Due to the logarithmic nature of the determinative process we have not used the ratio of hairies to total achenes directly but its logarithm to the bases 0.618 (see above). Thus a head bearing all hairies has an lf of zero, one showing a simple Fibonacci ratio, say 34 hairies in 55, has an lf value of unity, and so on to very small ratios of hairies. The determination becomes difficult below about 3.4% hairies, i.e. an lf value of 7.

The pair of genes that we have identified as operating on this ratio has been designated 'hairy achenes-4' and 'hairy achenes-5', because only the homozygous recessive genotype *ha-4/ha-4* permits the lf value to go beyond 4 (14.6% hairies or fewer) while *ha-5* has to be homozygous in addition to *ha-4* in order to achieve lf values above 5 (9.0% hairies or fewer, figure 2). As a 1st approximation both genes have dominant alleles in the *M. bigelovii* genome, and *ha-4*$^+$ is epistatic over *ha-5*.

This interpretation is based on the observation that only 11 of 142 F2 plants had fewer than 9% hairies. 1 F3 family raised from such a plant bred true for lf values above 5 (15 specimens). The ratio of 11/142 (0.077) is near 1/16 (0.063) expected in a 2-gene system with dominance and epistasis.

The epistatic gene can be followed by 2 linked markers that affect achene morphology. One of these, hairy, with the alleles weak and dense (D) affects the degree of hairiness of the hairy achenes. Since the dominant allele, hy^D, is linked with *ha-4*$^+$, plants with a higher proportion of hairy achenes also have more densely furry ones. The other marker, absence of tuft, *at*, is recessive to an allele causing an apical tuft of hairs on the inner, non-hairy, achenes. Since the recessive allele of *at* is linked with *ha-4*$^+$, plants homozygous for *ha-4*$^+$ can be distinguished by the absence of a tuft on the inner achenes from heterozygous ones in which there is a tuft. On this basis the 3 genotypes +/+, +/*ha-4* and *ha-4/ha-4* occur in the ratio of 35:69:38 in the F2. The 11 plants with lf values above 5 belong to the latter 38.

This analysis of the genetics of capitulum differentiation is only a beginning. There are obviously more factors involved, and the interactions are more complex than they appear here. The table shows that an analysis of the F3 families reveals a more complex interaction between *ha-4* and *ha-5* than simple dominance. As mentioned above, there are also strain differences. Chambers has shown that the tuft in another cross between *M. pygmaea* and *M. bigelovii* is determined by 2 genes[4]. One of these 2 genes may be our *at*, but an unequivocal identification awaits further work.

Range of values for the lf (logarithm to base 0.618) of the ratio of hairy to total achenes for the 6 genotypes homozygous for *ha-4* alleles. The values are based on segregation in F3 families. Genotypes heterozygous for *ha-4*$^+$/*ha-4* should correspond exactly to the homozygous dominant ones

	ha-4$^+$/*ha-4*$^+$	*ha-4/ha-4*
ha-5$^+$/*ha-5*$^+$	2.1–2.9	3.0–3.9
ha-5$^+$/*ha-5*	2.9–3.0	3.9–4.9
ha-5/ha-5	3.3–3.9	5.1–∞

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Chromosome variability in Brazilian specimens of *Rattus rattus* (2n = 38)[1]

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Summary. In 8 specimens of *Rattus rattus* collected in the state of São Paulo, Brazil, a diploid number of 2n = 38 was found. Contrary to the supposed lack of karyotypic variability in South American populations, 5 specimens were found to be heterozygotes for a pericentric inversion in the autosome no. 8.

The black rat *(Rattus rattus)* which is widely distributed all over the world shows geographical chromosome variability as well as several types of intrapopulation polymorphism, due to Robertsonian fusions, pericentric inversions and supernumerary chromosomes[3–5]. Polymorphic variations of C-band patterns are also found[6]. 3 geographical variants, the Asian (2n = 42), the Ceylon (2n = 40), and the Oceanian (2n = 38) types have been described. It is suggested that the Asian karyotype is the ancestral form and that the 2 others developed sequentially by centric fusions[3,5,6].

It is supposed that *R. rattus* from European populations with an Oceanian karyotype was introduced in South America[3]. In fact, all specimens heretofore collected in Argentina, Brazil, Chile, Ecuador and Venezuela have disclosed the same karyotype (2n = 38)[7–10]. The lack of chromosomal variability is, according to Patton and Myers[10] characteristic of all introduced populations of black rats in Europe, Australia, Africa and America. However, in a sample of *R. rattus* from Europe, a polymorphism due to supernumerary chromosomes has been found[11].

