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## New markers and linkage data

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## New markers and linkage data

### Abstract

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Perkins, D. D., M. R. Smith and D. R. Galeazzi.

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have not been completed. Strain T51M171 is probably a point mutant at a new locus, with poor ascospore ripening and viability, but chromosome aberration has not been excluded. The requirements of T51M152(t), T42M59(t), T51M147(t) have been identified and confirmed by H. Inoue and T. Ishikawa (personal communication). Locus assignments for 1003 at act-1, T51M147(t) at asp, and 76P.5 at rib-1 are based on map location rather than direct allelism tests.

Linkage data are given in Tables 2 and 3. [following pages] There concern not only markers in Table 1, but also give new information on other markers and intervals. The usual conventions are followed: the top number of each pair of complementary classes represents progeny of the genotype that contains the wild-type allele of the leftmost marker scored. Regions are numbered from left to right. Where dashes replace numbers, the corresponding classes of segregants were not scored. Interval lengths have usually been rounded to the nearest digit, because it was felt that showing tenths of units conveyed a false impression of precision and predictability.

pi (B101) and col-10 (R2438) are distinctly different in appearance, and are capable of recombination to give true wild-type morphology. It is therefore suggested that separate names be retained, although Srb and Basl (1969 *Neurospora* Newsl. 15: 22) have reported that pi and col-10 do not show complementation with respect to ascus morphology. Genes thr-2 and thr-3 have never recombined in our experience. They were designated separate loci on the basis of phenotypic differences and complementation (Teas 1947 Ph.D. Thesis, Calif. Inst. Technol.; Emerson 1950 Cold Spring Harbor Symp. Quant. Biol. 14:40). Mutant T42M59(t) is designated thr-3 because it resembles thr-3 allele 44104(t) phenotypically and does not resemble thr-2. The mutant spco-15 (R2537), reported to be on III by Garnjobst and Tatum (1967 *Genetics* 57:579), shows no linkage in 111 when extracted from the original strain spco-15; inos A (FGSC# 1799). Possibly the III linkage was due to a reparable aberration.

Recently published linkage data: The following is an incomplete list of linkages that have been published from this and other laboratories since the 1969 tabulation of Perkins et al. in *Genetics* 40: 271.

#### Linkage Group I:

aza-1 (10-20) mt; aza-2 near mt (Jho 1971 *Mol. Gen. Genet.* 114: 156)  
leu-3 (12) mt (1.6) upr-1 (7) org-1 (Tuveson 1972 *Mutat Res.* 15:411)  
mt sru-2 sru-3 al-2 (Seale 1972 *Genetics* 70:385).  
m+ ret-3 arg-3 (Catcheside et al. 1971 *Austral. J. Biol. Sci.* 24: 107)  
cr (1 1) uvs-6 (6) al-2 (Schroeder et al. 1972 *Neurospora* Newsl. 19: 17)  
nit-2 (17) mig tre (20) al-2 (Sussman et al. 1971 *J. Bacteriol.* 108:59)  
ty-2 right of al-2 (Ho 1972 *Neurospora* Newsl. 19: 15)  
or-1 (13) arom-8 (4) R (Turner et al. 1969 *Can. J. Genet. Cytol.* 11:622)

#### Linkage Group II:

worn-1 (2) ff-1 (4) mo (P240at) (Ton 1972 *M. S. Thesis*)

#### Linkage Group III:

prol-1 ff-5 me-8 hist-7 (Tan 1972 *M. S. Thesis*)

#### Linkage Group IV:

cys-10 centromere un-8 (5) col-4 (Perkins et al. 1972 *Neurospora* Newsl. 19:24)  
pdx-1 (2) mtr (1) col-4 (0.2) org-2 (Boone et al. 1970 *Neurospora* Newsl. 16:12)  
cys-10 (25) pyr-1 (3) pdx-1 (2) col-4 (1) arg-2 (16) col-1 (25) uvs-2 (D. A. Smith 1968 *M. S. Thesis*)

#### Linkage Group V:

sp (5) am-1 (0.05) gul-1 (3) hist-1 (Smyth 1970 Ph. D. Thesis, Austral. National Univ.)  
al-3 near arg-8 and inos (Wang et al. 1971 *Neurospora* Newsl. 18:16)  
inos (15) pab-2 (9) pyr-6 (Caroline 1969 *J. Bacteriol.* 100: 1371)

