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SHORT PAPERS

The location of Cattanach's translocation in the X-chromosome linkage map of the mouse

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1. INTRODUCTION

In Cattanach's X-autosome translocation a piece of autosome of linkage group I has been inserted into the X-chromosome and a piece of X may have been reciprocally translocated to the autosome (Cattanach, 1961; Ohno & Cattanach, 1962). The present communication reports investigations to locate the autosomal insertion in the X-chromosome linkage map and provide evidence pertinent to the question of the possible reciprocal nature of the rearrangement; a brief summary of the results has already been reported (Cattanach & Isaacson, 1965).

The unbalanced form (Type II) of the translocation was employed since animals of this genotype, i.e. those possessing a normal set of autosomes and carrying the piece of autosome inserted into the X as a duplication, should be deficient for a piece of X if, in fact, the rearrangement is a reciprocal one. The linkage group I chromosomes of all animals employed in the crosses carried the marker gene, *albino* (*c*). All translocation-bearing animals could thus be identified by an *albino*-variegated phenotype in females and a wild-type phenotype in males; the chromosomally normal animals were uniformly *albino*. In most crosses the linkage data was estimated from the analysis of the *albino* male progeny only; females could not always be classified for the sex-linked genes, and viability problems were encountered with the translocation-bearing males. To simplify the presentation of the data the autosomal insertion will here be designated, *T*II.

2. CROSSES AND RESULTS

(i) *Crosses involving the translocation*, Tabby *and* Bent-tail

In an earlier report it was shown that the insertion (*T*II) and *Tabby* (*Ta*) lie close together on the X-chromosome. From a two-point repulsion backcross the recombination frequency was estimated to be of the order of 4%, or 3·5% if only the *c* male progeny were considered. The coupling backcross has now been carried out and provides essentially the same answer (Table 1). From both sets of data the recombination frequency between *T*II and *Ta* may be estimated to be 4·11% (lower and upper 95% confidence limits, 1·90 and 7·66 respectively). Since *Ta* is one of the central markers in the X-chromosome linkage map it would seem probable that other marker genes might be found on either side of the autosomal insertion (*T*II).

Bent-tail (*Bn*) recombines with *Ta* with a frequency of the order of 11% (Falconer, 1953) to 15% (Phillips, 1954). Two-point tests of *T*II and *Bn* were therefore carried out (Table 1) but the estimation of the recombination frequency was made difficult by the low viability of *Bn* males and the incomplete penetrance of the gene in the females. However, when

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Table 1. *Phenotype and numbers of offspring from two-point linkage backcross*

Heterozygous parent	Females				Males			
	Non-crossovers	Crossovers		Non-crossovers	Non-crossovers	Crossovers		Non-crossovers
Tu Ta/+ +	*Tu Ta* 46?	*Tu* + 1?	+*Ta* 1?	+ + 88?	*Tu Ta* 17	*Tu* + 2	+*Ta* 4	+ + 70
Tu +/+*Bn*	*Tu* + 43?	*Tu Bn* 3?	+ + 12?	+*Bn* 23?	*Tu* + 22	*Tu Bn* 0	+ + 11	+*Bn* 20
Tu Bn/+ +	*Tu Bn* 11?	*Tu* + 5?	+*Bn* 4?	+ + 23?	*Tu Bn* 2	*Tu* + 0	+*Bn* 2	+ + 36
Tu +/+Mo^{Br}	*Tu* + 80	*Tu* Mo^{Br} 1	+ + 4	+Mo^{Br} 81	*Tu* + 45	*Tu* Mo^{Br} 0	+ + 2	+*Br* 90
Tu Mo^{Br}/+ +	*Tu* Mo^{Br} 17	*Tu* + 1	+Mo^{Br} 1	+ + 34	*Tu* Mo^{Br} 4	*Tu* + 0	+Mo^{Br} 0	+ + 36
Tu +/+*jp**	*Tu* + (119)	*Tu jp*	+ + (141)	+*jp*	*Tu* + 36	*Tu jp* 0	+ + 1	+*jp* 153
Tu +/+*spf***	*Tu* + (47)	*Tu spf*	+ + (41)	+*spf*	*Tu* + 9	*Tu spf* 1	+ + 24	+*spf* 24
spf +/+*jp****	*spf* + (206)	*spf jp*	+ +	+*jp*	*spf* + 47	*spf jp* 45	+ + 54	+*jp* 52

Numbers in brackets indicate that non-crossovers and crossovers were not distinguishable. A question mark after a number indicates uncertainty in classification. **jp* not classifiable in females. ***spf* not classifiable in females. ***Neither gene classifiable in females.

allowances were made for these factors most calculations placed the recombination frequency at approximately 20%. This indicates that *T11* lies further away from *Bn* than it does from *Ta* and that the order probably is *T11–Ta–Bn*. This was confirmed in three-point linkage tests using *T11 Ta* + / + + *Bn* and *T11 Ta Bn*/ + + + females. Neither class of female produced any offspring in which *Ta* crossed over in relation to both *T11* and *Bn*, although a number of the other crossover types were found among eighty-two unambiguously classified offspring. This implies that *Ta* crossovers represent the double recombinant, i.e. that *Ta* is the middle locus.

