_4

164. 31a-29

165. 5T-60

166. 5T-51

167. 31a-30

168. 5T-52

169. 16-5 greenish ylo from (5T-16 ylo) from 5t

170. 5T-f "FAWN"

171. 5T-38 (2, arom$^-$)

172. 31a-9 paba w

173. 31a-10 paba w

174. a-10 paba fawn from 5t

175. 31a-5 ∅ al w

176. 31a-6 ∅ al w

177. 16-7 paba$^-$ ylo from 5t (via 5t-16 ylo)

178. a-17 a-17 arom$^-$ f

179. 5T-38 arom t

180. a-25 arom f

181. a-13 paba f

182. 5t-10 met + cys t

183. 31-55 bi w

184. 5t-1 pdx t

185. 31-49a lys w

186. 5t-33 lys t

187. 31-36b nic tryp w

188. a-15a nic f

189. 31a-25 met w

190. 31-59b ad w

191. a-1 nic f

192. a-26a paba f

193. 5T-35 amino acid(s)? t

194. 31-50 nic w

195. 31-23b leaky arg, glu prol, asp. w

196. 31a-21 nic w

197. 16-27 bi⁻ ylo from (5t)

198. 31a-51a arg + prol w

199. 31-8 lys w

200. 31-48 met cys w

201. a-20 nic f

202. 31-19 pdx w

203. 5t-7 nic t

204. a-28b nic f

205. 5T-36 met t

206. 5T-37 amino acid(s)? t

207. 5T-38 (1) arom t

208. 5T-40 nucleate?

209. 28-1 red pigment w from 5642

210. 114-1 (67) prol⁻ leaky green from 5642

211. 79-1 (110) prol⁻ t from 5642

212. 5642 produces only B_2 - from Schroader & Carlton (Appl. Microbiol.) (probably A. parasiticus) 25: 146-148, 1973)

213. lys-2 ylo A. parasiticus from Joan Bennett, Tulane

214. pdx-1 br-1 " " "

215. ad-1 br-1, red-1" " " norsolorinic

216. 5319 prototrophs from R. T. Hanlin

217. 5325

218. 5329

219. 5351

220. 5332

221. 5337

222. 5350

223. 5359

224. 5350-14 white prototroph from 5350

225. 5350-39 ylo prototroph B > G

226. 5350-14 (1) ad^{-1} w

227. 5350-14 (3) met^- w

228. 5350-14 (27) met^- w

229. 5350-39 (2) ad^- ylo-w

230. 5350-39 (14) met^- org

231. Diploid 5350-14 (1) + 5350-39 (14)

232. 5350-39 (22) ad^- ylo-w

233. 5350-39 (58) met^- org

234. 34-4 (1) pdx^- bi^- from #34 [isolate from (31a-17 + 5T-9)]
$B_2/B_1 > 1$ (NG as mutagen)

235. 34-4 (2) $B_2/B_1 > 1$

236. 34-4 (3) $B_2/B_1 > 1$

237. 34-18 low B_1 (~0) from #34

238. ~~34-26 high B_1 (~16,000) from #34~~ LOST

239. 35-6 thi^- from #35 [isolate from 31a-17 + 5T-17]

240. T37-3 low B_1 from T37 (NG as mutagen)

241. T37-10 B_1 = 0 pdx afl-4 Ts 1

242. T37-13 pdx^-

243. T37-14

244. T37-17 B_1 ~0 afl-5

245. T37-17a

246. T37-17b

247. T37-18 high B_1

248. #40 from (T37-13 + 31a-22) pdx^- low B_1 red pigment

249. 34-8 (B_1 - 14,000) from #34

250. Diploid (T37-17 + 31a-22)

251. Diploid (T37-13 + 31a-22)

Box V

252. Diploid (T37-17 + 31a-14)

253. Diploid (T37-17 + 31a-19)

254. 34-15 high B_1 (10,000) from #34

~~255. 34-8 low B_1 from #35~~ LOST

256. Diploid (T37-14 + 31a-22)

~~257. #4 from (T37-13 + 31a-22) low B_1 red pigment~~ LOST

258. Diploid (#4 above + 31a-22)

259. Diploid (#4 + 31a-14)

260. Diploid (#4 + #18, leu^-)

261. Diploid (#4 + #9, nic^-)

261a. Diploid (# + 31a-19)

262. Diploid (34-4 + 31a-14)

263. Diploid (34-4 + 31a-19)

264. Diploid (34-4 + #9, nic^-)

265. Diploid (34-4 + #18, leu^-)

~~266. Diploid (34-4 + 31a-22)~~ LOST

267. Diploid (34-4 + 16-7)

268. #5 leu^- $B_2/B_1 > 1$ from (34-4 + #18) W

269. #34 pdx^- leu^- $B_2/B_1 > 1$ from (34-4 + #18) W

270. #13 $paba^-$ pdx^- $B_2/B_1 > 1$ from (34-4 + 31a-14)

271. #19 pdx^- $B_2/B_1 > 1$ from (34-4 + 31a-14)

272. #109 pdx^- $B_2/B_1 > 1$ from (34-4 + 31a-22)

273. #25 pdx^- bi^- $B_2/B_1 > 1$ from (34-4 + 31a-19)

274. #31 bi^- t $B_2/B_1 > 1$ " "

275. #38 Bi^- t $B_2/B_1 > 1$ " "

276. #28 pdx^- bi^- $B_2/B_1 > 1$ " "

277. #40 pdx^- nic^- $B_1 = B_2 = 0$ from (34-4 + #9)

278. #50 nic^- t $B_2/B_1 > 1$ ($B_1 + B_2 = 0$) (34-4 + #9)

279. Diploid (34-4 + #5, above)

280. Diploid (#25 + #5)

281. Diploid (#40 + #5)

282. Diploid (#50 + #5)

283. Diploid (#31 + #5)

284. Diploid (#19 + #50)

285. #42 leu^- w $B_2/B_1 > 1$ from (#50 + #5, above)

286. Diploids: T44 + 31a-22

287. 5T-2 + met^- $pro1^-$ pdx^-

288. T37 + 31a-22

289. 5T-18 + 31a-14

290. 5T-1 + 31a-19 (2)