#### Linkage Group VI:

ad-8 (8) ssu-7 (14) ylo-1 (Seale 1972 *Genetics* 70: 385)

#### Linkage Group VII:

nit-3 (31) me-7 (3.5) wc (2.5) aga (27) arg-10 (Morgan 1969 *John Inner Inst., Ann. Rept.* 60:46)  
thi-3 ars-1 (<1) me-7 me-9 wc (Murray 1970 *Genet. Res.* 15: 109)  
nit-3 ssu-4 me-7 ssu-1 Su-1 nt (Seale 1972 *Genetics* 70:385)

We propose henceforth to limit the publication of routine mapping data from this laboratory to the Newsletter, which seems ideally suited for the purpose, unless such data are logically presented in the context of a journal paper devoted to a broader subject.

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Table 1. Mutants previously unassigned to linkage groups.

Locus symbol and name	Isolation No.	Linkage group and arm	Approximate location or evidence of allelism	Phenotype	Origin (strain, mutagen)	Reference to origin
<u>atr-1</u> : aminotriazole-1	RC2(r)	IL	0/39 recombination x <u>suc</u> /	Resistant 3-AT 1 mg/ml Abnormal morphology	74A, diethyl sulfate	M. L. Pall, unpubl.
<u>acr-7</u> : acriflavine-7	P1676(r)	VIR	Near <u>ws-1</u>	Resistant to acriflavine 0.5 mg/ml	Mixed, spontaneous?	
<u>bg</u> : brown ascospore	AR62	IR	R. of <u>un-i</u> (9%)	Autonomous, viable	OR23-1A, UV	
<u>un-9</u> : unknown-9	<u>T54M56</u> (t)	VR	R. of <u>pyr-6</u> (2%)	Irreparable temperature-sensitive (34° vs 25°)	74A, UV	Inoue & Ishikawa, 1970 un(42)
<u>un-10</u>	<u>T42M25</u> (t)	VIIR	R. of <u>wc</u> (7%)	"	74A, UV	" un(11)
<u>un-11</u>	<u>T42M30</u> (t)	VR	0/47 x <u>al-3</u>	"	74A, UV	" un(10)
<u>un-12</u>	<u>T51M118</u> (t)	IVR	0/73 x <u>col-4</u>	"	74A, X-rays	" un(17)
<u>un-13</u>	<u>T42M24</u> (t)	VI	2/106 x <u>ylo-1</u>	"	74A, UV	" un(9)
<u>un(T42M56)</u>	<u>T42M56</u> (t)	VI	0/81 x <u>ylo-1</u>	"	74A, UV	" un(12)
<u>un(T42M69)</u>	<u>T42M69</u> (t)	IL	0/86 x <u>mt</u>	"	74A, UV	" un(16)
<u>un(T51M154)</u>	<u>T51M154</u> (t)	VIL	0/44 x <u>lys-5</u>	"	74A, X-rays	" un(22)
<u>un(T51M171)</u>	<u>T51M171</u> (t)	IIIR	R. of <u>tyr-1</u> (5%)	"	74A, X-rays	" un(25)
<u>un(T54M55)</u>	<u>T54M55</u> (t)	III	Linked <u>acr-2</u> (8%)	"	74A, UV	" un(36)
RECURRENCES:						
<u>acr-2</u>	<u>1001</u> (r)	IIIL	0/46 wt x KH2		SL, UV	Howe & Terry 1962
<u>acr-2</u>	<u>1002</u> (r)	IIIL	0/38 wt x KH2		SL, UV	"
<u>act-1</u> (probable)	<u>1003</u> (r)	IR	Linked <u>aur</u> (10%), M. Flavin		SL, UV	"
<u>asp</u>	<u>T51M147</u> (t)	VR	Between <u>al-3</u> , <u>hist-6</u>	Temperature-sensitive	74A, X-rays	Inoue et al. 1970 un(19)
<u>fl</u>	P4499	IIR	0/37 wt x <u>fl</u> <sup>P</sup>		Mixed, spontaneous	
<u>hist-2</u>	<u>T51M152</u> (t)	IC	0/600 wt x Y152M14	Temperature-sensitive	74A, X-rays	" un(20)
<u>inos</u>	P47231	VR	0/200 wt x 37401		Mixed, spontaneous	
<u>os-1</u>	NM204(t)	IR	0/90 wt x B135	Nearly wild at 25°	Ema, UV	
<u>os-5</u>	P5341	IR	0/82 wt x NM2160		Mixed, spontaneous	
<u>rib-1</u>	76R5	VIR	0/193 x <u>pan-2</u>		Mixed, UV	
<u>thr-3</u> (probable)	<u>T42M59</u> (t)	IIL	0/73 wt x 44104(t)	Temperature-sensitive	74A, UV	Inoue et al. 1970 un(14)
<u>un-2</u>	ALS9(t)	IC	0/87 wt x 46006(t), D. Newmeyer		SL, UV	
<u>wc</u>	P4723w	VIIR	0/47 wt x P829		Mixed, spontaneous	
<u>ylo-1</u>	P5241	VIL	0/38 wt x Y30539y		Mixed, spontaneous	

