LINKAGE OF LOOP-TAIL, LEADEN, SPLOTCH AND FUZZY IN THE MOUSE

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INVESTIGATIONS by Dickie and Woolley (1950) and Fisher (1953) have established a linkage group (number thirteen) in the mouse carrying the genes *leaden* (*ln*), *fuzzy* (*fz*), *polydactyly* (*py*), and probably *Splotch* (*Sp*). The published crossover values are : *ln*—*fz*, 40·9±3·7 per cent. where the heterozygous parent is the female and 41·5± 4·5 per cent. where the heterozygous parent is the male (Dickie and Woolley, 1950) ; *fz*—*Sp*, 41·3±5·2 per cent. (Dickie and Woolley, 1950) ; *ln*—*py*, 40·3±1·77 per cent. where the heterozygous parent is the female and 23·0±2·00 per cent. where the heterozygous parent is the male (Fisher, 1953). No three-point or four-point data have been reported.

Table 1 shows the results from two sets of crosses, one involving *ln*, *Sp* and *fz* and the other *Lp* (Loop-tail : Strong and Hollander, 1949 ; Stein and Rudin, 1953), *ln* and *fz*. It will be seen that the data establish the linkage of these four genes with the order and crossover per cents. as follows :

	Lp	*ln*	*Sp*	*fz*
Heterozygous ♂ . .	35·1	5·8	31·6	
Heterozygous ♀ . .	38·1	8·5	39·8	

While these were the two most important crosses, two others gave results which deserve mention.

The *leaden Splotch* linkage was first discovered by Mrs Ann Ingalls (data previously unpublished) in a backcross of *Sp* to the V stock, a multiple-factor stock carrying *a*, *ln*, *s*, *v*, *wa*-1. The segregation of *piebald* (*s*) in this cross complicated the classification of *Sp*. However, a frequency distribution of the animals classified according to the total area of white spotting gave an indication of four modes which presumably corresponded to the four classes *spspSs*, *SpspSs*, *spspss* and *Spspss*. There was more overlapping between the *SpspSs* and the *spspss* classes than between these and the two extreme classes. The class with maximum white included animals with up to 90 per cent. of the coat unpigmented, considerably more than is ever seen in the V stock due to *piebald* alone. Evidently the effect of *Sp* and *s* in combination is more than additive. The selection of lines to divide the four classes was necessarily somewhat arbitrary ; the lines finally

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TABLE 1

Data from matings establishing the linkage and order of Lp, ln, Sp, fz. *All matings are of the backcross type*

Crosses	Phenotypes and number of mice								Totals	Crossover per cents.		
♀ ♂	*ln+fz*	*ln++*	*lnSpfz*	*lnSp+*	*++fz*	*+++*	*+Spfz*	*+Sp+*		*ln-Sp*	*Sp-fz*	*ln-fz*
$\frac{ln+fz}{ln+fz} \times \frac{ln+fz}{+Sp+}$ . . .	92	44	0	3	12	3	52	107	313	5·8±2·8	31·6±2·8	35·5±2·8
$\frac{ln+fz}{+Sp+} \times \frac{ln+fz}{ln+fz}$ . . .	42	37	1	3	9	2	30	52	176	8·5±3·8	39·8±3·8	44·9±3·8
	+lnfz	*+ln+*	*++fz*	*+++*	*Lplnfz*	*Lpln+*	*Lp+fz*	*Lp++*		*Lp-ln*	*ln-fz*	*Lp-fz*
$\frac{+lnfz}{+lnfz} \times \frac{+lnfz}{Lp++}$ . . .	46	35	15	36	14	3	19	26	194	35·1±3·6	37·1±3·6	53·6±3·6
$\frac{+lnfz}{Lp++} \times \frac{+lnfz}{+lnfz}$ . . .	8	9	5	4	6	1	2	7	42	38·1±7·7	40·5±7·7	50·0±7·7

selected yielded a figure for crossing over between *ln* and *Sp* of 9·7± 4·5 per cent. in heterozygous males, and 9·8±7·8 per cent. in heterozygous females.

Data indicating an apparent linkage of *Sp* and *Sd* were reported in a previous publication (Dickie, Kelton *et al.*, 1949). Since *Sd* was subsequently shown to belong in linkage group five (Wallace, 1950), some explanation of this case is necessary. The data came from matings of a single heterozygous male, with *Sp* and *Sd* in repulsion, to C57BL females. Final tabulation, including published and previously unpublished data, gave results as follows :

++	*Sp*+	+*Sd*	*SpSd*
38	64	39	29

It will be seen that the apparent linkage is due to the excess of animals in the *Sp*+ class. Only additional tests, not now contemplated, could establish definitely the reason for this unequal distribution. One possible explanation is a second spotting factor actually closely linked with *Sd*, which mimics *Sp* in phenotype and has, as *Sp* sometimes does, incomplete penetrance. *Sp* and the postulated gene are assumed to have entered the cross from one parent, *Sd* from the other.

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