291. 5T-1 + 31a-17

292. 5T-1 + 31a-18

293. T37 + 31a-17

294. 31a-22 + 5T-2

295. 5T-17 + met^- $pro1^-$ pdx^-

296. 31a-22 + 5T-13

297. 31a-15 + 5T-18

298. 5T-1 + A30-6

299. T44 + met^- $pro1^-$

300. 31a-22 + 5T-17

301. T44 + pdx^- met (t)

302. D5 = 5T-1 + 31a-22

303. D17 = T44 + A30-6

304. D25 = T44 + A30-6

305. D7 = 5T-1 + 31a-22

306. D28 = T44 + Lg 82

307. D16 = T44 + A30-6

308. Diploids: D26 = T44 + A30-6

309. 31a-22 + T44

310. D15 = Lg 82 + A30-6

311. 5T-13 + met$^-$ pro1$^-$ pdx$^-$

312. 31a-15 + 5T-17

313. 5T-13 + 31a-22

314. D8 = T44 + A30-6

315. 5T-17 + A13-3

316. met$^-$ pro1$^-$ + pdx$^-$ cys (t)

317. 5T-2 + 31a-17

318. 31a-17 + met$^-$ pro1$^-$ pdx$^-$

319. 31a-15 + T37

320. 5T-9 + 31a-17

321. 5T-13 + 31a-17

322. 5T-9 + A14-1

323. 5T-15 + met$^-$ pro1$^-$ pdx$^-$

324. Diploids: 5T-17 + 31a-22

325. 5T-18 + 31a-17

326. 5T-9 + 31a-22

327. 31a-15 + 5T-1

328. 5T-18 + A14-1

329. 5T-1 + 31a-19 (w)

330. T37 + 31a-19

331. 31a-19 + met$^-$ pro1$^-$ pdx$^-$

332. 31a-17 + #1 (w) #1 (f16rom 5T-1 + 31a-22) pro1$^-$

333. 5T-1 + 31a-22

334. 31a-19 + T44

335. 5T-1 + 31a-19 (1)

336. Diploids: 5T-18 + #40 #40 pdx^- from T37 + A30-6

337. 31a-17 + 5T-17 (w), #25

338. 5T-9 + #40 (t) #40 pdx^- from T37 + A30-6

339. 31a-22 + 5T-18

340. 5T-9 + 31a-14

341. T37 + A14-1

342. D27 = T44 + Lg82

343. 31a-17 + 5T-17 (w) #35

344. T44 + A14-1

345. 5T-1 + A13-3

346. 5T-38 + A13-3

347. D12 = Lg82 + A30-6

348. D5 pro1 + pdx^- met^- (t)

349. 31a-13 + T37

350. 5T-18 + A13-3 (1)

351. 16-7 + a-17 (2)

352. a-17 + T37

353. 5T-38 + 31a-19

354. 31a-19 + #34 #34 = thi from 5T-9 + 31a-17

355. 16-7 + T37

356. 5T-9 + A13-3

357. 5T-18 + A13-3 (2)

358. 31a-19 + 16-7

359. 5T-38 + 31a-22

360. #10 + 5T-8 #10 = $paba^-$ $pro1^-$ met^-

361. 5T-9 + #4 #4 = leu^- from 5T-18

362. 16-7 + A14-1

363. 5T-18 + 31a-19

364. Diploids: 16-7 + a-17 (1)

365. 5T-9 + 31a-9

366. 5T-38 + #9 #9 = nic^-

367. 31a-6 (Ø al) + #1 #1 $prol^-$

368. #18 + 5T-9 #18 = leu^-

369. a-17 + A14-1

370. 31a-6 (Ø al) + T37

371. a-17 + 5T-18

372. 5T-18 + #9 #9 = nic^-

373. 31c-18 + T44

374. #5 + 31a-18 #5 =

375. #1 + 31a-18

376. 5T-38 + 31a-14

377. #44 + 31a-18 #44 arg^- cys^-

378. 5T-38 + 31a-18

379. T44 + a-17

380. #18 + 5T-38 #18 = leu^-

= PARENTS =

381. Diploids: 5T-9 + #9

382. 9-17 + 5T-9

383. 5T-38 + #32 #32 = iv^-

384. #13 + a-25 #13 = $paba^-$ $prol^-$ met^-

385. 5T-38 + #40 #40 = pdx^-

386. a-17 + 5T-1

~~387. a-17 + 5T-18~~ lost

388. 31a-18 - 16-7

389. Isolates: #21 ad^- cit^- w from 31a-18 + T44 → ad^- + NG → cd^- cit^-
(No linkage) leaky

390. Isolates: #18 ad^- arg^- w " " ad^- arg^-
(No linkage) arg^- linked to leu = (arg-7) NG → ad^- orn^-

391. #14 ad^- orn w " " " ad^- orn^-
(No linkage) - leaky

392. #4 (A14-1 + 16-7) B_1 = 500

393. #40 (T37 + 16-7) B_1 = 0

394. #6 (A14-1 + 16-7) B_1 = 2500

395. #32 (5T-38 + #18) B_1 = 4500

396. #34 (31a-19 + T37) B_1 = 4500

397. #48 leu^- t^- B_1 = 2000

398. #22 (5T-38 + 31a-18) B_1 = 4000

399. #55 (A14-1 + 16-7) B_1 = 0

400. #10 (5T-38 + 31a-18) B_1 = 2500

401. #45 (5T-9 + #18) B_1 = 2800

402. #35 (T37 + 16-7) B_1 = 4500 $paba^-$

403. #40 $paba^-$ iv t (5T-9 + 31a-14)

404. #20 prol iv w (5T-9 + 31a-22)

405. #15 leu paba t (5T-18 + 31a-14)

406. #37 leu met w (5T-18 + A14-1)

407. #1 pdx iv w (5T-9 + #40) #40 = pdx^-

408. #40 $arom^-$ bi^- t (5T-38 + 31a-19)

409. #28 $arom^-$ prol w (5T-38 + 31a-22)

410. #56 $arom^-$ t (a-25 + #13)

411. #6 pdx^- ylo (16-7 + T37)

412. #7 paba ylo (16-7 + T37)

413. 69 lys prol paba met t (#10 + 5T -8)

414. 33 arom prol t (5T-38 + 31a-22)

415. 54 iv^- bi^- t (5T-9 + 31a-19)

416. 16 pdx^- f (a-17 + T37)

