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Abstract
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Catcheside, D. E. A. A new carotenoid mutant of Neurospora.

A mutant, MN58p, found amongst the survivors of UV-irrodioted conidio, is pigmented somewhat like ad-3 strains grown on limiting adenine. The 'purple' pigmentation of MN58p is due to a lock of neurosporaxanthine and at least two yellow carotenoids which ore, as yet, unidentified. The new mutant is epistatic to ylo-1 (Y30539y).

Crosses of MN58p to markers on linkage groups II (pe), III (try-1), IV (lys-5, try-2) and VII (nit-3), foiled to detect linkage (Table 1). However, MN58p proved to be closely linked to nic-1, aur, al-2 and alY on linkage group IR. Failure to detect a single recombinant amongst 5,742 progeny of a cross of al-2 (15300) suggests that MN58p may be on allele of al-2.

A forced heterocaryon (A, MN58p; me-5 (86304)) + (A, al-2 (15300); cot-1 (ClO2); am (47305). hist-1 (K83)) was found to be phenotypicolly MN58p, although the purple pigmentation is less intense than in the MN58p parent, ond not wild type. A heterocaryon (A, MN58p; lys-5 (DS6-85 ylo-1 (Y30539y); nit-3 (Y31881)) + (fr (B110), A, our (34508)), phenotypically fr^+ and able to grow on minimal medium, has a normal distribution of pigment, unlike the our parent, which has pigmented conidia but locks colored polyenes in the mycelium, and is wild type in color. MN58p complements our (34508) but not al-2 (15300).

The ability of MN58p to complement various mutants deficient in carotenoids has also been investigated by examining the color phenotype of the escape growth of the initially slow-growing progeny, containing a duplication, of crosses between normal sequence and a translocation T(IR:VL) AR190 (Table 2). Wild type pigmentation was observed amongst the progeny of crosses of MN58p with alY (AL54) and aur (34508), but not with al (al^5), al (K96) or al-2 (15300).

As MN58p complements and recombines with our (34508) and alY (ALY), it is probable that MN58p is in a gene separate from there two mutations. However, as no complementation is observed with al-2 (15300), al (al^5) and al (K96), it would seem thot MN58p is allelic to these mutations, although it has a phenotype distinct from each of these albino mutants, which foil to produce colored polyenes. This suggests that the al-2 gene product is concerned in two steps in carotenoid biosynthesis; the conversion of colorless polyenes and a later step concerned in the conversion of colored polyenes. The MN58p mutation would affect only the latter function, whilst al-2 (15300) affects both. However, this interpretation should be considered in conjunction with Huang's findings (1964 Genetics 49:453) that complementation may not be observed between albino mutants which, on the basis of recombination frequency, could be considered to be in different cistrons. Although some cases of complementation failure con be considered as due to unfavorable nuclear ratios in forced heterocaryons, the phenomenon is not inconsistent with the hypothesis that all of the mutations affecting polyene biosynthesis and located in this region of linkage group IR result in on alteration in the structure of one functionally integrated unit possessing heterocatalytic sites, analogous to the products of the arom gene cluster (Giles, Case, Partridge and Ahmed 1967 Proc. Natl. Acad. Sci. U. S. 58: 1453) and the hist-3 region of Neurospora (Minson and Creaser 1969 Biochem. J. 114:49; Catcheside, D. G. 1965 Biochem. Biophys. Res. Commun. 18:648; Ahmed, Core and Giles 1964 Brookhaven Symp. Biol. 17:55). The properties of the new mutant, MN58p, are consistent with this and similar suggestions which hove been mode by Huang (op. cit.) and by Subden and Threlkeld (1968 Con. J. Genet. Cytol. 10:351).

Table 1. Two-point linkage data for MN58p.

Cross No.	Locus	Allele	Linkage Group	Progeny parental	Progeny recombinant	Map Distance upper limit[g]
898	pe	L	II R	45	17[a]	-
1046	lys-5	DS6-85	VI L	134	124	-
1046	try-2	75001	VI R	133	125	-
1110	try-1	A10	III R	65	60	-
1110	cot-1	C102	IV R	66	59	
1116	nic-3	Y31881	VII L	59	67	
1106	nic-1	3416	I R	119	6	9.2
1105	al-2	15300	I R	5742[b]	0[a]	0.1
2242	aur	34508	I R	208	1[a,c]	4.5
2348	aur	34508	I R	35	1[a,d]	e
3771 f	al y	ALS4	I R	49	1[a,d]	e

a - only one recombinant class distinguishable from parental classes: b - 2430 albino, 2812 purple. Ascospores were germinated and grown 3 days at 25°C in the dark on sorbose:glucose:fructose (1: 0.025 : 0.025 %) medium and then transferred to 4°C under fluorescent lighting for up to 14 days (Huang op. cit.) Progeny of all other crosses were scored, following total isolation, in 4" by 1/2" tubes incubated at 25°C for 5 days in the dark and subsequently for 3-7 days at ca. 23°C in diffused daylight: c = not pseudowild: d = not tested for pseudowild: e = contains translocation T(IR:VL) AR190. Scores of non-duplicated progeny only: f - D.D. Perkins data and cross number: g - 95% confidence level.

Table 2. Complementation between carotenoid mutants in the escape growth of duplications from crosses containing T(IR:VL) AR190.

Allele crossed to MN58p	Presumptive duplications examined*	Number showing wild type color in escape growth
al y (ALS4)	26	19**
al (al[s])	17	0
al (K96)	20	0
al-2 (15300)	28	0
aur (34508)	40	22

* The escape growth moy have either type of parental pigmentation and is frequently sectored with both. Conidial re-isolates normally include both parental phenotypes, but the nuclear ratio appears to be unstable and may favor either parental type.

* * Data of D. D. Perkins.

I should like to thank D. D. Perkins for suggesting the use of AR190, for breeding MN58p into this translocation and for making his unpublished observations available to me. • • • Research School of Biologic.1 Sciences, Australian National University, Box 475 GPO, Canberra, A.C. T., Australia.