

New morphological mutants

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New morphological mutants

Abstract

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LINKAGE DATA

Perkins, D. D., C. W. Taylor, D.C. Bennett
and B.C. Turner. New morphological mutants
that have been localized to linkage group.

New morphological mutants have been accumulated in our laboratory over several years. Some that appear potentially useful have been mapped to linkage group, usually by crosses with alcoy and follow-up linkage testers (Neurospora Newsl. 6:22, 1964; 9:11, 1966). Forty-seven such mutants are listed in Table 1, with information on origin, characteristics, and linkage. A few of the mutants have been further localized by 3-point tests (Table 2).

Locus symbols or names have not been assigned because we do not feel that our tests have been adequate for pinpointing mutants within the linkage groups so as to establish that each is at a previously unmapped locus, nor have the mutants been subjected to the necessary tests of allelism with each other or with already named and mapped morphological mutants at established loci. It is unlikely that we will soon obtain the information necessary for locus designations to be made critically. Some of the strains may nevertheless be useful either for investigating morphogenesis or as genetic markers, even without critical information on allelism. The 47 mutants have therefore been deposited with the Fungal Genetics Stock Center in order to make them freely available, but are not listed in the stock list, pending further critical information.

We are grateful to persons named in Table 1 for donation of mutant strains, to D. Newmeyer for linkage data on M184 and P2615, to A. L. Schroeder for data on NM213t and P1163, to Mrs. E. D. Anderson and Mrs. Marie J. Grindle for technical assistance, and to Public Health Grants AI 01462 and K6-GM-4899 for support. - * - Department of Biological Sciences, Stanford University, Stanford, California 94305.

Please Note: The tables for the above paper are on the following five pages.

Table 1. Information on 47 morphological mutants mapped LO linkage group.

Isolation No.	Linkage group	Origin: treatment and strain	Evidence of linkage	Characteristics and remarks	Suggested temporary designation
AR2	IR	Spont., <u>pyr-1 pdx-1</u> x <u>me-1</u> (A. Radford)	0 w.t. recomb./95 x <u>os</u> (B135), which it resembles.	Sensitive to high osmotic pressure.	os(AR2)
AR5	I	UV, <u>pyr-1 pdx-1</u> (A. Radford)	40 units left of <u>aur</u> (Table 2)	Uniform conidiation flat over entire surface of slant. Light pigment.	morph(AR5)
D5	IR	UV, <u>inos</u> (89601) (S. R. Gross)*	18 units right of <u>nic-2</u> (Table 2)	Colonial with restricted growth, no conidiation, little pigment. Free of <u>T(D5)</u> .	col(D5)
M184	I	Spont., <u>pdx-1</u> x <u>col-4</u> (B. D. Maling)	0 recomb./86 x <u>hist-2</u> (Table 2)	Flat surface growth with small wisps of dense growth at top of slant, a few protruding onto glass and conidiating.	morph(M184)
M193-1	IC	From <u>pdx-1</u> x <u>pyr-1</u> (B. D. Maling)	0 w.t. recomb./94 x <u>sn</u> . 0 recomb./17 x <u>hist-2</u>	Flat surface growth; initially forms large balls of conidia at top of slant. Resembles <u>col-4</u> . Distinguishable from <u>sn</u> , but possible allele.	morph(M193-1)
NM203	I	UV, <u>Ema</u> (N. E. Murray)*	10.9 units from <u>sex</u> , probably right (Table 2)	Starts as flat colonial; some spread, but not over entire slant. Late conidiation in thick smooth, coherent masses.	morph(NM203)
NM204t	IR	*	0 w.t. recomb./70 x <u>os</u> (B135) (possibly 2 w.t.)	Temp. sens. Some isolates may overlap wild type at 25°, not 34° or 39°. Some conidiation. Sterile hyphae tend to bleed. Possible <u>os</u> allele.	morph(NM204t)
NM216o	IR	*	0 w.t. recomb./82 x <u>os</u> (NM233t). 1 recomb./129 x <u>al-2</u>	Resembles <u>os</u> (B135); perhaps more conidiation on GCP. Named <u>os-5</u> by Laura R. Livingston, who has evidence of nonallelism.	os(NM216o)
NM216s	I	*	3 recomb./56 x <u>nic-2</u>	Smooth appearance, light pigment, conidia not loose. Aerial growth nearly fills 12 mm tube diameter.	morph(NM216s)
NM233t	IR	*	0 w.t. recomb./130 x <u>os</u> (B135),	Resembles <u>os</u> (B135) at 39°. Nearly w.t. morphology at 25°.	os(NM233t)
0301	IR	+	3 recomb./59 x <u>aur</u>	Light-colored irregular growth in a thick mat, with conidiation throughout.	morph(D301)
P1417	IR	Spont., <u>thi-3</u> x <u>wc</u>	Right of <u>nic-2</u> ; left of <u>ad-9</u> (Table 2)	Leathery pigmented surface growth with scattered conidiation. Conidia later form in rim at top of slant.	morph(P1417)
P1798	IR	Spont., <u>T(I;VII)</u> 17084, <u>thi-1</u> x <u>T(IV;V)45502</u> , <u>pyr-3</u>	6 units right of <u>hisf-2</u> (Table 2)	Resembles <u>ropy</u> . Separated from aberrations.	morph(P1798)
P2615	I	Spont., <u>T(I;II)39311</u> , <u>ser-3</u> x <u>un(b39)</u>	19 units left of <u>al-2</u> (Table 2)	Restricted colonial. No conidia. (separated from aberration.)	col(P2615)
P3282	IR	Spont. from OR8-la x <u>cot-1</u> ; <u>inos A</u>	0 w.t. recomb./60 x <u>os</u> (B135), which it resembles.		os(P3282)
NM201f	II	*	9 recomb./94 x <u>arom-1</u>	Thin, skin-like surface growth without aerial hyphae. Thickest low in slant. Resembles 0318 (V).	morph(NM201f)