417. omit

418.	8	arom f	(a-17 + T37)
419.	43	arom$^-$ t	(#13 + a-25)
420.	35	pdx$^-$ arom$^-$ t	(a-17 + T37)
421.	8	arom$^-$ bi$^-$ w	(5T-38 + 31a-19)
422.	1	arg pdx t	(T44 + pdx$^-$ met$^-$)
423.	52	arg pdx t	(T44 + pdx$^-$ met$^-$)
524.	70	arg pdx met (slow) t	(T44 + pdx$^-$ met$^-$)
425.	9	nic w	(5T-13 + 31a-19)
426.	T-1	met$^-$ prol$^-$	(5T-1 + 31a-22)
427.	4	prol nic w	(31a-22 + 5T-13)
428.	8	prol leu t	(31a-22 + 5T-18)
429.	1	nic t	(31a-15 + 5T-1)
430.	22	paba met w	(met prol pdx + 5T-17)
431.	2	bi nic w	(5T-13 + 31a-19)
432.	W-2	met$^-$ prol$^-$	(5T-1 + 31a-22)
433.	31	met bi prol pdx w	(met prol pdx + 31a-19)
434.	58	met w	(31a-15 + 5T-1)
435.	w-1	met prol	(5T-1 + 31a-22)
436.	10	paba prol met w	(met prol pdx + 5T-17)
437.	13	paba prol met t	(met prod pdx + 5T-17)
438.	76	arg$^-$ met$^-$ t	(T44 + pdx$^-$ met$^-$)
439.	16	paba prol t	(met prol pdx + 5T-17)
440.	18	ad met w	(5T-1 + 31a-18)
441.	2	arg met t	(T44 + A14-1)
442.	100	nic met t	(nic #1 + #37 met$^-$ bi$^-$)
443.	63	arg met t	(T44 + pdx$^-$ met$^-$)
444.	10	met pdx t	(met$^-$ prol$^-$ + T37)
445.	2	prol t	(5T-1 + 31a-22)
446.		omit	
447			
448			
449			

450.	59	thi t	(5T-18 + 31a-17)
451.	1	pdx w	(T37 + A14-1)
452.	34	thi t	(5T-9 + 31a-17)
453.	1	prol t	(5T-1 + 31a-22)
454.		met t	[(T44) + (T37 + ?)]
455.	82	met g	(5T - 18 + A14-1)
456.	23	prol pdx w	(T37 + 31a-22)
457.	115	arg pdx met w	(T44 + pdx met)
458.	37	met bi w	(5T-1 + 31a-19)
459.	24	prol cys w	[(T37 + A30-a) + (5T-1 + 31a-22)]
460.	17	paba w	(met prol pdx + 5T-17)
461.	55	bi t	(5T-13 + 31a-19)
462.	47	paba t	(5T-18 + 31a-14)
463.	1	bi t	(5T-1 + 31a-19)
464.	9	prol leu w	(31a-22 + 5T-18)
465.	15	paba prol w	(met prol pdx + 5T-17)
466.	1	ad w t	(31a-18 + T44)
467.	18	leu w	(5T-18 + #40)
468.	21	bi prol w	(met prol pdx + 31a-19)
469.		bi paba w	(5T-17 + 31a-19)
470.	2	pdx w	(T37 + A30-6)
471.	79	leu thi t	(5T-18 + 31a-17)
472.	9	leu paba w	(5T-18 + 31a-14)
473.	1	met w	(5T-1 + 31a-22)
474.	20	pdx met w	(T37 + A30-6)
475.		pdx met w	" "
476.	17	prol pdx t	(met prol + 37)
477.	6	bi met prol pdx w	(met prol pdx + 31a-19)

478.	44	nic met t	(mic #1 + met⁻ ki⁻ #37)
479.	37	bi nic t	(5T-13 + 31a-19)
480.	9	met arg t	(met prol + T44)
481.	10	bi w	(5T-2 + 31a-17)
482.	104	prol cys w	[(T37 + A30-6) + (5T-1 + 31a-22)]
483.	1	pdx met w	(T37 + A14-1)
484.	85	met lt g.	(5T-18 + A14-1)
485.	86	met lt t	" "
486.	8	thi nic w	(5T-13 + 31a-17)
487.	1	prol nic t	(31a-22 + 5T-13)
488.	4	prol pdx t	T37 + 31a-22
489.	76	thi nic t	5T-13 + 31a-17
490.	37	thi pada t	
491.	6	leu pdx t	(5T-18 + #40)
492.	2	bi thi w	(5T-2 + 31a-17)
493.	t-2	met prol	
494.	34	paba met w	(met prol pdx + 5T-17)
495.	40	pdx w	(T37 + A30-6)
496.	14	bi pdx t	(met prol pdx + 31a-19)
497.	3	prol paba t	(31a-22 + 5T-17)
498.	27	ad met w	(5T-1 + 31a-18)
499.	6	leu w	(5T-18 + 31a-14)
500.		pdx pale g	[(Lg 82) + (T37 + A30 - 6)]
501.	9	w⁻ t⁻ ad	31a-18 + T44
502.	9	nic paba w	31a-15 + 5T-17
503.	4	prol paba w	31a-22 + 5T-17
504.	9	pdx thi w	met prol pdx + 31c-17
505.	1	bi prol t	met prol pdx + 31a-19

Bx XV

506.	22	leu pdx w	5T-18 + #40
507.	2	pdx bi w	T37 + 31a-19
508.	44	bi paba t	5T-17 + 31a-19
509.	1	pdx bi t	T37 + 31a-19
510.	4	leu w	5T-18 + 31a-17
511.	35	leu met	5T-18 + A14-1
512.	26	bi pdx w	met prol pdx + 31a-19
513.	2	leu thi w	5T-18 + 31a-17
514.	4	thi I-l/v w	5T-9 + 31a-17
515.	35	iv/thi t	5T-9 + 31a-17
516.	32	iv w	5T-9 + 31a-17
517.	10	paba prod pdx met w	(met prol pdx + 5T-17)
518.	17	ad pdx or ad pdx prol met w	(met prol pdx + 5T-15)
519.	3	paba iv w	5T-9 + 31a-14
520.	46	prol iv t	(5T-9 + 31a-22)
521.	7	arom⁻ met w	9-17 + A14-1
522.	66	lys prol met paba t	(#10 + 5T-8)
523.	39	lys prol w	" "
524.	9	arom pdx f	a-17 + T37
525.	5	leu arg w	5T-18 + A13-3
526.	45	leu arg w	" "
527.	15	arom ylo	16-7 + a-17
528.	39	Ø al t	(31a-6 = Ø + # 1)
529.	4	arom w	5T-38 + 31a-22
530.	18	arom w	5T-38 + A13-3
531.	16	Ø al pdx⁻ w	(31a-6 = Ø + T37)
532.	44	arg cys t	D26
533.	5	arom w	5T-38 + 31a-18

