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Properties and strains of additional
DNA repair defective mutants in known
and new genes of Neurospora crassa

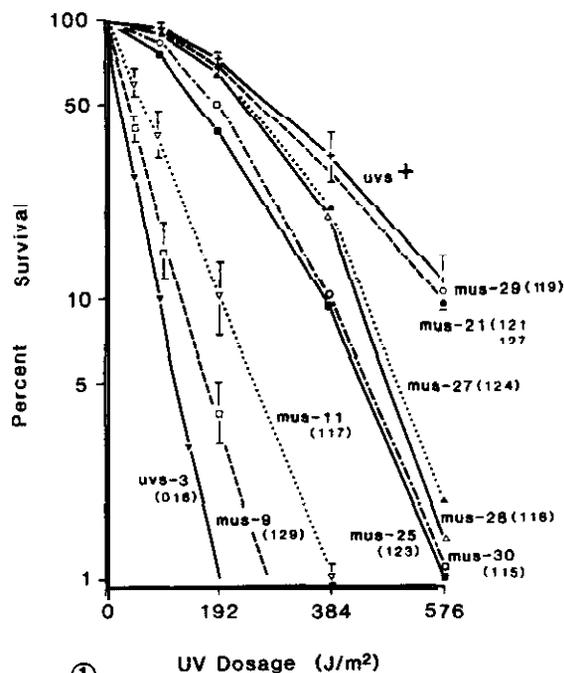
Some time ago, a number of mutants hypersensitive to MMS (methyl methane-sulfonate) were induced in Neurospora to obtain further types of DNA repair-deficient mutants; e.g., rec⁻ types not yet identified in Neurospora (meiotic-defective mutants generally are "hyperrec"; Schroeder 1984 Curr. Genet. 10:381-387). To characterize the new mutants, they were tested for cross-sensitivities to radiation and various chemicals, including histidine (HIS) (Newmeyer 1984 Curr. Genet. 9:65-74). Results for UV, mitomycin C (MC) and HIS are summarized in Table 1. All new mutants were found to be cross-sensitive to some mutagenic agents and are, therefore, likely to be defective in DNA repair rather than uptake or metabolism of MMS.

Most of the mutants listed in Tables 1 and 2 have been induced by 4NQO (4-nitroquinoline-1-oxide) as described for Aspergillus by Bal et al. (1977 Mutat. Res. 56:153-156). More recently, 3 further cases, mus (131 to 133), were isolated after UV-treatment. In both cases, a sn cr-1 strain (FGSC 4159) was mutagenized and the resulting colonies were tested on MMS (0.01% and 0.03%) and HIS (1 and 3 mg/ml) using velveteen replication. All mutants were backcrossed 2-4 times to wild type (74-ORS-1VA, FGSC 2489) as indicated in Table 2. The same wild type was also used as the control strains for all tests of hypersensitivity.

Genetic characterization of mus started usually with complementation tests in heterokaryons, using first prototroph strains on MMS-media and subsequently forced heterokaryons for confirmation, especially of negative results (Käfer and Perlmutter 1980 Can. J. Cytol. 22:535-552). Non-complementing pairs were further checked for recombination in intercrosses. However, since the latter were often sterile, most mutants were simultaneously crossed to alcoy; csp-2 (FGSC 3434) and mapped further to linked markers (Table 1). They were routinely checked for fertility in homozygous crosses and intercrossed to all available mus or uvs located on the two chromosomes involved in the linked alcoy translocation.

Tests for hypersensitivities to MMS and HIS were semi-quantitative (as described for HIS, Käfer 1981 Mutat. Res. 80:43-64) and UV survival was determined in several experiments (Figure 1). The obtained results permit a rough comparison between new and "old" alleles, and also between mutants in different genes. For example, the new allele mus(FK129) of mus-9 more closely resembles mus(FK109) than mus(FK104) (Table 1). The latter appears to be more defective than the other two and may well be a null allele. Furthermore, for MMS and HIS sensitivity, mus(FK133) resembles mus-21(SC10) while (FK131) and (FK132) are somewhat less sensitive. However, their UV survival is about normal, similar to that of mei-2 (Schroeder and Olson 1983 Can. J. Genet. Cytol. 25:16-25).

Five new genes are clearly identified by the various tests, namely mus-21, and mus-27 to -30 (Table 1). Five other cases which are included at the end of that table may also represent new genes. These mutants, mus(FK125), mus(FK128), and mus(FK131 to 133) need further backcrossing, and both (FK124) and (FK128) have shown certain problems. mus(FK125) produces very low and highly variable survival of conidia (0-5 to 40% when plated on standard minimal media and is unlinked to all mus and many other markers on linkage groups IV and V (in the absence of translocations). The mutant mus(FK128), on the other hand, produces two types of progeny in backcrosses which show different survival on MMS. It is uncertain whether is this related to the inability to identify linkage to alcoy; csp-2 (Table 1), but attempts to separate out two different mutants have so far been unsuccessful.