Reig et al.[9] suggested that the 2n = 42 form might have migrated to South America also, but the descendants of such stocks either have not yet been discovered or they were unsuccessful as colonizers. The present paper reports the cytogenetic studies on *R. rattus* collected from different areas of the state of São Paulo (Brazil), which reveal a structural rearrangement in the autosome No. 8 in some of the specimens.

3 males were collected from Americana, 2 males and 2

females from Taubaté and 1 female from Pindamonhangaba. For chromosome analysis air-dried preparations of bone marrow, spleen and testis were made after in vivo colchicine treatment; 0,075 M KCl was used as hypotonic solution and 3:1 methanol-acetic acid as fixative. Conventional staining was done with buffered Giemsa 2%, pH 6.8. G-bands were obtained by trypsin treatment[12], and Q-bands according to Caspersson et al.[13].

All specimens had a diploid number of 2n=38. 2 males from Americana and 1 female from Taubaté presented a typical Oceanian karyotype. The G-band patterns were similar to those found in 2n=38 *R. rattus* from Australia and India[14]. The remaining specimens, 3 males (2 from Taubaté and one from Americana) and 2 females (1 from Taubaté and 1 from Pindamonhangaba) also had 38 chromosomes, which included an autosome heteromorphic pair, consisting of an acrocentric and a subtelocentric (figure 1). Q-bands allowed the identification of the heteromorphic pair as No. 8, with a pericentric inversion giving rise to the subtelocentric (figure 2). However, the heterozygote inversion was not detectable by meiotic analysis in male rats.

The diploid number of 2n=38 in our sample is not surprising, since all South American black rats studied so far, including Brazilian specimens from Rio Grande do Sul[7,8], have been found to have this diploid number. However, contrary to the supposed lack of karyotypic variability in the South American populations[9,10], heteromorphism due to a pericentric inversion is seen to occur with a high frequency. Since this rearrangement has never been found in the original populations from abroad, it is most probable that it has recently arisen and spread rapidly.

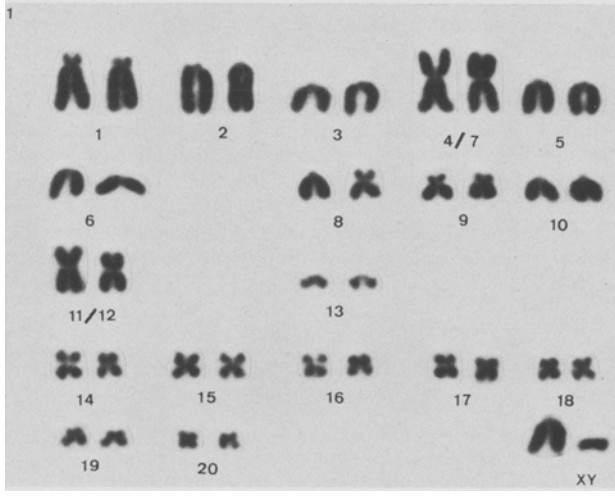

Fig. 1. Karyotype of a male *R. rattus* (2n=38) heterozygote for a pericentric inversion in pair No. 8.

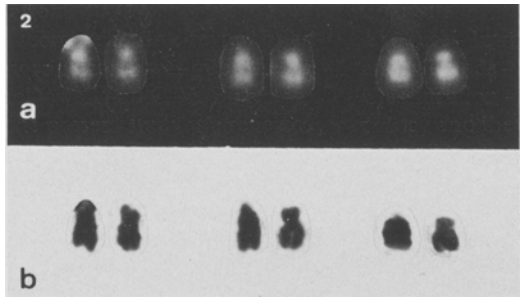

Fig. 2. Chromosome pair No. 8 from 3 metaphases of a male *R. rattus* heterozygote for a pericentric inversion. a) after Q-banding; b) the same chromosome pairs after Giemsa staining.

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Morphogenetic effect of precocene I and II on *Schistocerca gregaria* (Forsk)

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Summary. 4th instar nymphs of *Schistocerca gregaria* exposed to precocene I and II by topical application metamorphosed precociously. The ED_{50} of both compounds were evaluated and, unexpectedly, precocene I was found to be more active than precocene II. All adultiforms were identical and in an advanced form.

Although considerable interest has been devoted to insect juvenile hormones, molting hormones (ecdysones) and synthetic juvenile hormone mimics, there is relatively little work done on inhibitors of hormones regulating metamorphosis in insects[2]. Such inhibitors could be used to disrupt the hormone-regulated processes of insects and lead to new types of chemicals for safe, selective insect control. Precocene I (7-methoxy-2,2-dimethylchromene) and precocene II (6,7-dimethoxy-2,2-dimethylchromene) possess anti-allatotropic properties and induce precocious metamorphosis in several insect orders[3]. These activities have been explored mostly using *Oncopeltus fasciatus*[3-6] and