534.	9	paba f	(16-7 + a-17)
535.	15	arom g	5T-38 + 31a-18
536.	66	arg g	31a-18 + T44
537.	10	nic iv w	(5T-9 + #9 nic)
538.	44	arg g	D25
539.	63	arg ltg	31a-18 + T44
540.	7	arom ad w	(5T-38 + 31a-18)
541.	37	nic iv t	(5T-9 + #9 nic)
542.	33	Ø al pdx t	(31a-6 = Ø + T37)
543.	30	Ø al t	" "
544.	12	pdx arom w	(5T-38 + #40)
545.	34-4 (1)	high B_2	(from 3 single spore transfers) Feb. 1977
546.	34-4 (2)	"	"
547.	34-4 (3)	"	"
548.	34-4 (4)	"	"
549.	34-4 (5)	"	"
550.	34-4 (7)	"	"
551.	34-4 (9)	"	"
552.	34-4 (11)	"	"
553.	#35	met pro pdx w	(10 X 6)
554.	#70	leu met pdx t	(10 X 6)
555.	#28	high B_2	(T44 X #19)
556.	#39	high B_1	(T44 X #19)
557.	D #13 X 31a-6 (Ø a1)		
558.	D #13 X #22 (1)		
559.	D #13 X #22 (2)		
560.	D #13 X 31a-5 (Øa1) (1)		
561.	D #6 X 31a-5 (Øa1) (1)		

562. D #6 X 31a-5 (Øa1) (2)

563. D T38 + #22 (1)

564. D T38 + #10 (2)

565. D T38 + #10 (1)

566. D T38 + #22 (2)

567. #8 leu paba pdx t (10 X 6)

568. #27 leu paba pdx w (10 X 6)

569. #31 leu paba pro w (10 X 6)

570. D #10 X #6 (1)

571. D #10 X #6 (2)

572. D #13 X 31a-5 (2)

573. A83-7 his

574. A83-6 his

575. A83-4 his

576. A83-3 his

577. OMIT

578. A83-1 his

579. #51 t (T38 X #10) pab$^-$ pro$^-$ met$^-$ his$^-$ t

580. #4 leu pab prol t (10 X 6)

581. B188-9 anthr lgt.t

582. B188-2 anthr w

583. B188-1 anthr w

584. A118 tyr

585. #20 (#13 X #22)

586. D 31a-18 X #39 (Øa1)

587. D 34-4 X 31a-5

588. C65-31 B1 only-his

589. A103 thi

590. #5 Øal paba pro w

591. #62 w (#32 X #22)

592. #1 w pab pro met his (T38 X #10)

593. B144-30 (A)

594. D B144-26 X B43-21

595. A122-2 or amino acid

596. HERE

597. D #1 pro X 31a-5

598. D T38 X #19

599. D #40 X 31a-22

600. A43-27 nic

601. B11-1

602. C65-16 his

603. C66-29

604. A43-9

605. A108-5

606. D #40 + 16-7

607. D 31a-19 X #39 (2)

608. D B144-17 X B43-21

609. D B144-26 X B43-23

610. D B144-17 + B43-23

611. B11-5

612. A45-14 met

613. HERE

614. B11-3

615. A43-26

616. C53-6 pab

617. B43-23

618. OMIT

619. B144-17 lys

620. #9 (#40 + 31a-22) nic⁻ t

621. A43-7 ——— orange nic afl-1

622. C65-15

623. B43-2

624. B144-26 ——— w-met Afl-2

625. A43-8

626. B144-30 (C)

627. D 5T-18 X 31a-5 (Øal)

628. B144-30 (B)

629. B144-30 (D)

630. B50-2

631. B27-14

632. C53-30 paba lemon buff low producer (close to NP)

633. 24551-4 pab

634. 18168-46 ad

635. 18168

636. 24551

637. OMIT

638. Diploid 1-17 + A14-1

639. OMIT

640. A44-26 pab t np

641. A43-9 nic ylo-or np —

642. C53-5 pab or np

643. C53-23 pab or np

644. C53-26 pab w np

645. C56-12 ad or buff np

646. C66-30 pro olive np

647.	B50-20	leu	gn buff	np		
648.	B21-4	arg	or	np		
649.	5T-18-2	leu	t	np	afl-1	ts4
650.	5T-18-6	leu	t	np	afl-2	
651.	5T-18-7	leu	t	np	afl-3	
652.	16-7-4	pab	ylo	np	afl-6	
653.	16-7-8	pab	lgt ylo	np	afl-7	
654.	A17-19	arom	fawn	np	afl-14	
655.	A14-1-3	met	w	np	afl-8	
656.	A-14-1-4	met	w	np	afl-9	
657.	A14-1-5	met	w	np	afl-10	
658.	9-2	nic	w	np	afl-11	
659.	9-6	nic	w	np	afl-12	
660.	9-7	nic	w	np	afl-13	
661.	18168-46-10		ad	t	B_2	
662.	18168-46-2	ad	w		B_2	
663.	24551-4-4	pab	w	low B & G	averufin	
664.	24551-4-10	pab	ylo	low B & G		
665.	24551-2	pdx				
666.	24551-6	bi				
667.	18168-27	nic				
668.	18168-68	met				
669.	18168-67	lys				
670.	omit					
671.	18168-33	leu				
672.	18168-45	met				
673.	75 (C66-17 X C70-46)	g buff	pro	met		
674.	54 (C65-24 X C70-46)	or buff	his	met		

675. 1 (C65-20 X c70-46) or his met

676. 96 (Cgg-17 X C70-46) or buff pro met

677. 7 (C66-17 X C70-46) or pro met

678. 28 (B43-6 X B11-2) W pro lys

679. 61 (B43-6 X B11-2) or pro lys

680. 34 (C65-24 X C70-46) buff his met

681. 61 (A43-1 X B43-21) ylo nic pro

682. 5 (A43-1 X B43-21) or nic pro

683. 2 (A26-7 X A45-13) or ad met

684. 10 (A43-7 X B144-17) lys^- nic^-

685. 86 (A26-7 X A45-13) or^- met^- ad^-

686. 78 (A26-5 X A45-13) or ad met

687. 6 (A26-5 X A45-13) or ad met

688. 43 (B11-6 X B12-8) buff lys^- met^-

689. 89 (B11-6 X B12-8) buff lys^- met^-

690. 17 (C65-31 X C53-30) pab^- his^-

691. 1 (A26-3 X A45-5) w^- ad^- met^-

692. B144-30-D54 ad NP

693. B144-30-D48 leu NP

694. B144-30-C37 pab NP

695. B144-30-B27 arg NP

696. B144-30-A6 pad NP

697. 29 (C66-17 X C7046) arg^- met^-

698. 46 (C53-7 X C70-11) w met^- pab^-

699. #56 (T37-10 + 592) pro^- his^- pdx^- np

700. #32 (T37-10 + 592) pab pro met his np

701. #33 (T37-10 + 467) pdx^- leu^- t np

702. #35 (T37-10 + 467) pdx^- leu^- t np

703. #92 (T37-10 + 592) pro his pdx t np

704. #58 (T37-10 + 592) pab pro met his np

705. #53 (5 X 6) ad$^-$ met$^-$ nic$^-$ or

706. #42 (5 X 6) ad$^-$ met$^-$ nic$^-$ or

707. #43 (5 X 6) ad$^-$ met$^-$ nic$^-$ or

708. #88 5T-18-2 + 592 his leu pro w

709. #91 5T-18-2 + 592 his leu pro w

710. #139 5T-18-2 + 592 leu pro w

711. #50 " " his leu pab pro t

712. #49 42 X 61 (706 X 679) ad met nic lys or

713. #53 42 X 48 (706 X ?) ad met nic his or

714. #74 42 X 48 (700 X ?) ad met nic his or

715. #33 42 X 49 (706 X ?) ad met nic his or

716. #29 " " ad met nic his or

717. 1-11-105-13 requirement? mutant of #722

718. 1-11-105-4 " "

