A second 'leaky' histidine mutant in linkage group IV

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Abstract
A second 'leaky' histidine mutant in linkage group IV

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This linkage data is available in Fungal Genetics Reports: http://newprairiepress.org/fgr/vol1/iss1/22
Su-2a, one of the genes which suppress the td-2 (tryp-3) phenotype, is located on linkage group I, roughly 15 units from al-2 (15300). This value is based on examination of the td- classes only (260 spores) as it is difficult to distinguish with certainty between td+su-2a+ and td+su-2a-.

Su-2, another of the genes suppressing the td-2 phenotype, appears to be located on linkage group III, approximately 22 units from leu-1 (33757). Again, this value is based on examination of td- classes only (153 spores).

Morrow, John. A new morphological marker in Neurospora. Through ultraviolet treatment, has been mapped and assigned to linkage group I. Igloo is characterized by small, spherical colonies which are densely packed and form no aerial hyphae. The linkage data are as follows:

<table>
<thead>
<tr>
<th>Cross</th>
<th>Igloo, al-2</th>
<th>x++</th>
</tr>
</thead>
<tbody>
<tr>
<td>PD</td>
<td>NPD</td>
<td>TT</td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>7</td>
</tr>
</tbody>
</table>

The criterion used for linkage was a ratio of parental ditypes to non-parental ditypes significantly in excess of one to one. Applying the chi-square test gives a probability of about 0.02. Several asci from the above cross were tested for mating type and on the basis of these considerations Igloo appears to be located to the left of al-2 on chromosome I. Igloo could be allelic or identical to the morphological mutant Cushion, isolated by P. St. Lawrence (unpublished), but no evidence is available on this point.

Murray, N. E. and M. Glassey. A second 'leaky' histidine mutant in linkage group IV

Subsequently, it was shown that the methionine strain PI43 (isolated by filtration enrichment technique following U.V. irradiation of Emerson a) required both methionine and histidine for normal growth. The histidine requirement resulted from a second mutation located a few units distal to the me-2 locus. It is proposed to designate the me-2 mutant isolation number PI43m and the hist 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 C141 (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 (PI43) 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 histi-
It is concluded that hist (P143h) is closely linked to hist-4 and that if P143h and Cl41 (hist-4) are alleles, they are physiologically dissimilar. A complementation test has not been made.

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

<table>
<thead>
<tr>
<th>Zygote genotype and recombination per cent</th>
<th>Parental combinations</th>
<th>Single exchanges in per cent</th>
<th>Total and per cent germination</th>
</tr>
</thead>
<tbody>
<tr>
<td>+ me hist +</td>
<td>198</td>
<td>12 9 0 0</td>
<td>455 91%</td>
</tr>
<tr>
<td>tryp + pan</td>
<td>223</td>
<td>7 5 1 1</td>
<td></td>
</tr>
<tr>
<td>+ me hist +</td>
<td>125</td>
<td>8 2 - -</td>
<td>258 64%</td>
</tr>
<tr>
<td>+ cot +</td>
<td>116</td>
<td>7 0 - -</td>
<td></td>
</tr>
</tbody>
</table>

On the basis of a single isolate hist (P143h) is proximal to pan-l, whereas hist-4 is distal to pan-l (Perkins, Glassey and Bloom, Canad. J. Genet. Cytol., in press). However, the second cross indicates that P143h is distal to cot, and there is evidence (Mitchell and Mitchell, 1954, P.N.A.S. 40:436) that cot is distal to pan-l. The region adjacent to pan-l comprises a cluster of very closely linked genes, making it difficult to demonstrate the linear order.

Smith, B. R. Linkage data for

In the course of locating the hist-5 gene, further linkage data between group four markers have been obtained. The loci used in these studies with the standard alleles are as follows: arg-2 (33442), col-4 (70007), flic (P623), hist-5 (K517, K534, K550), leu-2 (37501), me-1 (38706), pyr-3 (1298) and tryp-4 (All). The results of three point crosses are listed in Table 1. The order of genes shown by the three point crosses together with the approximate map distance between them is: (centromere) me-1 4.5 col-4 1.5 arg-2 0.8 pyr-3 1.0 hist-5 4.3 tryp-4 1.6 leu. In addition pyr-1 is proximal to arg-2 and probably is proximal to me-1. The morphological mutant flic is proximal to hist-5 and is probably closely linked with arg-2.