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TRANSDUCTION MAPPING.

The following remarks were instigated by certain data in the mapping of gene sequences in Salmonella kindly furnished for our inspection by Dr. M. Demerec. We found that the usual trial-and error method for analysis of multipoint linkage data was especially tedious and therefore attempted a more analytical procedure. The same principles may be applicable to tetrad analysis. We postulate the generally accepted model (cf. Symposium on Genetic Recombination, Jour. Cell. Comp. Physiol., 45, Suppl. 2) that transduction involves the transfer of a linear fragment which then exchanges in some manner with a homologous region of the recipient chromosome. Whether each fragment overlaps all the genes in the sequence being studied is not crucial for the following discussion, so long as the incorporation of an uninterrupted linear segment is the principal condition for a frequent exchange type.

Two procedures are shown. For the more practical requirements of 3- and 4-point tests, tables are presented. A more general, but non-symbolic, procedure is also available for hypothetical, more complex linkage tests.

A. Tables for testing transduction map sequences. 3- and 4- point tests.

Instructions:

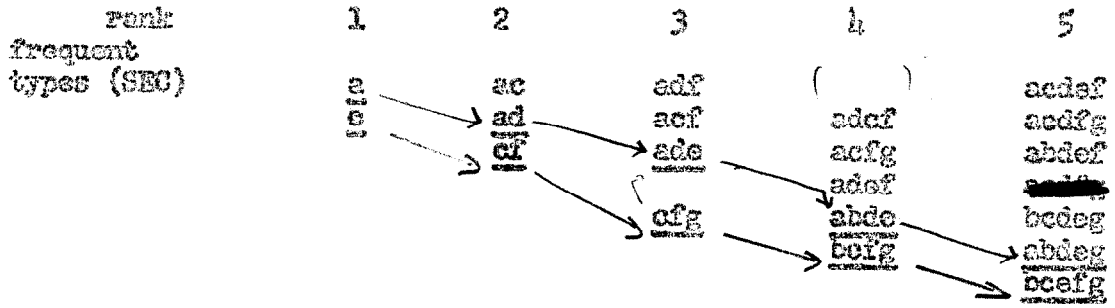
1. Write down the donor genotype (differential markers only) in any arbitrary sequence, e.g. W- X+ Y+ Z-....
2. Group the experimental results into the rare and frequent classes.
3. Code these classes as transformations of the donor genotype. The code "a" means "reverse the sign of the first locus written", "b" the same for the second, etc. Thus, (ac) (W-X+Y+Z-) would be W+X+Y-Z-.
4. The table gives the codes for the multiple exchange classes (mec) corresponding to each sequence. Those models are excluded where frequently found types are included in the mec codes, and vice versa.
5. The sequence codes can be translated into maps by writing $\begin{bmatrix} W & X & Y & Z \\ A & B & C & D \end{bmatrix}$ and transposing accordingly. Thus, BCAD would be the map XYWZ.
6. For the reciprocal transduction, superimpose the operation abcd, so that, e.g., ac becomes bd; c becomes abd in the mec codes.

	Sequence Operator	MEC types as transforms of donor genotype				
3-point test	ABC	b				
	ACB	c				
	BAC	a				
4-point test	ABCD	b	c	ac	bc	bd
	ABDC	b	d	ad	bd	bc
	ACBD	c	b	ab	bc	cd
	ACDB	c	d	ad	cd	bc
	ADBC	d	b	ab	bd	cd
	ADCB	d	c	ac	cd	bd
	BACD	a	c	bc	ac	ad
	BADC	a	d	bd	ad	ac
	BCAD	c	a	ab	ac	cd
	BDAC	d	a	ab	ad	cd
	CABD	a	b	bc	ab	ad
	CBAD	b	a	ac	ab	bd

The complete table can be generated as the permutations of (a'b+cd'), where a'b = (b+c+d) b = b+bc+cd and cd' = C(a+b+c) = ac+bc+c.

B. N-point tests.

1. Follow coding instructions A:1-3. For higher values of n, however, it is more economical to tabulate the frequent (SEC, single exchange classes) rather than the infrequent (MEC) genotypes.
2. Classes with r letters will be said to have the rank r. The SEC will include r+1 genotypes in the rth rank (except r=n-1 which will comprise each single-factor-transduction and r=n, which corresponds to non-transduction). Classify frequent genotypes according to rank and begin with r=1. Rank 0 (completely linked transduction) should be frequent.
3. In rank 1, there should be two types corresponding to the peripheral loci.
4. In rank 2, there should be 3 frequent types. One of these is the combination of the two peripheral loci; the other two show the linkage of the penultimate factors.
5. In rank 3, look for the additional factors associated with the peripherals just established. Ignore combinations of factors previously located.
6. In rank 4, and subsequently until all factors are located, repeat the same process as in 5. Each rank should establish the location of the next two factors, starting from the periphery of the sequence to its center.
7. Working example for n=7. Informative types in each rank are underlined.



Steps:

r=1	A.....C	
r=2	AD...FC	
r=3	ADE..GFC	Hence sequence must be ADEBGFC, and following steps are to check only.
r=4	ADEBGFC	
r=5	ADEBGFC	

8. The sequence operator (e.g., ADEBGFC) is then applied to the arbitrary gene sequence (WXYZ...) to obtain the map order, as outlined in A-5.
9. Due consideration has to be given to the limitations imposed by the selective methods on the variety of genotypes that can be detected. The inadvertent inclusion of an unlinked factor can be readily detected by abnormalities in frequencies in ranks 0 and 1. Data from reciprocal transductions can be readily combined as indicated in A-6.

J. Lederberg and M. Kimura, Department of Genetics, University of Wisconsin.

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