the probability that a female will oviposit on decaying fruits which will then be sent a long distance away. This constitutes a great advantage if we consider the capacity of long distance migrations and colonization of new places. Moreover, the possibility for these species to thrive within man-made constructions affords them a new type of habitat. This behavioral property is surely involved in the well known 'liking' of *D. melanogaster* for garbage cans. Also the occurrence of huge populations of *D. melanogaster* in wine cellars of temperate countries is not only due to the high alcohol tolerance of the species[6], but also to the behavioral characteristics described here.

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Cytogenetics of South American akodont rodents (Cricetidae). V. Segregation of chromosome No. 1 polymorphism in *Akodon molinae*[1]

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Summary. Akodon molinae is polymorphic with 2n = 42, 43, 44, where the metacentric autosome No. 1 is homologous to 2 acrocentrics 1a and 1b. Matings between 2n = 43 heterozygotes 1/1a, 1b gave a surplus of 1/1 offspring, a moderate reduction of heterozygous and a strong reduction of homozygous 1a, 1b/1a, 1b offspring. The latter type also has a highly reduced fertility.

Most species of the genus *Akodon* (Rodentia Cricetidae) exhibit noteworthy chromosomal rearrangements involving the sex chromosomes or the autosomes[2,3]. Among these species, *Akodon molinae* shows a remarkable polymorphism of chromosomes 1. Thus, in a given population of *A. molinae* it is possible to find animals with 42, 43 and 44 chromosomes[3,4]. Specimens with 42 chromosomes have the pair 1 formed by 2 large submetacentric chromosomes easily identifiable; animals having this karyotype are named simple homozygous (SH). Specimens with 43 chromosomes show 1 chromosome No. 1 and 2 medium-sized subterminal chromosomes, 1a and 1b, which pair with the long and short arms of chromosome 1, respectively. The homology of chromosomes 1a and 1b with the arms of chromosome 1 has been determined by the appearance of trivalents in male meiosis and by the equivalent pattern of G-banding exhibited by the long arm of chromosome 1 and the chromosome 1a and by the short arm of chromosome 1 and the chromosome 1b[3,4], animals with 43 chromosomes are designated as heterozygous (Ht). Finally, the specimens with 44 chromosomes have one pair of chromosomes 1a and one pair of chromosomes 1b; these animals are named double homozygous (DH). The remaining chromosomes in the complement of *A. molinae* are acrocentrics, with the exception of the smallest autosomal pair (pair 20) which is metacentric. The X pair is the 2nd acrocentric pair in size while the Y chromosome is one of the smallest acrocentrics of the set.

Material and methods. A laboratory colony of *A. molinae* was started from several mating pairs collected in the area of Chasico, Province of Buenos Aires, in 1972. At the present time, the colony comprises approximately 150 animals in the F_6 or F_7. The karyology of most laboratory specimens was determined in vivo by the diffusion microchamber technique[5]. Heterozygous animals from the F_3 generation were selected and mated. Chromosome analyses of the next filial generation (F_4) were also performed in vivo by the microchamber method. A total of 160 animals in the F_4, derived from 10 pairs of Ht × Ht specimens, are included in this report. The results obtained were statistically analysed by the chi square and the Student t-test.

Results and discussion. Table 1 shows the observed and expected frequencies of SH, Ht and DH animals. The χ^2 test shows that the observed frequencies deviate significantly from the theoretical expectations. Moreover, the t-test indicates that differences between observed and expected numbers result from an increase in SH, a significant decrease in DH animals and a decrease in Ht specimens which is on the borderline of statistical significance.

A preferential segregation of chromosomes 1, 1a and 1b during oogenesis is one of the mechanisms to be considered to explain the observed frequencies of SH, Ht and DH animals. In this process, the chromosomes 1a and 1b would be preferentially included in the polar body nuclei while chromosome 1 would mainly migrate into the egg nucleus. Such a mechanism has been proved regarding the behaviour of sex chromosomes in *Drosophila pseudobscura* and related species[6,7] and also in *Sciara*, in aphids[8,9] and in the moth *Talaeporia*[10,11]. In the case of mammals it has been demonstrated that in XO mice the X chromosome does not segregate randomly but remains preferentially in the oocyte[12]. A non-random segregation would automatically pro-

Table 1. Segregation of chromosomes No. 1, 1a and 1b in *A. molinae* among the offspring of 10 Ht × Ht matings