Table 2. Data from 2- and 3-point crosses.

Zygote genotype and % recombination	Parentals	Crossovers			Isolation Numbers
		1	2	1,2	
<b>LINKAGE GROUP I:</b>					
A - <u>flm-2</u> a - <u>acr-3</u> + 10 1"	5 1"	2 0	2 0	0 0	mt KH14(r) Y256M223
+ <u>flm-2</u> suc + 8	43 6"	7 2			66702 Y256M223
+ <u>flm-2</u> cut + 3 (126 coral)		2			T(I;IV)cut Y256M223
+ <u>aur arom-8</u> flm-2 + + 47 41	17 12	14 1"	9 1"	9 9	Y256M223 34508 DH8
<b>(B. c. Turner)</b>					
A <u>atr-1</u> + a + <u>un-2</u> 10 17		3		0	mt RC2(r) 46006(t)
+ + <u>bs</u> cr <u>un-1</u> + 9 9	27	2	2	1	B123 44409(t) AR62
+ <u>os-5</u> + act-1 + <u>al-1</u> 12 4	3" 33	4 5	2 1	0 0	KH52(r) NM2160 ALS4
+ <u>aur os-1</u> un-7 + + 3 22	2" 24	2 0	6 7	0 0	T53M50(t) 34508 B135
+ <u>al-2 arg-6</u> un-7 + + Selective, un <sup>+</sup> arg <sup>+</sup> . Therefore, <u>un</u> not between.		9	2		T53M50(t) T5300 29997
+ <u>al-2</u> os-5 + 0.4 (206 total)	0 1				NM2160 153"
+ <u>aur</u> os-5 + 6	21 26	3 0			P5341 34508

zygote genotype and % recombination	Parentals	Crossovers			Isolation Numbers
		1	7.	1,2	
<b>LINKAGE GROUP 11:</b>					
+ <u>col-10</u> pi + 1.2	32 48	1 0			B101 R2438
het-c + + het-C pyr-4 ro-3 0.8 (236 total) Therefore <u>ro-3</u> not between.			1 1		het-c 36601 R2354 T(II-V) homozygous
+ <u>ro-3 thr-2</u> pyr-4 + + 2 8	52 64	2 0	4 6	0 0	36601 R2354 35423
+ + <u>da</u> pyr-4 <u>thr-3</u> + 15 3	32 4"	7 5	2 0	0 1	36601 44104(t) R2375
+ + <u>lp</u> pyr-4 <u>thr-3</u> + 15 10	3"	6	4	0	36601 44104(t) P736
+ + <u>m</u> pyr-4 <u>thr-3</u> + 3 10	26	1	3	0	36601 44104(t) NM218
+ <u>thr-3</u> + ro-3 <u>thr-2</u> arg-5 16 17	15 18	6 1	1 4	0 0	R2354 T42M59(t) 35423 27947
+ <u>arg-5 mo</u> thr-2 + + 3 24	23 26	2 0	1" 6	0 0	35423 27947 D309
+ <u>arg-5 mo</u> thr-2 + + 18 2	21 27	7 4	0 1	0 0	35423 27947 NM220
+ <u>arg-5 pe</u> ro-9 + + 3 3	28 -	1 0	1 0	0 0	R2526 27947 Y8743m
+ <u>mo</u> + arg-12 + <u>fl</u> 0 13	31 38	0 0	4 6	0 0	UM107 D309 1.

Table 2 (continued).

