Linkage data on phen and tyr mutants

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Abstract
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sults was obtained from the two isolations in every case.

The mechanics of utilizing the alocy strain have been described in detail by Perkins (1964 N. europsor Nws. 6: 22) for mapping new mutants to linkage groups. Perkins (1966 Neuropsora News. 9: 11) stated that translocations from wild type also may be mapped using the alocy tester stmin. Normally independent alocy markers will show linkage to each other if the new translocation has breaks close to the breakpoints of two of the marked alocy translocations. Therefore, a linkage between \( a l \) and \( ylo \) would indicate that the new translocation involved linkage groups I or II and III or VI. Similarly, a linkage between \( a l \) and \( cot \) would indicate the involvement of linkage groups I or II and IV or V, while a linkage between \( cat \) and \( ylo \) would indicate involvement of IV or V and III or VI. If the alocy markers \( a l \) and \( ylo \) remains independent, one of the following situations exists:

- (1) Linkage group VII is involved in the new translocation;
- (2) The new translocation involves linkage groups I and II, III and VI, or IV and V; or
- (3) One of the two linkage groups involved in the new translocation is common to one alocy translocation and the other linkage group is common to another alocy translocation, but with the two breaks widely separated in at least one of the groups.

The linkage results (Table 1) are grouped into four categories; (A) Independence, (B) Linkage of \( a l \) and \( ylo \); (C) Linkage of \( al \) and \( cat \); and (D) Complex results not expected of simple reciprocal translocations (note the \( al \)/non-\( al \) ratios). The recombinant values calculated from the data in categories Bond C give a measure of the total genetic length of the two differential (between breaks) segments separating the linked alocy markers and are not extremely valuable in mapping the actual breakpoints of the new translocations.

Fewer \( cot \) than \( cot^+ \) germlings were obtained from crosses involving all but two of the translocation strains (AR17 and AR18). NM150 and NM161 were "morphs" and NM141 and NM170 were "peach", but progeny with these phenotypes are considered as wild types for the purposes of Table 1. An interaction of "peach" with some of the alocy markers is suspected.

The results from NM180 crosses are particularly intriguing since they indicate independence between the alocy markers in the \( cot^+ \) class but an \( al-cot \) linkage in the cot class. This unusual genetic behavior might be expected if NM180 involved two translocations involving three linkage groups (IV, V, and I or II) with breaks located such that an association of six chromosomes plus a "pair" carrying only the \( cot^+ \) allele would result from a cross with the alocy strain instead of an association of eight. This strain will be investigated farther.

In summary, translocations NM107, 111, 112, 114, 121, and 131 are independent of the alocy translocations, NM141, 163, 163, and P2648 involve linkage groups I or II and III or VI, and NM170 involves linkage groups I or II and IV or V. Translocations ALS6, AR9, 12, 17, NM109, 127, 150 and 180 appear to be more complicated than simple reciprocal translocations. Undergraduate Research Project by the first author under the direction of the second author conducted as part of Special Problems Course No. 25.

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Newmeyer, D. C. T. Taylor and D. C. Bennett

Gene sequences in linkage group I.

1) \( cyt-1(C115) \), \( cys-5(35001)^* \), and \( leu-4(D133)^* \) are all between \( leu-3(R156) \) and \( ser-3(47903) \). (The relative order of \( cyt-1 \), \( cys-5 \), and \( leu-4 \) has not been determined directly, but \( cys-5 \) and \( leu-4 \) are very close to \( wr-3 \), while \( cyt-1 \) appears to be considerably further from \( wr-3 \).)

2) \( ser-3 \) is left of \( un(55701) \).

3) \( sor(D5)^* \) is between \( suc(66702) \) and \( arg-1(8369) \). (The order of \( suc \) and \( arg-1 \) is uncertain.) \( sor(D5)^* \) is a sarbaw-resistant mutant derived from David Stadler's patch. Our limited evidence suggests that the \( sor(D5)^* \) patch may be due to the same gene. \( sor(D5) \) has not been tested for allelism with Klingmüller's \( sor(15) \).)

4) \( me-10 \) is right of \( eth-1 \). (\( me-10(Y6994) \) was isolated by Peter Dodd (Univ. of Washington); probably UV, 74A.)

5) \( un(46006)^* \) is left of \( hist-2(Y152M14) \).

6) \( dot^*(P789) \) is right of \( thi-1(56501) \).

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The following sequences have been determined since publication of the map in Table 2 of Newmeyer and Taylor (1967 Genetics 56: 771). All sequences are based on 3-point crosses. An asterisk indicates that the order depends on less than three critical crossovers. The data will be published elsewhere.

The phenylalanine requiring mutants \( phen-z(E5212) \) and \( phen-3(Y16329) \) are both alleles at the same locus and are in the right arm of linkage group III at 2.2 map units to the left of \( tyr-1(Y6994) \). The tyrosine requiring strain tyr \( (NM170) \) is also tryptophan and leucine just as \( phen-1 \) does.

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