84. Studies on the Karyotype Differentiation of the Norway Rat. VI

*Linkage Analysis of the Bared (ba) Gene to the Inversion Pair No. 1 Chromosome**

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As previously reported by Yosida (1980a), an LEM strain rat with an inversion pair no. 1 was established from a mosaic rat consisting of two cell types; 1-12 translocation/normal no. 1 and 1-12 translocation/inversion no. 1. In the 5th inbreeding generation of the LEM strain rat, a bared (*ba*) mutant spontaneously appeared (Yosida 1981) (Fig. 1). Based on the mating between the mutant

Fig. 1. Bared rat (*ba*) occurred in the LEM strain rat.

and the normal haired LEM rats, it was shown that the bared character was due to a simple and recessive mutant gene. Since the bared rat appeared in the LEM strain rat with inversion no. 1, there is a possibility that the *ba* gene is located on the inversion no. 1 chromosome. To know this problem a segregation ratio in the F_2 generation from hybrids between the bared rat with inversion pair no. 1 and the normal rat without inversion was investigated. The present paper deals with the results of observations on the segregation ratio in a total of 76 F_2 offspring.

Material and methods. Bared rats (*ba*) from the LEM strain with inversion pair no. 1 was mated to the normal Wistar strain rat (WM) having no inversion. From the mating between bared

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and normal rats, 55 F_2 offspring were obtained for the analysis of the bared character. A correlation between the karyotype and the bared character was analysed from 21 F_2 offspring newly obtained from the other 5 litters. The karyotype was analysed using being made of the tail cultured cells prepared by our routine technique (Yosida 1980b).

Results and discussion. 1) Characteristics in F_1 rats. All F_1 rats had the normal hair coat, but their karyotypes showed without exception an inversion/normal heterozygous pair no. 1 ($1^{inv}/1^+$) as expected. Namely, one of the pair no. 1 chromosomes was characterized by metacentrics resulted from the pericentric inversion, but the other partner was normal subtelocentrics (Fig. 2).

Fig. 2. Karyotype of the F_1 hybrids between the LEM and the normal WM strain rat. Pair no. 1 is heteromorphic due to the inversion (1^{inv}) and normal (1^+) chromosomes.

2) Segregation of bared rats and inversion pair no. 1 in F_2 rats. Among 55 F_2 offspring obtained from matings between the F_1 hybrids described above, 16 rats were bared, while the remaining 29 rats were normally haired (Table I). The segregation ratio was not significantly different from the expected value as a simple and recessive mutant gene. A relation between the segregation ratio of karyotypes and that of the bared rats examined in 21 F_2 offspring was shown in Table II. Namely, 3 rats among them were bared, but the remaining 18 rats were normal. The ratio of the bared to the normal rats was not significantly different from the expected one (5.2:15.8). A fewer occurrence of the bared rats than the expected one is due to a slight weakness of the mutants. The karyotype of the bared rats was all

characterized by having the inversion and normal heteromorphic pair no. 1 ($1^{inv}/1^+$). On this basis it was suggested that the bared gene might not be linked to the inversion pair no. 1, but to any other

Table I. Segregation in F_2 offspring in matings between the bared (ba/ba) and normal rats (ba^+/ba^+)

	No. of rats observed ($\varphi : \sigma$)	Expected values*
Bared (ba/ba)	16 (9 : 7)	13.8
Normal hair (ba^+/ba^+ , ba^+/ba)	39 (21 : 18)	41.2
Total	55 (31 : 25)	55.0 ($\chi^2=1.0$, $p<0.3$)

* Expected values are calculated as the ba gene is simple and recessive.

Table II. Segregation in the F_2 offspring in mating between bared rats with the inversion pair no. 1 and the normal rats without inversion (ba/ba , $1^{inv}/1^{inv} \times ba^+/ba^+$, $1^+/1^+$)

No. 1 chrom.	Bared	Bared (ba/ba)	Normal (ba^+/ba , ba^+/ba^+)	Total
$1^+/1^+$		0(1.0)* (0)** (0)***	4(4.0)* (5.0)** (5.0)***	4(5.0)
$1^{inv}/1^+$		3(3.0) (0) (1.0)	11(8.0) (11.0) (9.5)	14(11.0)
$1^{inv}/1^{inv}$		0(1.0) (5.0) (4.0)	3(4.0) (0) (1.5)	3(5.0)
Total		3(5.0)	18(16.0)	21(21.0)

* Numbers in the parentheses denote the expected values calculated as the ba gene is not linked to the inversion pair no. 1 ($\chi^2=3.1$, $p\div 0.7$). ** The numbers are calculated as the ba gene is linked to the inversion pair no. 1 ($\chi^2=31.3$, $p<0.01$). *** The numbers are calculated as the ba gene is linked to the inversion pair no. 1, but 20% crossing over is taken in F_1 hybrids ($\chi^2=18.5$, $p\div 0.01$).

pair. There is no significant difference between the observed and expected numbers which were calculated from an assumption that the bared gene was not linked to the inversion pair no. 1 ($\chi^2=3.1$, $p\div 0.7$) (Table II). If the ba genes would be located in the inversion pair no. 1, the bared rats should have the inversion homologous pair no. 1, while the normal haired rat would have either one of the normal homologous pair no. 1 ($1^+/1^+$) or the heterologous pair no. 1 ($1^{inv}/1^+$). Although this possibility was examined by χ^2 test (see two asterisks in Table II), there was a significant difference between the observed and expected values ($\chi^2=31.3$, $p<0.01$). Another account was made based on an assumption that the gene was located on the inversion pair no. 1, but the 20% crossing over to the normal partner was taken in F_1 hybrids. The segregation ratio of the bared rat and

inversion pair no. 1, however, was significantly different from the expected one ($\chi^2=18.5$, $p \div 0.01$) (see three asterisks in Table II). Based on the above results, the bared gene should be located on the some autosome pair other than the pair no. 1. Since the bared rats appeared in both females and males, it seems not to be linked to the sex chromosome. At present, it cannot be determined which chromosome pair the mutant gene is located on. This problem will be determined by further linkage analyses by the use of more chromosome markers.

Genetical hypotrichotic mutants of the rat have already been described by Robert *et al.* (1940) as the hairless (*hr*), by Castle *et al.* (1955) as the naked (*n*), by Palm and Ferguson (1976) as the fuzzy (*fz*) and by Festing *et al.* (1978) as the nude (*rnu*). According to Castle *et al.* (1955), the *hr* and *n* genes were in the linkage group III, while the *fz* was in the linkage group I (Palm and Ferguson 1976). As already reported (Yosida 1981) the bared mutant was different in its external character from the above mutants, but rather similar to the nude rat. However, the bared rat had the thymus, although it was slightly smaller than the normal one. There is no any information on the relation between the hypotrichotic rat mutants already reported and the present bared one. We also do not know whether, or not, the bared mutant is an allele to either one of the other hypotrichotic mutants. This has been remained as an important problem to be solved in future.

Summary. Bared (*ba*) gene occurred as a hypotrichotic mutant in the LEM strain rat, which is characterized by having the inversion pair no. 1, is analysed whether the gene is located on the inversion chromosome no. 1. Based on statistical analyses of the bared rats and the inversion pair no. 1 in the F_2 offspring, it is shown that the *ba*-gene is not located in the pair no. 1, but in any one of the other autosome pairs.

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