LINKAGE DATA ON THE REX CHARACTER IN THE HOUSE MOUSE

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Rex has been described as a new autosomal dominant in the house mouse, and it was stated that once its linkage group was determined it should prove a very useful chromosome marker on account of its dominant character, the fertility and viability of Rex animals, and the ease of classification within a few days of birth. Accordingly linkage experiments with a number of chromosome markers present in our stocks (the most important one supplied by L. C. Dunn) were started. As the work has to be discontinued for the time being, we publish the data obtained so far. Though they are not as large as desirable and intended, they still seem sufficient to exclude at least close linkage with any of the tested genes.

Data from ordinary backcrosses with an expected 1 : 1 : 1 : 1 ratio for independent segregation are presented in Table I.

TABLE I

Data from backcrosses of heterozygotes for R and a recessive marker gene (designated by m) to the homozygous recessive

Gene tested for linkage with Rex	Type of cross	Number of					*P* for a 1 : 1 : 1 : 1 ratio
		Rm	*R+*	*+m*	*++*	Total	
albino (*c*)	repulsion	26	22	18	17	83	0·5–0·3
non-agouti (*a*)	repulsion	7	9	9	9	34	0·95
blue dilution (*d*)	repulsion	10	14	16	20	60	0·3
brown (*b*)	coupling	9	12	14	8	43	0·7–0·5
pink dilution (*p*)	coupling	13	8	8	14	43	0·5–0·3

The column "type of cross" indicates whether Rex and the recessive marker gene had been introduced into the heterozygote from the same parent (coupling) or from different parents (repulsion).

The particularly meagre data for non-agouti are supplemented below by data from another cross. The figures for brown are also very small, but whatever deviation they show is in the direction opposite to what would be expected in the case of linkage. With pink, on the other hand, the direction of the deviation is in the direction of linkage; but apart from the fact that with the present material a significant deviation from a 1 : 1 : 1 : 1 ratio could not be demonstrated, the fact that the independent segregation from albino seems well established makes a loose linkage with

pink, which is on the same chromosome as albino at a distance of about 15 cross-over units, unlikely.

Another set of data was obtained from the following cross:

$$\frac{R}{+}\ \frac{+}{a}\ \frac{+}{w_1}\ \frac{+}{v}\ \frac{+}{l}\ \frac{+}{s} \times \frac{a}{a}\ \frac{w_1}{w_1}\ \frac{v}{v}\ \frac{l}{l}\ \frac{s}{s}$$

(a = non-agouti; w_1 = wavy-1; v = waltzing; l = leaden; s = piebald), in which Rex had been introduced from one parent, the recessive markers from the other. A difficulty arose through the fact that Rex, wavy-1, and their combination are so much alike phenotypically that no attempt was made to record them separately. All three genotypes were classified together under the neutral designation "curly". With this classification, the following results were expected for independent segregation of Rex with all the genes concerned:

a ratio of 3 curly to 1 non-curly over all mice; and

a ratio of 3 curly and 1 non-curly in each of the eight classes formed by classification for presence or absence of the four remaining characters.

In contrast, linkage of Rex with wavy-1 would result in a deficiency of the non-curly individuals in the total, down to complete absence with perfect linkage. Linkage with one of the other genes would result in the deficiency or absence of curly animals in the class heterozygous for this gene (e.g. in the case of piebald in the non-piebald class), and a 1 : 1 ratio of curly to non-curly in the homozygous class (e.g. the piebald class). The results actually obtained are given in Table II.

TABLE II

Backcross data with a multiple recessive stock

Gene tested for linkage with Rex	Class examined	No. of curly animals	No. of non-curly animals	Class examined	No. of curly animals	No. of non-curly animals	P for a 3 : 1 ratio	P for a 2 : 1 ratio
wavy-1 (w)	All animals	54	24	—	—	—	0·3–0·2	0·7–0·5
non-agouti (a)	aa	25	10	$a+$	29	14	0·5–0·3	0·9–0·8
waltzing (v)	vv	20	10	$v+$	34	14	0·5–0·3	0·9–0·8
leaden (l)	ll	32	15	$l+$	22	9	0·5–0·3	0·9–0·8
piebald (s)	ss	22	11	$s+$	33	13	0·5–0·3	0·9–0·8

The values of P in the last two columns have been arrived at by considering the two classes in each line separately (D.F. = 2).

It is seen from this table that with the number of animals tested the data agree in every case with the 3 : 1 ratio expected for independent segregation. The last column, however, shows that the fit for a 2 : 1 ratio of curly to non-curly animals is considerably better not only in respect of the total population but also in respect of every individual class. This

suggests the existence of an inviable class among the curly animals not connected with any of the other genes tested. No differential postnatal mortality in the backcross litters was observed; prenatal mortality was not studied. The curly class should be composed of equal numbers of three genotypes: $R+w+$, $R+ww$, $++ww$. Since it is known that homozygous wavy and heterozygous Rex are viable the suspicion of inviability attaches to the $R+ww$ class in which it might be due to an interaction of the two genes. As no breeding tests of the surviving curly animals could be carried out this hypothesis could not be verified.

REFERENCE

CREW, F. A. E. & AUERBACH, CH. (1939). "Rex: a dominant autosomal monogenic coat texture character in the mouse." *J. Genet.* **38**, 341–4.