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Abstract

Recombination frequencies of mutations located in *wc-1* and *wc-2.*

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Eight white collar (wc) mutants were isolated after UV mutagenesis of ST a. These mutants and the three already located (wc-1), allele P829, linkage group VIIR, FGSC No. 143, mt a; wc-1, allele P4723, linkage group VIIR, FGSC No. 3628, mt a; wc-2 allele 234w, linkage group IR, FGSC No. 3818, mt a) were crossed with isogenic arg-1 and arg-10 strains in order to perform forced heterokaryons. A quantitative complementation analysis of photoinduction of carotenoids indicates that they fall into two complementation groups: wc-1 (7 mutants and wc-2 (4 mutants) (Russo and Innocenti, manuscript in preparation). All the wc mutants are impaired in the photoinduction of carotenoids, in the production of protoperithecia in the dark and in the photoinduction of protoperithecia (Innocenti and Russo, manuscript in preparation). Therefore the wc genes seem to have a 'very important role in photoregulation and in sexual differentiation. It is of interest to know whether these new mutations which belong to two complementation groups are closely linked to the wc loci already mapped (Perkins et al., 1982 Microbial. Rev. 46: 426-570), and to estimate the degree of linkage between mutations.

Strains of mt a and A containing the seven mutations in complementation group wc-1 were crossed with each other in all possible combinations (49 crosses). The same was done for the four wc-2 mutations. After 6-8 weeks some ascospores (much less than in wt crosses) were shot. The ascospores, after heat shock, were incubated at 34°C in the dark for three days, than at 26°C with white light for a further 24 h. Germination for the wc-1 crosses was 15-90%:(in particular in the cross AxF of Table I it was 45%); and for wc-2 germination was 40-60%. 0range colonies were likely wc^{+} recombinants. A further phenotypic check was then done. The recombination frequencies between the wc-1 mutations are given in Table I; those between the wc-2 mutations in Table 2. The recombination frequencies between the mutations in the locus wc-2 are in agreement with the value

TABLE I

Inter-allelic recombination at the wc-1 locus

	P829	ER53	ER57	P4723	MK2	MKI	ER45
P829	0 (0/10,375)						
ER53	0 (0/5,105)	0 (0/5,615)					
ER57	0 (0/3,587)	0,27 (l/7,240)	0 (0/2,360)				
P4723	0 (1/4,240)	0 (0/5,725)	0,046 (2/8,540)	0.027 (2/14,440)			
MK2	0.23 (9/7,765)	0 (0/7,625)	0 (0/7,010)	0.025 (2/15,753)	0 (0/3,259)		
MKl	0.42 (47/22,100)	0.24 (7/5,715)	0.27 (7/5,080)	0.043 (2/9.300)	0.15 (7/9.532)	0 (0/3.885)	
ER45	0 (0/8,956	0 (0/5,780)	0.03 (1/6,606)	0.06 (2/6,650)	0.09 (3/6,593)	0.2 (10/9,663)	0 (0/3,395)

Frequencies of recombination (in %). In parentheses the number of wt and the total viable colonies are given.

of 0.06 map unit per gene.found by DeSerres (1969, Mutat. Res. 8: 43-50) In contrast to that, a distance of 0.42 map unit was found for the wc-1 locus, a value seven times greater than the one found by DeSerres. A probable explanation for this finding is that either the crossover frequencies in the wc-1 locus are higher than in the region studied by DeSerres, or that it is due to gene conversion. An alternative hypothesis is that the wc-1 locus is a large gene (perhaps with introns) or it is composed of several genes which do not complement. Only further analysis can determine which is the correct interpretation. In any case, this analysis shows that each of the two loci is recombinationally a very small region.

TABLE II

Inter-allelic recombination at the wc-2 locus

	ER44	ER33	ER24	234w
ER44	0 (0/8,800)			
ER33	0.017 (1/12,020)	0 (0/5,475)		
ER24	0.014 (1/14,395)	0 (0/15,375)	0 (0/4,927)	
234w	0 (0/10,682)	0 (0/13,890)	0,043 (3/14,025)	0 (0/6,500)

Frequencies of recombination (in %) In parentheses the number of wt and the total viable colonies are given.

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