719. 1-11-105-9 met$^-$ or pab$^-$ "

720. 1-11-105-7 met$^-$ or pab$^-$ "

721. 1-11-105-6 nic$^-$ "

722. 1-11-105- wh-1 A parasiticus from J. Bennett, 1978 -accumulates versicolorim A

723. P3 mutants induced in 700 P = PFA resistant

724. P6

725. P9

726. P13

727. P14

728. P15

729. P16

730. P17

731. P19

732. P20

733. P21

734. P22

735. OMIT

736. P24

737. P25

738. P29

739. P35

740. P36

741. T14-2 mutants reduced in 700 T = thiophanate resistant

742. T14

743. T14-9

744. T14-9

745. T14-10

746. T14-4

747. T14-3

748. T14-13

749. T14-15

750. T18-16

751. T18-18

752. T18

753. T19

754. T20

755. B1 good growth on benlate up to 5 µg/ml

756. B2 fair growth up to 5 µg/ml

757. B12 fair growth up to 2.5 µg/ml

758. B14 fair growth up to 2.5 µg/ml

759. B15 " "

760. B17 fair growth up to 2.5 µg/ml

761. C22

762. C30

763. P28

764. 700-59

765. 700-510

766. 700-5-13

767. 86 vol (650 X 700-5) np leu pab w (afl-

768. Diploid (C53-26 + B144-17)

769. #13 ad arg pdx leu w

770. #13 A26-11 + 49

771. #59 A26-11 + 49

772. #68 his arg met w

773. #47 (14 X 491) ad arg pdx leu w

774. 19-1 pdx w afl-b2$^-$ np from #19

775. 19-5 " " prod " " golden pigment Rf-.33

776. 19-8 " " np " "

777. 700-1 afl-4 w (see 700) = same requirements

778. 4-16 leu w np (trace) from #4

779. 16-2 pdx fwn spot within B_1 spot?

780. 16-5 pdx fwn orange spot below B_2 high B_1 none on benzene-acetic acid

781. 16-6 pdx fwn " " no orange spot on benzene acetic acid

782. 17-2 pab w red pigment above B_1 to below B_2 none on benzene

783. 31a-608 $B_2 > B_1$ Ø al w + another requirement pab met w red spot allelic to (#19) 34-4 since diploid w/34-4 is $B_2 > B_1$

✓ = requirement tested

784. ~~31a-18-1 ad w nap afl 17~~ LOST (can be obtained from 1028 leaky (LOST)
784-797 tested on benzene acetic acid

785. 31a-18-2 ad w np leaky ✓

786. 32-2 iv w np ✓

787. 32-3 iv w np ✓

788. 4n-1 nic w np leaky ✓

789. 4n-7 nic w np leaky ✓

790. 59-6 thi t np leaky ✓

791. 59-18 thi t np (trace) ✓

792. 31a-17-8 thi w np ✓

793. 31a-17-11 thi w np ✓

794. 5T-38-12 nic t prod (red pigment) ✓
no red pigment on benzene acetic acid

795. 5T-38-13 nic t np (trace) ✓

796. 31a-25-3 arg w np ✓ afl=15

797. 31a-25-6 arg w np ✓

798. 8 bi t selected from (5T-18 + 31a-19)

799. 17 bi t " " "

800. 38 (C66-7 + C70-27) pro met or

801. 67 (" ") pro met ylo

802. 1 (C66-7 + C70-11) pro met w

805-815 tested on benzene acetic acid 817-836 retested

803. 28 (C65-14 + C66-24) his pro ylo

804. #6 his w (from dip T38 + 22)

805. 4n-12 nic w np (leaky) ✓
4n-12 has three faint yellow spots on benzene-acetic acid

806. 4n-5 nic w np ✓

807. 5T-38-10 nic t afl^{+} pigment ✓

808. 30-22 Øal t np leaky ✓

809. 5T-17-12 pab t trace leaky ✓

810. 5T-17-10 pab t afl^+

811. 5T-17-4 pab t afl^+ trace of B_1 ✓

812. 59-7 thi t afl^+ ✓

813. 59-9 thi t afl^+ ✓

814. T44-13 arg t np ✓

815. T44-7 arg t afl^+ (strange spots on TLC) ✓
yellow spot Rf. 16

816. #17 $afl\text{-}1^-$ $afl\text{-}b2^-$ leu t ✓

817. 31a-18-8 al w np ✓ (leaky)

818. 31a-18-5 al w np ✓

819. 4n-16 nic w np ✓

820. 31a-25-9 arg w np not tested on benzene-acetic acid ✓

821. 31a-18-10 ad w tr on retest produced 765 $\mu g/B_1/g$ ✓

822. 32-10 iv w low toxin ✓

823. 32-9 iv w np ✓

824. 31a-22-11 pro w np ✓

825. 31a-22-25 pro w np ✓

826. 31a-22-26 pro w np ✓

827. 31a-6-2 lys lys w produces red spot (norsolorinic acid) on benzene acetic acid red spot has Rf 43

828. 2-22 pro t low toxin ✓

829. 5T-17-14 pab t np trace B_1 on retest ✓

830. 5T-17-16 pab t np ✓

831. 5T-17-20 pab t trace w/red spot no red spot on benzene acetic acid

832. T38-4 his t low toxin

833. 8-1 nic w high B_1 (ylo, blue, red spots) ✓
on retest benzene acetic acid only light yellow and blue

834. 5T-8-5 lys t low toxin

835. 5T-8-7 lys t high B_1 (ylo - red, red spots)
same ylo spot as T44-7 (Rf=) retest high B_1 Rf_{ylo}^{21} $blue^{37}$ org^{39} org^{42}