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NM218	II	*	6 recomb./38 x <u>arg-5</u>	Flat carpety surface growth, with smooth, velvety puff of deep orange conidia at top of slant.	morph(NM218)
NM220	II	*	10 recomb./66 x <u>arg-5</u>	Characteristic matty conidiation. Min may be preferable to GCP for scoring.	morph(NM220)
D309	II	†	6 recomb./56 x <u>arg-5</u>	Thin transparent pigmented surface growth, free of conidia; irregular, large ragged patches of orange conidia at top of slant.	morph(D309)
B8	IIIR	UV, STA (V. W. Woodward)	5 recomb./73 x <u>tryp-1</u>	Fuzzy, pale-yellow aerial growth without conidia. Free of Ab(B8).	morph(B8)
M126	IIIR	Spont., <u>arg-10 nt</u> x <u>pab-1</u> (B. D. Maling)	1 recomb./71 x <u>tryp-1</u>	Aconidial aerial and surface growth, resembling fluffy. Pigment develops slowly, becoming cream-colored or yellow.	morph(M126)
NM211	IIIR	*	Right of <u>un(83106t)</u> (Table 2)	Smooth, dense, filling 12 mm tube-diameter above slant. Conidia distributed throughout aerial mycelium.	morph(NM211)
NM219	III	*	8 recomb./60 x <u>tryp-1</u>	Thick, spreading aconidial surface growth, later developing blooms of dense smooth orange conidiation high in slant.	morph(NM219)
B235r	IIIR	UV, STA (V. W. Woodward)	3 recomb./59 x <u>tryp-1</u>	Nonspreading colonial. Dense. No conidia. Forms warty, yellow aerial protrusions with age.	col(B235r)
D302	IIIC	†	7 recomb./70 x <u>acr-2</u> 1 recomb./39 x <u>thi-4</u>	Restricted colonial. No conidia.	col(D302)
D308	III	†	24 recomb./76 x <u>tryp-1</u>	Distinctive lush velvety growth hugging surface and forming rim all around edge of slant, to resemble a bird's nest.	morph(D308)
P1710	III	Spont., <u>cot-1</u> x <u>cot-1</u>	18 recomb.170 x <u>tryp-1</u>	Colonial without conidia. Large aerial knobs formed erratically.	morph(P1710)
B28	IVR	UV, STA. (V. W. Woodward)	2 recomb./223 x <u>cot-1</u> . See Table 2 .	Dense, nonconidiating, poorly pigmented, slow-spreading colonial. Called <u>col-5</u> (Garnjobst and Tatum 1967). No allelism test x <u>col-1</u> .	col(B28)
NM119	IVR	*	0 recomb./58 x <u>cot-1</u>	Pale, loose conidiation at top of slant, not below. Poor scorability. Free of <u>T(I;IV)NM119</u> .	morph(NM119)
NM213t	IV	*	Left of <u>cot-1</u> (Table 2)	Reverse temp. sens.: w.t. at 34°, <u>fl</u> -like aconidial at 25°, on min.	morph(NM213t)
D306	IVR	†	Between <u>tryp-4</u> and <u>pan-1</u> (Table 2)	Spreading colonial doesn't entirely cover slant. Conidiates in puffs high in slant. More restricted on GCP than min.	morph(D306)
D314	IVR	t	6 recomb./49 x <u>cot-1</u>	Large flat colonial with defective pigment. May form large aerial knobs high in slant.	morph(D314)
NM359	IVR	*	Between <u>cot-1</u> and <u>cys-4</u> (Table 2)	Irregular spreading colonial doesn't entirely cover agar. Blooms and conidiates in large orange puffs at top of slant, expanding from surface tongue of growth.	morph(NM359)
P1898	IV	Spont., <u>lys(66202)</u> x <u>lys-2</u>	Left of <u>tryp-4</u> (Table 2)	Very light scattered conidiation and weak "ivory" pigmentation.	morph(P1898)