Karyotype	SH	Ht	DH	χ^2
Observed frequency	74	64	22	$p < 0.0005$
Expected frequency	40	80	40	
Student's t-test	$p < 0.001$	$p > 0.05$	$p < 0.005$	Total: 160 animals

Table 2. Percentage of dead newborns in litters from different mating pairs

Crosses	Number of mating pairs	Number of litters	Newborns ♂	♀	Deads before weaning	Total	Deads (%)
SH × SH	13	30	42	43	19	104	18.2
Ht × Ht	13	35	45	43	37	125	29.6
SH × Ht	8	22	44	32	26	102	25.5
SH × DH	3	12	16	14	11	41	26.8
DH × DH	2	2	2	4	-	6	0.0

Table 3. Fertility of different mating pairs

Crosses	No. of mating pairs	Days of pairing	No. of litters	Total of newborns	Litter size (average)	Fertility index (x) (xx)
SH × SH	13	240	30	144	4.8	1.38 (100%)
Ht × Ht	13	660	35	135	3.8	0.55 (39.7%)
DH × DH	2	720	2	6	3	0.008 (0.58%)

(x) Fertility index $= \frac{\text{No. of litters} \times \text{No. of newborns}}{\text{No. of mating pairs} \times \text{days of pairing}}$. (xx) Numbers between brackets are the fertility expressed in percent.

duce an increase in SH proportional to the decrease of DH animals, maintaining at 50% the proportion of Ht specimens. The data in table 1 apparently deviate from the predictions of the preferential segregation hypothesis.

It is a rule that gametes unite at random. However, this rule breaks down in certain plants[13,14] and in at least one well-documented case in mice, in which the gametes with certain genotypes are better able to effect fertilization[15-18]. Accordingly, it might be surmised that gametes carrying chromosome 1 are preferentially combined with same, less preferentially combined with gametes carrying 1a, 1b, and that the combination of 2 gametes of the last type is selected against.

Our results could be explained also by assuming that SH embryos are better suited to implant and to successfully complete their intrauterine life than Ht embryos; and that the DH embryos are the least viable. Moreover, since the chromosome studies were performed in adult animals, it is possible to speculate that there is an increased mortality of DH with respect to Ht and SH newborns during lactation or weaning periods.

To test the last of these hypotheses we determined the percentage of dead newborns in the litters derived from different crosses. It is clear that if animals with 44 chromosomes die before weaning, the number of survivors will be approximately 25% higher in litters arising from SH × SH matings than in litters from Ht × Ht matings. The data in table 2 show that, as predicted, there is an increase of about 25% in the number of dead newborns in crosses of Ht × Ht compared to SH × SH. However, the number of dead newborns is also high in crosses of SH × Ht or SH × DH animals in which no DH newborns are expected. Accordingly, the above results are far from being conclusive. Therefore, at the present time it is not possible to decide which is the cause underlying our observations regarding the chromosome 1 of *Akodon molinae*. In spite of this, it can be assumed that there is a correlation between the number of chromosomes 1a and 1b in the complement and the viability of the embryos (or newborns). Specimens with a pair each of 1a and 1b are the least viable; 1a and 1b singly represented produce an intermediate viability, while the most frequent animals observed are those lacking the 1a and 1b elements.

Table 3 shows another interesting finding. According to the data in this table, the fertility of Ht and DH animals is only 39.7% and 0.58% the fertility of SH specimens. The testicular histology of DH and Ht males was normal. Therefore, the decreased fertility of these specimens is apparently not related with impairments of spermatogenesis. The decreased viability and remarkably low fertility of DH specimens present a very interesting point. Chromosome 1 may have appeared via pericentric inversion and centric fusion of 1a and 1b chromosomes, or conversely, chromosome 1 may have given rise to chromosomes 1a and 1b by centromeric fissioning followed by pericentric inversion[4]. Bearing in mind that DH animals have decreased survival rates and fertility in laboratory and perhaps also in natural populations, we favour the latter hypothesis concerning the origin of the polymorphism in chromosome 1. The appearance of acrocentric chromosomes by fission of a metacentric element is an evolutionary mechanism which has been proposed and documented by different authors[19-22]. The case of chromosomes No 1 in *A. molinae* may be an example of Robertsonian rearrangement by centromeric fissioning of relatively recent origin.

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