Fungal Genetics Reports

Volume 1

Article 22

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Recommended Citation

Murray, N. E., and M. Glassey (1962) "A second 'leaky' histidine mutant in linkage group IV," *Fungal Genetics Reports*: Vol. 1, Article 22. https://doi.org/10.4148/1941-4765.1036

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A second 'leaky' histidine mutant in linkage group IV

Abstract

A second 'leaky' histidine mutant in linkage group IV

<u>Murray, N. E. and M. Glassey</u> A second 'leaky' histidine mutant in linkage group IV The methionineless isolates from a cross of $\underline{me-2}$ (P143) x tryp-4 (Y2198), pan-1 (5531) grew very slowly on medium supplmented with methionine, indole and pantothenic acid.

Subsequently, it was shown that the methionine strain PI43 (isolated by filtration enrichment technique following U.V. irradiation of Emerson <u>a</u>) required both methionine and histidine for normal growth. The histidine requirement resulted from a second mutation located a few units distal to the <u>me-2</u> locus. It is proposed to designate the <u>me-2</u> mutant isolation number PI43m and the <u>hist</u> PI43h.

Further information was sought for two reasons. First, a marker distal to me-2 was required to facilitate an analysis of recombination within the me-2 gene using marker genes which, like the me-2 alleles, had been induced in the Emerson wild type strain. Secondly, the new 'leaky' histidine mutant probably represents a class of mutants not readily recoverable by the filtration enrichment technique. Approximately 1,100 histidine mutants have been isolated (Catcheside, 1960, Proc. R. Soc. B 153:179; Webber and Case, 1960, Genetics 45:1605) by a filtration enrichment procedure, but no hist-4 allele was obtained. It was suggested that hist-4 mutants may all be 'leaky' and are therefore selected against by filtration. Both PI43h and Cl41 (hist-4) grow appreciably on minimal medium and both are located in the right arm of linkage group IV, distal to me-2. None of the other six histidine genes is located in this region. No histidine independent isolate was found amongst 87 progeny from a cross of me-2, hist (P143) x hist-4 (C141), but preliminary chromatographic evidence of accumulation products detected by Pauly reagent (Ames and Mitchell, 1952. J. Amer. Chem. Soc. 74:252) indicates a difference between the two histidine mutants. It is concluded that $\underline{\text{hist}}$ (P143h) is closely linked to $\underline{\text{hist-4}}$ and that if P143h and C141 ($\underline{\text{hist-4}}$) are alleles, they are physiologically dissimilar. A complementation test has not been made.

Random spores were isolated from crosses of <u>me-2</u>, <u>hist</u> (P143) x <u>tryp-4</u> (Y2198), <u>pan-1</u> (5531) and <u>me-2</u>, <u>hist</u> (P143) x <u>cot</u> (C102). The data are tabulated below. No double crossovers were observed.

Zygote genotype and <u>recombination per cent</u>	Parental combi- <u>nations</u>	<u>Single</u> Region I	e exchanges Region 2	<u>in</u> Region 3	Total and per cent germination
4.1 3.1 0.2 + me hist + tryp + + pan	198 223	12 7	9 5	0 1	455 91%
5.8 0.8 <u>me + hist</u> + cot +	125 116	8 7	2 0	-	258 64%

On the basis of a single isolate <u>hist</u> (Pl43h) is proximal to <u>pan-1</u>, whereas <u>hist-4</u> is distal to <u>pan-1</u> (Perkins, Glassey and Bloom. Canad. J. Genet. Cytol., in press). However, the second cross indicates that Pl43h is distal to <u>cot</u>, and there is evidence (Mitchell and Mitchell, 1954. P.N.A.S. <u>40</u>:436) that <u>cot</u> is distal to <u>pan-1</u>. The region adjacent to <u>pan-1</u> comprises a cluster of very closely linked genes, making it difficult to demonstrate the linear order.