836. 5T-8-8 lys t low toxin

837. D 31a-17-11 + 5T-18-2

838. D 31a-17-11 + 5T-17-12

839. D1 19-1 + 5T-38-10

840. D1 19-5 + 5T-18-2

841. D1 T44-13 + 700-1

af1-1 = 5T-18-2
af1-4 = T37-10

842. D1 31a-18-1 + af1-4

843. D1 31a-6-8 + 34-4 (no complimentation - diploid is $B_2 > B_1$ as is both singely)

844. D1 19-8 + 30-22

845. D2 19-1 + 30-22

846. D1 31a-17-11 + 5T-38-10

847. D1 19-1 + 5T-17-12

848. D1 19-8 + 5T-38-10

849. D1 31a-25-3 + af1-4

850. D1 31a-18-1 + af1-1

851. D2 31a-17-8 + 5T-18-2

852. 59-1 thi t np

853. T38-2 hist np not tested on benzene-acetic

854. 31a-22-13 pri w trace

855. 2-27 pro t np np on retest ✓ not tested on benzene-acetic acid

856. D1 31a-18-5 + af1-1 ✓

857. T44-13 + 710

858. D1 5T-38-10 + 700-1

859. D1 30-22 + 700-1

860. D1 31a-17-8 + T37-10

861. D1 4-16 + T37-10

862. D1 31a-17-8 + 5T-38-10

863. D1 31a-18-10 + af1-1

864. D1 31a-25-3 + af1-1 ✓ 864

865. D1 19-1 + 5T-18-2

866. D1 31a-25-6 + af1-4

867. D1 31a-25-6 + af1-1 867

868. D1 30-22 + 710

869. D 4-16 + 5T-17-12

870. D1 31a-25-9 + af1-4

871. D1 5T-17-10 + 710

872. D1 4-16 + 30-22

873. D2 T44-13 + 19-5

874. D2 31a-18-5 + af1-4

875. D1 19-8 + 5T-17-12

876. D1 19-5 + 704

877. D2 31a-18-10 + af1-4

878. D1 31a-17-8 + 30-22

879. AF10 y1 ben 1 benlate 5 ppm - no success (growth) From Makins in London ↓

880. AF11 w^3 teo^2 met teoquil chloride (Hedoquinium chloride) 0.125 mg/ml

881. AF12 w^3 thi^2 met thiram (tetramethyl thiuran disulfide) 0.125 mg/ml

882. 16-4 pdx fwn low toxin (2 µg B_1)

883. 16-5 pdx fwn low toxin (21 µg B_1)

884. 5T-19-2 ad t low toxin (15 µg B_1)

885. T38-5 his t low toxin (33 µg B_1)

886. D1 2-22 + 31a-18-1

887. D1 793 + 4 (af1)

888. D1 31a-6-2 (lys) + 4 (afl)

889. D1 31a-6-2 (lys) + afl-1 ✓

890. D1 31a-22-26 + afl-4

891. D1 31a-22-11 + afl-4

892. D 700-1 + 794

893. D1 4 + 782

894. D1 4 + 783 (781 704)?

895. D1 779 + 704

896. D1 776 + 704

897. D1 T38-4 + 700-1

898. D1 774 + 704

899. D1 4 + 31a-22-13

900. D1 4 + 820

901. D1 4 + 31a-22-25

902. D1 700-1 + 807

903. D1 700-1 + 795

904. D1 5T-17-12 + 710

905. D1 808 + 700-1

906. D1 700-1 + T38-2

907. D1 780 + 704

908. Af15 y nys1 12 units/ml mycostatin from Mackins (London)

909. D1 4 + 787

910. D1 4 + 786

911. D1 700-1 + 2-27

912. D1 781 + 704 (44783)?

913. D1 4 + 32-9

914. 31a-22-27 (dark pigment-slow growing)

915. D1 30-22 + 506

916. D1 814 + 506

917. D1 796 + 579

918. D1 796 + 491

919. D1 822 + 4

920. D1 16-4 + 704

921. AF16 $\underline{y^2}$ $\underline{cob1}$ cobalt sulphate resistance (6 mg/ml) from Makins in London

922. D1 836 + 710

923. D1 5T-19-12 + 700-1

924. D1 814 + 592

925. D1-4 + 789

926. ver-mu-39 averantin Bennett 7/80 ↓

927. ATCC 36537 ver-1

928. ATCC 15517 averutin (Donkerslotts mutant)

929. ATCC 24690 Nor-1

930. D T44-13 + 506

931. D 5T-17-4 + 31a-6-2

932. D 5T-38-10 + 31a-6-2

933. D 5T-18 + 827

934. D 827 + 491

935. D T44 + 827

936. #60 (5T-38-10 + 31a-6-2)

937. #19 (5T-17-14 + 31a-6-2)

938. #7 (5T-17-14 + 31a-6-2)

939. su 1-17

940. su 1-18

941. su 1-14

942. su 1-23

943. su 1-26

944. su 1-27

945. su 4-19

946. su 4-20

947. su 4-21

948. su 4-23

949. su 4-9

950. su 4-27

951. su 4-28

952. su 4-29

953. su 4-30

954. su 4-32

955. su 4-33

956. su 4-39

957. D (su 1-14 + 592)

958. D9 827 + T44-7

959. D8 827 + T44-7

960. D6 827 + T44-7

961. D4 (827 + 5T-18)-22 + 31a-18-1

962. D2 " "

963. D1 " "

964. 73 (827 + 491) nor lys t

965. 59 (827 + 491) nor lys w

966. 22 (827 + 5T-18) nor lys t

967. 61 (827 + T44) arg t nor

968. 62 (927 + T44) arg lys t nor

969. 17 (659 + 491) afl-12 leu t

970. D T44-70 + 710

971. D3 (827 + 5T-18-2) afl-1
+ nor +/+ nor +

972. D4 ( ) + nor +/+ nor leu (contamin. ?)

973. D (827 + 5T-18)-22 + 31a-18-1 nor/+ het diploid

974. D (827 + 5T-18)-22 + 31a-25-3

975. D (827 + 491)-73 + 31a-25-3

976. D (31a-18-5 + [827 + 5T-18]-22) nor/nor (20-N)

977. 31a-18-5 + (827 + 491)-73 nor g (1-5)

978. 31a-18-5 + (827 + 5T-18)-22 nor w (3-9)

