

## SHORT PAPERS

### Curly-whiskers and its linkage with tail-kinks in linkage group II of the mouse

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Curly-whiskers (*cw*) is a recessive gene which was found in 1958 by Mr C. J. W. Smith of the Chester Beatty Research Institute, London. It arose in a subline of the CBA/Cbi inbred strain. The first mutant animals were one male and one female in a litter of five. The two mutants were mated together and a sib-mated subline was continued from them in which 500 mice were bred, all of which were curly-whiskered. This established the mutant to be fully penetrant. Curly-whiskers resembles the hair-waving genes in causing waving of the vibrissae, but it has no obvious waving effect on the hairs of the coat. The coat texture is, however, slightly abnormal and Mr Smith noted also that on the CBA background there was an appreciable darkening of the coat colour. Homozygotes (*cw/cw*) are easily classifiable soon after birth by the curled vibrissae. Heterozygotes (*+ / cw*) often have slightly curled vibrissae, and the gene is therefore not fully recessive; but the distinction between *+ / cw* and *+ / +* could not be relied on, and in the linkage tests *cw* was treated as a recessive gene.

Curly-whiskers was obtained from Professor H. Grüneberg, who had obtained it from Professor P. C. Koller of the Chester Beatty Institute. Proof that curly-whiskers is a single recessive gene was obtained from the segregation in intercross and backcross matings. There was a slight, but non-significant, deficiency of *cw/cw* progeny. The proportions of *cw/cw* progeny obtained were 22.2% in 797 intercross progeny, and 47.3% in 474 backcross progeny. Curly-whiskers was tested for allelism with rough (*ro*) (Falconer & Snell, 1952), which it resembles in some respects. The two genes were proved to be non-allelic. Tests for the linkage of curly-whiskers were made with the stocks maintained in Edinburgh, and it was found to be linked with short-ear (*se*) in linkage group II. This was reported in *Mouse News Lett.* 27, 30. The results given in Table 1 here include additional data. Another gene, tail-kinks (*tk*) described by Grüneberg (1955) had previously been found to be linked with short-ear (*Mouse News Lett.* 25, 30) (Table 1). Three-point backcross tests (Tables 2 and 3) were therefore made, and the order and recombination frequencies between the three genes were proved to be

*cw*—38—*se*—6—*tk*

By extending the known limits of linkage group II, curly-whiskers should prove to be a useful marker gene.

We are much indebted to Professor H. Grüneberg, F.R.S., for supplying us with stocks of both curly-whiskers and tail-kinks, and to Professor P. C. Koller for permission to study the genetics of curly-whiskers.

Table 1. Linkage tests by intercross matings, with recombination frequencies estimated from the tables of Finney (1949)

Genes tested	Genotype of parents	No. of matings	Phenotypes of progeny				Tot.	Recombination (%) ± S.E.
			++	cw+	+se	cwse		
<i>cw-se</i>	$\frac{cw+}{+se}$	8	140	45	44	5	234	36.2 ± 5.6
	$\frac{cwse}{++}$	11	207	43	44	40	334	30.8 ± 3.1
	$\frac{cwse+}{++tk}$	9	157	28	28	16	229	32.8 ± 3.7
				++	+tk	se+	setk	
<i>se-tk</i>	$\frac{se+}{+tk}$	6	90	31	49	1	171	16.2 ± 7.4
	$\frac{cwse+}{++tk}$	9	112	73	44	0	229	0
			Joint estimates: <i>cw-se</i>					32.8 ± 3.7
			<i>se-tk</i>					10.1 ± 4.9

Table 2. Three-point linkage tests by backcross matings of the types:

$$A = \frac{cw\ se\ tk}{++} \times \frac{cw\ se\ tk}{cw\ se\ tk} \qquad B = \frac{cw\ se\ +}{++\ tk} \times \frac{cw\ se\ tk}{cw\ se\ tk}$$

The results are tabulated by the type of mating and sex of segregating parents. The symbols in brackets indicate the type of gene-exchange represented.

Phenotype of progeny	Mating type A		Mating type B	
	Female	Male	Female	Male
+++	(none) 57	24	(tk) 4	2
cwse tk	30	19	1	2
+se tk	(cw) 16	8	(se) 0	0
cw++	41	16	2	0
cwse+	(tk) 4	2	(none) 38	21
++tk	5	3	55	22
+se+	(se) 1	0	(cw) 41	12
cw+tk	1	0	28	19
Total	155	72	169	78

Table 3. Recombination frequencies (%) and their standard errors, estimated from the data in Table 2

	Segment <i>cw-se</i>		Segment <i>se-tk</i>	
	Female	Male	Female	Male
Mating type A	38.1 ± 3.9	33.3 ± 5.6	7.1 ± 2.1	6.9 ± 3.0
B	42.0 ± 3.8	39.7 ± 5.5	4.1 ± 1.5	5.1 ± 2.5
Combined	40.1 ± 2.7	36.6 ± 3.9	5.5 ± 1.3	6.0 ± 1.9
Sexes combined	39.0 ± 2.2		5.7 ± 1.1	
Mean of sexes	38.4 ± 4.8		5.8 ± 2.3	

## REFERENCES

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