Table 1 - page 3

B107	VR	UV, <u>STA</u> (V. W. Woodward)	0 w.t. recomb./92 x <u>bis</u> (B6)	Some conidiation high in slant. Morphologically distinct from <u>bis</u> , and asci from B107 x <u>bis</u> (B6) are linear. not bulb-shaped: not allelic.	morph(B107)
M111	VC	Spont., <u>tryp-4</u> <u>chol-1</u> x <u>ad-6</u> (B. D. Maling)	Between <u>aspt</u> and <u>lys-1</u> (Table 2)	Conidia in small flecks; later in granular clumps, in crescent at top of slant. Min preferred for scoring. Probably allelic 0307.	morph(M111)
NM221t	VR	*	Between <u>lys-1</u> and <u>val-1</u> (Table 2)	crisp-like. Flat crescent of grainy conidia high in slant. Scorable good on min at 34°, poor on GCP.	morph(NM221t)
D307	VC	†	2 recomb./45 x <u>lys-1</u> 0 w.t. recomb./82 x M111.	Resembles probable allele, "111.	morph(D307)
D315	V	†	10 recomb./37 x <u>inos</u>	Light surface conidiation in small clumps; crescent of grainy conidia at top of slant.	morph(D315)
D318	V	†	8 recomb./37 x <u>inos</u>	Thin, skin-like surface growth without aerial hyphae. Thickest low in slant. Resembles NM201f (II). Scores well at 34°.	morph(D318)
P904	V	Spont., <u>hist-2</u> x <u>erg-4</u>	9 recomb./42 x <u>cot-1</u> in alcoy. 10 recomb., 68 x <u>inos</u> in <u>T(I;VII)S1007</u> , <u>un(55701t)</u> ; <u>T(V;VI)46802</u> <u>inos</u>	Resembles <u>ropy</u> . Not tested for allelism with <u>ro-4</u> .	ro(P904)
P1135	VI	Spont. in germinat- ing ascospore	0 recomb.190 x <u>ylo-1</u>	Twisted "Wiry" hyphae at ascospore germination. Gross morphology de arly scorable: Small yellowish aerial clumps above flat aconidial surface.	morph(P1135)
36703-4-20	"I	Spont., <u>arg-1</u> (367031) x <u>STA</u> (D. Newmeyer)	0 recomb./61 x <u>ylo-1</u>	Creamy-buff pigment; characteristic adherent aerial growth. (Separated from translocations.)	morph(36703-4-20)
C-L2B	VIIL	beta-propiolactone, <u>74A</u> (J. c. Murray)	27 units left of <u>thi-3</u> (Table 2)	Restricted nonconidiating colonial. Described and called <u>mei-1</u> by Murray and Srb (1962). Possible allele: do. not tested.	col(C-L2B)
NM226	VII	*	0 recomb./70 x <u>thi-3</u>	Fine-grained hazy golden aerial growth fills tube diameter high in slant. No loose conidia.	morph(NM226)
P1163	VIIR	Spont., <u>arg-9</u> x <u>ro-3</u>	Between <u>for</u> and <u>arg-10</u> (Table 2)	Dense matty conidia high in slant. Scores better on min than GCP.	morph(P1163)
P1718	VIIR	Spont., <u>cr</u> x <u>leu-3</u> (R156)	2 recomb./39 x <u>nt</u>	Flat, thick surface growth, with irregularly expressed light-colored clumps just above surface. Not tested x <u>sk</u> .	morph(P1718)

Table 1 Footnotes

min = minimal agar medium (Vogel's Medium N), with or without supplement. GCP = glycerol complete agar medium.
recomb. = recombinant random isolate. spont. = spontaneous or segregating from cross where parents did not possess trait. w.t. = wild type. temp. sens. = temperature-sensitive. R = right arm, L = left arm, C = centromere region.

Descriptions are based largely upon gross morphology as observed on agar slants in 12 x 75 mm tubes, at either 25° or 34°.

*All mutants with numbers prefixed NM were recovered following filtration enrichment of wild type Emerson a following ultraviolet treatment to allow 55-25% survival, in experiments of Noreen E. Murray.

†All mutants with numbers prefixed D were obtained by S. R. Gross after inositol-deprivation following ultraviolet irradiation of inos (89601) a.