979. D 30-22 + 31a-18-1

980. D 19-1 + T44-7

981. D 31a-25-3 + 31a=18-5

982. D #19 + 5T-18-2

983. D T44-13 + 31a-25-6

984. D 19-8 + T44-13

985. D T37 + 31a-25-6

986. D 31a-25-6 + (31a-18-5 + 579)-20

987. D T44-7 + 31a-25-6

988. D 30-22 + (T44-7 + 592)-20

989. D T44-13 + 19-1

990. D 16-4 + (31a-18-1 + 579)-33

991. D 31a-25-6 + (31a-18-1 + 579)-33

992. D 31a-25-3 + (19-1 + 579)-14

993. D 16-4 + (31a-18-5 + 579)-20

994. D 16-4 + 5T-18-2

995. D 16-4 + T44-7

996. D T44-7 + 31a-18-2

997. D 31a-18-2 + (31a-18-5 + 579)-20

998. D 31a-25-3 + (19-1 + 579)-3

999. D 30-22 + 31a-18-5

1000. D 19-8 + 30-22

1001. D 19-1 + 5T-18

1002. D T44-7 + 31a-18-5

1003. D 19-8 + T44-7

1004. D 30-22 + 31a-25-6

1005. D 5T-18-2 + 19-8

1006. D 19-8 + 5T-18

1007. D 19-8 + (31a-18-5 + 579)-20

1008. D 19-1 + (31a-18-5 + 579)-20

1009. D 19-8 + (31a-18-1 + 579)-33

1010. D 19-1 + (31a-18-1 + 579)-33

1011. D 16-4 + T44-13

1012. D 31a-10-2 + (19-1 + 579)-3

1013. D 31a-18-2 + (19-1 + 579)-14

1014. D T44-7 + 31a-18-1

1015. D 31a-18-5 + T44-13

~~1016. D 31a-25-3 + (31a-18-5 + 579)-20~~ Lost

1017. (827 + 5T-18)-22 lys t nor

1018. (31a-25-6 + 491)-6 arg t af1-23

1019. (31a-25-3 + 579)-22 arg his t af1-15

1020. (19-8 + 579)-16 pab met his t af1-25

1021. D 31a-18-1 + (31a-18-5 + 579)-20

1022. (16-4 + 5T-18)-28 leu t af1-24

~~1023. (659 + 491)-17 leu t af1-12~~ Lost

1024. (31a-25-3 + 579)-16 arg his t af1-15

1025. (T44-7 + 592)-20 his w af1-19

1026. (19-1 + 579)-3 pab pro t af1-21

1027. Omit

1028. (31a-18-1 + 579)-33 met his t afl-17

1029. (T44-7 + 592)-10 his w afl-19

1030. D [31-1 ($\underline{NO_3}^-$ w) + afl-4]

1031. D [31-1 ($\underline{No_3}^-$ w) + T44]

1032. 31-1 $\underline{No_3}^-$ w

1033. 31-4 $\underline{No_2}^-$ w

1034. 31-7 (H8) hypoxanthine w (from 31a) ← PC7
↓
hc group 17 tester

1035. 81-12-17 No_3

1036. 81-12-18 HX

1037. 81-12-33 No_2

1038. 81-1-24 No_3

1039. 81-1-38 No_2

1040. 81-1-41 HX
↓
hc group 1 tester

1041. 81-15a-44 No_3 w

1042. 81-15a-55 No_2 w

1043. 81-156-121 No_3

1044. 81-156-123 No_2

1045. 81-156-124 HX
↓
hc group 5 tester

1046. 81-8-129 No_3

1047. 81-8-131 HX
↓
hc group 4 tester

1048. 81-30a-136 HX

1049. 81-30a-137 No_3

1050. 81-30a-139 No_2

1051. 81-37a-141 HX
↓
hc group 6 tester

1052. 81-32a-142 No_2

1053. 81-13-157 No_3

1054. 81-13-158 No_2

1055. 81-47-213 No_2

1056. 81-47-211 HX
↓
hc group 21 tester

1057. 81-28a-210 HX

1058. 81-28a-208 No_2

1059. 81-28a-207 No_3

1060. 81-46-193 No_2 hc group 3 tester

1061. 81-51-174 HX

1062. 81-51-171 No_3

1063. 81-6-160 No_3
↓
hc group 3 tester

1064. 81-6-159 No_2

1065. 81-49-223 No_2

1066. 81-33b-227 HX

1067. 83-76-269 No_3

1068. 83-96-271 No_3

1069. 83-6-282 No_3

1070. 83-6-284 No_2

1071. 83-50-386 No_3

1072. 83-75-428 No_2

1073. 83-52-456 No_2

1074. 83-52-457 No_3

1075. 84-59c-574 No_2 A. clavatus (formed hets only with 631)

1076. 84-59c-629 No_2 A clavatus (formed hets well with 631; poorly w/630)

1077. 84-59c-630 No_3 " "

1078. 84-59c-631 HX " "

1079. 83-50 wild-type isolates from which nitrate mutants were obtained

1080. 83-52

1081. 83-76

1082. 83-90

1083. 83-6

1084. 83-75

1085. 83-96

1086. 81-1

1087. 81-15a

1088. 81-30a

1089. 81-13

1090. 81-15b

1091. 81-12

1092. 81-28b

1093. 83-47

1094. 81-37a

1095. 81-51

1096. 81-33b

1097. 81-28a

1098. 81-49

1099. 81-8

1100. 81-47

1101. 81-6

1102. 81-46

1103. 81-5

1104. 81-4

1105. 83-14

1106. 83-11

1107. 84-24

1108. 84-23

1109. 83-23

1110. 83-72

1111. 83-89

1112. 81-30b

1113. 81-4-93

1114. 81-4-96 HX hc group 2

1115. 81-5-152

1116. 81-5-154 No_3

1117. 81-30b-177

1118. 83-30b-180

1119. 81-28b-214

1120. 81-28b-216

1121. 83-47-260

1122. 23-47-261

1123. 83-14-373

1124. 83-11-374

1125. 84-24-583

1130-1136 all A. clavatus collected from maize weevils by Doug Dix

1126. 84-24-584 ✓ HX
↓
hc group 23

1127. 83-89-618

1128. 83-72-626 ✓ No_3

1129. 84-23-588

1130. 10-50 ✓ A. clavatus surface contaminent of maize weevil collected 10-22-82, Midville, Ga row 10 in corn field, plant 50

1131. 10-40-1 " "

1132. 22-20 " "

P41

The A. clavatus was in preparation for a graduate student's study on parasexuality. If you ever need any clavatus we have 190 isolates, incl. diploids, which are clearly identified.

gar

1133.	104-20	maize weevils collected 8-31-82 Griffin, Ga.		
1134.	126-60	"		" "
1135.	4-10	"		" "
1136.	26-25	"		10-27-82 "
1137.	47-1	arg⁻	w	(from 31-1 + T44)
1138.	1114-1	w	HX	white
1139.	1114-2	or	HX	leiteous 19b
1140.	1114-3	ol	HX	lt. olive buff 21'''d
1141.	1114-7	ylo	HX	amber 21'b
1142.	1068-9	w	No_3	lt. olive buff 21'''d
1143.	1068-4	ol	No_3	lt. olive buff 21'''d
1144.	1068-3	ylo	No_3	luteous 19b
1145.	1068-2	w	(dirty) No_3	pale buff 19"d*
1146.	1068-1	or	No_3	luteous 19b
1147.	1045-1	ol	HX	primrose 23"d
1148.	1045-2	or	HX	lt. sienna 13i
1149.	1045-5	ylo	HX	amber 21'b
1150.	1047-1	cr	HX	white
1151.	1047-2	ol	HX	primrose 23"d
1152.	1047-3	w	HX	white
1153.	1047-4	ylo	HX	luteous 19b
1154.	1047-8	or	HX	luteous 19b
1155.	1128-4	or	No_3	luteous 19b
1156.	1128-5	ylo	No_3	lt. luteous 19b
1157.	1128-7	w	No_3	white
1158.	116-1	al	No_3	primrose 23"d
1159.	1116-4	or	No_3	dk. luteous 19d
1160.	1116-5	w	No_3	white