①

Table 1

Genetic Properties and cross-sensitivities of new musResults relative to mus⁺ control: 0 - like wild type;

1.5x, 8x, etc., - dose modifying factors; ±, +, ++ - increased levels of sensitivities:

NT - not tested; ? - preliminary results

<u>mus</u> Gene - allele numbers	Linkages Group Linked & arm marker ^a		Fertility: homozygous crosses	Approx. conidial viability ^b	Sensitivities to mutagens and inhibitors			
					MMS	HIS	MC	uv
<u>1) Alleles of known genes</u>								
-7 (FK116)	IIR	nuc-2	barren	100%	>8x	>100x	NT	NT
(FK107) ^b		p:12%	barren	100%	>8x	>200x	±	0
-9 (FK129)	IR	al-2	sterile	80%	>8x	>10x	+	4x
(FK104) ^b		p:6%	sterile	25%	>8x	>100x	+	5-6x
(FK109) ^b			sterile	75%	>8x	>50x	+	5-6x
-11 (FK117)	VR	pab-2	barren	75%	>10x	>100x	0	3x
(FK111) ^b		d:23%	barren	80%	>10x	>200x	+	2x
-25 (FK123) ^c	VIIR	met-7	barren	90%	6x	20x	±	>1.5x
		d:6%						
<u>2) Mutants in new genes</u>								
-21 (FK121)	IIIR	trp-1	barren	100%	6x	5x	0	0
(FK120)		d:20%	barren	80%	6x	>5x	NT	NT
(FK127)			barren	90%	>6x	2x	NT	0
(SC10) ^d			±sterile	80%	>6x	>15x	NT	2x
-27 (FK124)	IIR	nuc-2	fertile	85%	>8x	50x	0	<1.5x
		d:16%						
-28 (FK118)	VL	lys-1	fertile	100%	2x	>2x	0	<1.5x
		d:10%						
-29 (FK119)	VIL	cho-2	sterile	50%	2x	20x	0	0
		p:14%						
-30 (FK115)	IVR	trp-4	fertile	80%	>4x	2x	0	>1.5x
		p:4%						
<u>3) Unmapped new <u>mus</u></u>								
<u>mus</u> (FK125)	VL?	Alcoy cot T(IV;V) 32%	fertile	2-20%	3x	>20x	NT	±
<u>mus</u> (FK128)	NT	Alcoy unlinked	barren	85%	4x	>5x	0	0
<u>mus</u> (FK131)		Complementing all <u>mus</u> listed	NT	80%	>3x	15x	NT	0
<u>mus</u> (FK132)		above, <u>mus</u> -8, <u>mus</u> -10, all MMS.	NT	75%	>3x	15x	NT	0
<u>mus</u> (FK133)		sensitive <u>uvs</u> and <u>mei</u> -2.	NT	85%	5x	20x	NT	0

^aa p or d = proximal or distal to linked marker indicated.^bb Compared to published cases (Käfer 1981. ref. cit.).^cc Allelic with mus-25(SA3) (Inoue and Ishii 1984 Mutat. Res. 125:185-194 and pers. comm.).^dd Mutant of DeLange and Mishra (1982 Mutat. Res. 96:187-199).

All these mutants are being deposited at FGSC (Table 2) and additional detailed information will be made available to anyone interested in analyzing them further (their investigation is being discontinued).

Table 2. New mus strains available from FGSC

<u>mus</u>		Prototroph		strains		Simple requiring		strains		
Gene	Allele	Level of backcross		FGSC no.		Marker gene	allele	FGSC no.		
				A	a			A	a	
mus-7	FK116	II(A)	I(a)	6401	6402	--	--	--	--	
mus-9	FK129	IV		6403	6404	leu-3	R156	6405	--	
						nic-2	43002	6407	6408	
mus-11	FK117	IV		6409	6410	pan-1	5531	6411	6412	
						lys-1	33933	6413	--	
mus-21	FK121	VI		6414	6415	trp-1	10575	6416	6417	
	FK120	II		6418	6419	trp-1	acr-2	10575	KH5	
	FK127	II		6422	6423			--	--	
mus-25	FK123	IV		6424	6425	nic-3	Y31881	6426	6427	
mu-27	FK124	IV		6428	6429	arg-5	27947	6430	6431	
						nuc-2	T28M2	6432	6433	
mus-28	FK118	IV		6434	6435	leu-1	33757	6436	6437	
mus-29	FK119	IV		6438	6439	trp-2	41	6440	6441	
					yl0-1	pan-2	Y30539y	Y153M96	6442	6443
mus-30	FK115	IV		6444	6445	pan-1	5531	6446	6447	
						met-2	K43	6448	6449	
	mus(FK125)	IV		6450	6451	rib-1	51602(t)	6452	6453	
						pan-1	5531	6454	6455	
	mus(FK128;	IV		--	6457	lys-5	DS6-85	6458	--	
	mus(FK131)	II		6459	6460	trp-2	41	6461	6462	
	mus(FK132)	II		6463	6464	rib-1	51602(t)	6465	6466	
	mus(FK133)	II		6467	6468	met-1	M105	6469	6470	

Tests of mus(FK115), (FK119) and (FK123) for allelism to recently mapped genes by Dr. H. Inoue are gratefully acknowledged. This work was supported by NSERC of Canada. --- Biology Dept., McGill University, 1205 Avenue Docteur Penfield, Montreal, Quebec, H3A 1B1, Canada