Table 2. Three-point data on selected mutants from Table 1.

Zygote genotype and recombination %	Parental combinations		Recombinations				Total, % germination, and linkage group	Marker isolation numbers
			Singles Region 1	Singles Region 2	Doubles Regions 1 and 2			
$\frac{+}{AR5} \frac{aur}{+} \frac{arg(RU3)}{+}$ 40 19	- 21	- 17	7	-	- 2	47 (100%) I	AR5 34508 RU3	
$\frac{+}{hist-2} \frac{+}{nic-2} \frac{D5}{+}$ 2.5 18	36 28	1 1	4	10	0 0	80 (80%) I	Y152M14 43002 D5	
$\frac{+}{M184} \frac{hist-2}{+} \frac{nic-2}{+}$ 0 4.6	48 34	0 0	2	2	0 0	86 (86%) I	M184 Y152M14 43002	
$\frac{+}{a} \frac{+}{NM203} \frac{aur}{+}$ 11 23	25 19	0 5	7	6	1 1	64 (80%) I	(mt) NM203 34508	
$\frac{+}{P1417} \frac{ad-9}{+} \frac{nit-1}{+}$ 2.3 10	44 3 1	1 1	4	5	0 0	86 (86%) I	P1417 Y154M37 34547	
$\frac{+}{hist-2} \frac{+}{nic-2} \frac{P1417}{+}$ 11 10	39 32	3 7	3	6	0 0	90 (93%) I	Y152M14 43002 P1417	
$\frac{+}{arg-1} \frac{hist-2}{+} \frac{+}{P1798}$ 3.4 5.6	34 47	1 2	2	3	0 0	89 (91%) I	B369 Y152M14 P1798	
$\frac{+}{P2615} \frac{al-2}{+} \frac{hg}{+}$ 19 7.0	32 (39)*	8 (10)	3 (4)		0 (0)	43 (+53)* (96%) I	P2615 15300 51504	
$\frac{+}{acr-2} \frac{+}{un} \frac{NM211}{+}$ 17 12	14 34	5 4	3	3	2 0	65 (87%) III	KH5 83106t NM211	
$\frac{+}{ad-b} \frac{+}{\text{m p } \square \diamond \text{ e f } \text{ g h } \bullet}$ 17 12	88 67	5 3	2	0	0 0	165 (82%) I"	28610 C102t B28	

$\frac{+ \text{cot-1} \quad \text{cys-4}}{\text{NM213t}}$ 21 22	16 24	5 7	7 6	1 1	67 (67%) IV	NM213t C102t K7
$\frac{+ \quad 0306 \quad +}{\text{tryp-4} \quad + \quad \text{pan-1}}$ 1.8 1.8	52 58	2 0	0 2	0 0	114 (72%) IV	Y2198 D306 5531
$\frac{+ \quad \text{ml359} \quad +}{\text{cot-1} \quad + \quad \text{cys-4}}$ 16 16	40 17	7 7	9 5	0 0	85 (85%) IV	C102t NM359 K7
$\frac{+ \quad \text{tryp-4} \quad \text{pan-1}}{\text{P1898}}$ 17 19	31 7	- -	8 1	-	47 (69%) I''	P1898 Y2198 5531
$\frac{+ \quad \text{M111} \quad +}{\text{aspt} \quad + \quad \text{lys-1}}$ 3.1 2.1	49 42	2 1	1 1	0 0	96 (96%) V	44303e M111 33933
$\frac{+ \quad \text{NM221} \quad \text{val-1}}{\text{lys-1} \quad +}$ 7.4 8.4	37 43	4 3	2 6	0 0	95 (95%) V	33933 NM221 45201
$\frac{+ \quad \text{thi-3} \quad \text{me-7}}{\text{C-138} \quad +}$ 27 7.3	59 22	26 7	7 2	0 0	123 (67%) VII	C-L2B 18558 4894
$\frac{+ \quad \text{for} \quad \text{P1163}}{\text{me-7} \quad +}$ 5.8 3.2	107 36	2 7	5 0	0 0	157 (56%) " 11	4094 C24 P1163
$\frac{+ \quad + \quad \text{arg-10.}}{\text{me-7} \quad \text{P1163} \quad +}$ 18 12	55 60	15 12	9 9	1 1	162 (82%) VII	4094 P1163 B368

Loci designated by isolation number are mutants listed in Table 1; the symbol morph or col has been omitted. Crosses are arranged in order of linkage groups, and numerically by isolation number of morphological mutant within each linkage group. In the body of the table numbers at left within each pair represent the class having the + allele of the left-most marker (or A).

* Scoring uncertain for al-2 among morph classes, enclosed in parentheses.