Zygote genotype and % recombination	Parentals	Crossovers			Isolation Numbers	Zygote genotype and % recombination	Parentals	Crossovers			Isolation Numbers
		1	2	1,2				1	2	1,2	
LINKAGE GROUP 111:						<u>+</u> <u>leu-5</u> <u>+</u>	45	0	3	0	<b>KH53(r)</b>
<u>+</u> <u>arg-9</u> <u>+</u>	32	0	3	0	9185	<u>act-2</u> <u>+</u> <u>sp</u>	44	1	3	0	45208
Lhi-2 <u>+</u> ro-2	40	0	3	0	35401	1 6					<b>B132</b>
0 8					<b>B20</b>			29	20		83201(L)
<u>+</u> <u>un</u> <u>dow</u>	13	1	5	0	Y6994	<u>+</u> <u>al-3</u> <u>tryp-5</u>					RP100
tyr-1 <u>+</u> <u>+</u>	29	1	8	0	<u>T51M171(t)</u>	inos <u>+</u> <u>+</u>					A420
5 16					<b>P616</b>	Selective, inos <sup>+</sup> tryp <sup>+</sup> . Therefore inos not between.					
<u>+</u> <u>+</u> Chi-4	13	17	0	0	<b>R2537</b>	<u>+</u> <u>al-3</u>	43				<b>89601</b>
spco-15 <u>acr-2</u> <u>+</u>					<b>85902</b>	inos <u>+</u>		1			RP100
> 50 0					<b>KH5</b>	2					
LINKAGE GROUP IV:						<u>+</u> <u>al-3</u>	129				<b>83201(t)</b>
<u>+</u> <u>pyr-1</u>	23	0			<b>T27M9(t)</b>	inos <u>+</u>		1			RP100
un-8 <u>+</u>	24	0			<b>H263</b>	1					
0						<u>+</u> <u>+</u>	45	2			RP100
<u>+</u> <u>pdx</u> <u>un-12</u>	12	27			<b>T27M9 (t)</b>	al-3 <u>tryp-5</u>	37	1			A420
un-8 <u>+</u> <u>+</u>					<b>37803</b>	4					
Selective, un <sup>+</sup> .					<b>T51M118(t)</b>	<u>+</u> <u>un-11</u> <u>+</u>	34	0		0	RP100
Therefore <u>un-12</u>						al-3 <u>+</u> <u>hist-6</u>			13		T42M30(t)
not between.						0 27					Y152M105
<u>+</u> <u>col-4</u> <u>+</u>	35	2	0	0	37803	<u>+</u> <u>pyr-6</u> <u>+</u>	12		1	0	RP100
pdx <u>+</u> <u>un-12</u>	35	1	0	0	70007	al-3 <u>+</u> Mat-6	15	2	1	0	DFC37
4 0					<b>T51M118(t)</b>	19 6					Y152M105
LINKAGE GROUP V:						<u>+</u> <u>asp</u> <u>+</u>	19	6	1	0	RP100
<u>+</u> <u>at</u>	10	9			R2365	al-3 <u>+</u> <u>hist-6</u>	20	5	2	0	T51M147
spco-3 <u>+</u>					<b>M111</b>	21 6					Y152M105
<u>+</u> <u>+</u> <u>+</u>	37	5	5	0	33933	<u>+</u> <u>cot-2</u> <u>pab-2</u>	42	1	5	0	B6
lys-1 <u>aspt</u> <u>iv-1</u>	31	4	10	0	44304(C)	bis <u>+</u> <u>+</u>	38	6	1	0	R1006
10 16					16117	8 6					"193
<u>+</u> <u>act-2</u> <u>leu-5</u>	40	0	0	0	37101	<u>+</u> <u>un-9</u> <u>+</u>	31	0	2	0	DFC37
lys-2 <u>+</u> <u>+</u>	45	0	0	0	<b>KH53(r)</b>	pyr-6 <u>+</u> <u>hist-6</u>	14	1	1	0	T54M96(t)
0 0					45208	2 6					Y152M105
Selective, act <sup>R</sup> leu <sup>+</sup> .	-		9			LINKAGE GROUP "I:					
Therefore <u>leu-5</u> not	-			0		<u>+</u> <u>un</u> <u>+</u>	19	0	0	0	DS6-85
between.						lys-5 <u>+</u> <u>ylo-1</u>	24	0	1	0	T51M154(t)
Selective, lys <sup>+</sup> leu <sup>+</sup> .	-	33	7			0 2					Y30539y
Therefore <u>lys-2</u> not	-					<u>+</u> <u>ylo-1</u>	48	1			T42M24(t)
between.						un-13 <u>+</u>	56	1			Y30539y
						2					