(ii) *Crosses involving the translocation and* Brindled

Brindled (*Mo^{Br}*) recombines with *Ta* with a frequency of 4% and lies on the opposite side of *Ta* from *Bn* (Falconer, 1953, 1954). If the above calculations are correct *Mo^{Br}* and *T11* should be very closely linked. Two-point linkage tests (Table 1) fully confirmed this prediction; the recombination frequency was 2·16% (lower and upper 95% confidence limits, 0·59 and 5·45 respectively).

Since the translocation would be expected to suppress recombination in its immediate vicinity the observed recombination frequencies will not represent the true genetic distances, i.e. *T11* will be further away from the marker genes than the recombination frequencies indicate. It is therefore highly unlikely that *T11* lies between *Mo^{Br}* and *Ta*; almost certainly the order will be *T11–Mo^{Br}–Ta–Bn*. Linkage tests with marker genes further away from *Ta* on the *Mo^{Br}* side of this gene were therefore carried out.

(iii) *Crosses involving the translocation*, jimpy *and* Gyro

Jimpy (*jp*) recombines with *Ta* with a frequency of 20% and lies on the *Mo^{Br}* side of this gene (Phillips, 1954). It should therefore show little recombination with *T11*. Two-point linkage tests (Table 1) confirmed this to be the case; only one crossover was detected among 154 progeny scored. To ensure the recombinant phenotype was not a consequence of the animal possessing the exceptional XXY sex chromosome constitution, fertility tests and chromosome counts were carried out. Both tests indicated a normal XY condition, supporting the recombination hypothesis of origin. While demonstrating that the translocation almost completely suppresses crossing-over in the *Mo^{Br}–jp* region, the data do not distinguish the relative position of *jp*; it could lie on either one or the other side of *T11*.

Gyro (*Gy*) recombines with *Ta* with a frequency of 30–40% and lies on the *jp* side of this gene (Lyon, personal communication). Linkage tests could not provide any accurate estimate of the recombination between *T11* and *Gy* because of the many technical difficulties associated with studies utilizing this gene. The data did however indicate that crossing over occurred, probably with a frequency of the order of 20%. It is therefore certain that *Gy* lies on the opposite side of the *T11* from *Ta*.

(iv) *Crosses involving the translocation and* sparse-fur, *and* sparse-fur *and* jimpy

Sparse-fur (*spf*) is known to be closely linked to *scurfy* (*sf*) (Russell, personal communication) and *sf* has been tentatively located about 40 crossover units away from *Ta* on the *Bn* side of this gene (Welshons, personal communication). However, since evidence existed (Russell, 1963) which permitted the speculation that both *spf* and *sf* might rather lie on the *Gy* side of *T11* (Cattanach, 1965) this possibility was tested. Two-point linkage tests were carried out between both *spf* and *T11* and *spf* and *jp*. The results are shown in Table 1. The tests indicated that *spf* lies distant to both *T11* and *jp*, for the maximum recombination frequency (50%) was obtained in both cases (*spf–T11*, 50 ± 14%; *spf–jp*, 50 ± 7%). On the basis of the data presented in this communication it must be concluded that *spf* does in fact lie on the opposite side of *Bn* from *Ta*, not on the *Gy* side of *T11*.

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3. DISCUSSION AND CONCLUSIONS

The data clearly establish that the piece of autosome (*T11*) inserted into the X-chromosome in Cattanach's translocation is located within the X-chromosome linkage map. The order of the loci is *Gy–T11–Mo^{Br}–Ta–Bn–spf*. One other gene, *jp*, which is located between *Gy* and *Mo^{Br}* is closely linked to *T11* but the data do not distinguish on which side of *T11* it lies. The results also establish that *spf* lies in the position indicated above, i.e. on the opposite side of *Bn* from *Ta*, this confirming Welshons' data for the closely linked *sf*.

The translocation suppressed crossing over throughout most of the region between *jp* and *Mo^{Br}* (normally about 16 crossover units apart), only one cross-over being found among 154 offspring scored, and it is possible that the effect may extend a further distance beyond *jp* towards *Gy*. Since the rearrangement is insertional it would seem most likely that crossover suppression will operate on both sides of the insertion and hence, on the basis of the above information, the amount of suppression on each side must be fairly small. If this is so then it is unlikely that Type II translocation heterozygotes are deficient for a piece of X-chromosome, a condition which together with the autosomal insertion would be expected to cause a marked suppression of crossing over. In support of this conclusion is the observation that the translocation did not influence the phenotype of any of the tested sex-linked genes when either in coupling or repulsion with them. Type II animals cannot therefore be deficient for regions of X-chromosome which include any of the loci of these genes. Genetical evidence for a reciprocal exchange between the X and the autosome is therefore lacking. Recently, however, pachytene configurations of female translocation heterozygotes have been interpreted to indicate that the translocation had involved a chromatid-type reciprocal exchange (Slizynski, personal communication). It was considered that by this means a piece of X was translocated into the autosome without its loss from the X. The linkage data presented here do not conflict with this interpretation.

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