*refers to location on A Mycological Colour Chart Rayner

1161.	1126-1	ylo	HX	amber 21'b
1162.	1126-3	w	HX	white
1163.	1126-4	ol	HX	olive buff 2'''d
1164.	1126-5	or	HX	luteous 19b
1165.	1126-6	ol-ylo	HX	dk. amber 21'b
1166.	1126-7	t-g	HX	citrine 21K
~~1167.~~	~~1126-8~~	~~w (dirty)~~	~~HX~~	Lost
1168.	1040-1	w	HX	white
1169.	1040-4	glo-g	HX	dk. amber 21'b
1170.	1040-5	cr	HX	primrose 23"d
1171.	1117-1	or	No_3	lt. sienna 13i
1172.	1117-7	t	No_3	citrine 21K
1173.	1117-8	ylo	No_3	dk. amber 21'b
1174.	1059-1	ol	No_3	primrose 23"d
1175.	1059-2	or	No_3	lt. amber 21'b
1176.	1069-4	w	No_3	pale primrose 23"d
1177.	1069-3	al	No_3	primrose 23"d
1178.	1056-1	or	HX	luteous 19b
1179.	1056-5	ylo	HX	lt. luteous 19b
1180.	1056-6	ol	HX	sulfur yellow 25F
1181.	1056-7	ol-g	HX	olive buff 21'''d
1182.	1056-8	w	HX	white
1183.	1051-4	w (dirty)	HX	very pale buff 19"f
1184.	1051-3	w	HX	white
1185.	1051-2	t	HX	citrine 21K
1186.	1062-3	ylo	No_3	amber 21'b
1187.	1062-5	w	No_3	white

1188. 1062-7 ylo-g No_3 amber 21'b

1189. 1135-775 No_2 A. clavatus

1190. 1130-777 No_3

1191. 1130-778 NX

1192. 1134-781 No_3

1193. 1134-783 HX

1194. 1136-784 No_2

~~1195. 1136-786 HX~~ Lost

1196. 1133-788 No_2

1197. 1133-789 HX

1198. 1132-794 No_3

1199. 1132-797 No_2

1200. 1131-791 No_3

1201. 1131-793 No_2

1202. 1117-1 + 506 (2n)

1203. 1117 + 506 (2n)

1204. 1117-8 + 506 (2n)

1205. 1060-1 No_2

1206. 1060-2 No_2

1207. 1060-3 No_2

1208. 1060-6 No_2

1209. 1035-5 No_3

1210. 1035-6 No_3

1211. 84-78 (725) No_2

1212. 1117-4 w No_3

1213. 1035-7 w No_3

1214. 1064-7 w No_3

1215. 1064-4 or-g No_3

1216. 1064-2 w No_3 (dirty w)

1217. [506 + 1117-1]-8 or pdx No_3

1218. [506 + 1117-8]-67 or pdx No_3 leu

1219. [506 + 117-8]-19 ylo pdx No_3

1220. [506 + 117-8]-36 ylo pdx No_3

1221. A flavus

1222. A. flavus A266 36

1223. " 40

1224. " 23

1225. " 25

1226. " 30

NRRL 3357 from Shane Tucker supplied by D. T. Wicklow - isolated from subterranean seed caches of the desert kangoroo rat - Dipodomgs spectabilis - produce tan-beige sclorotia

1227. A. clavatus 1131-7 arg ? or ang + ?

1228. 1130-15 arg

1229. 1130-4 arg

1230. 1130-1 arg

1231. 1130-8 arg ? or arg + ?

1232. 1132-10 ad ? or ad + ?

1233. 1132-24 arg

1234. 1131-2 arg

1235. 1131-16 arg

1236. 1131-12 arg

1237. 1130-14 leu

1238. 1130-16 leu

1239. 1132-7 arg

1240. 1132-13 arg

1241. 1134-1 ad

1242. 1132-15 leu

1243. 1431 t

1244. 1132 light blue

1245. 1131 w

1246. 1130 w

1247. 1134 w

1248. 1134 t

1249. 1132 w

1250. 1130 golden tan (gt)

1251. 1134-8 arg

1252. 1134-3 arg

1253. 1134-6 arg

1254. 1133- w

1255. 1133-28 ad ? or ad + ?

1256. 1131-12 red arg

1257. 1131-12 w arg

1258. 1131-12 off w arg (bluish w) ?

1259. 1131-12 w arg

1260. 1134-1 ad w

1261. 1135 ad

1262. 1135 arg

1263. 1132 lt bl leu? or double mutant

1264. 1134 leu

1265. 1131 ad

1266. 1133 w arg

1267. 1136 arg

1268. 1132 met? or double mutant no. 1

1269. 1132 met? or double mutant no. 2

1270. 1130 met

1271. 1136 leu? or double mutant no. 1

1272. 1136 " " " no. 2

1273. 1131 met

1274. 1130 ad

1275. 1131 leu leaky

1276. 1132-24 ad w

1277. 1134 met

1278. 1133 leu w

1279. 1132 lt. blue met? or double mutant

1280. 1133 w met? (" ")

1281. 1136 met

1282.	81	81-18 w	h-c group	13 tester
1283.	58	81-17 w	"	12
1284.	46	81-17 w	"	12
1285.	91	81-16	"	"
1286.	118	81-11	"	10
1287.	109	81-9	"	9
1288.	107	81-9	"	9
1289.	133	81-7	"	8
1290.	75	81-2 w	"	7
1291.	67	81-2 w	"	7
1292.	92	81-18 w	"	13
1293.	23	81-20	"	14
1294.	21	81-20	"	14
1295.	128	81-29a	"	15
1296.	186	81-37b	"	20

1297.	187	81-37b	h-c group	20
1298.	196	81-36	"	19
1299.	197	81-36	"	19
1300.	163	81-32	"	18
1301.	204	81-32	"	18
1302.	201	81-29b	"	16
1303.	200	81-29b	"	16
1304.	102	81-52	"	22
1305.	103	81-52	"	22
~~1306.~~		End		
1307.				
1308.				
1309.				
1310.				
1311.				
1312.				