(Burroughs Wellcome, cat. No. HA 16) was added to the Cariama cristata culture in the amount of 0.2 ml/5 ml media. The purified PHA seemed to cause less agglutination of the cells than the regular PHA (Difco) which was used on the S. serpentarius cells. The cultures were interrupted with 0.13 ml of 0.001% colchicine added for 1 h and 15 min and then a hypotonic solution of 0.075 M KCl was added for 20 min. The cells were next fixed with 3:1 methanol/acetic acid and slides made in the usual manner.

Results and discussion. The karyotype of the secretary bird, Sagittarius serpentarius, had 36 macrochromosomes of quite large size and a diploid number of approximately 90. The macrochromosomes consist primarily of metacentric and a few submetacentric pairs. Only the first 21 chromosome pairs are shown in figure 1. In several karyotypes prepared there was 1 heteromorphic pair which is assumed to be ZW and shown as the first pair. While the identification of these sex chromosomes must be considered tentative, these elements are consistently different from other pairs, are not unlike what is 2 W in other birds and, most important for the present consideration, they differ remarkably from chromosomes in the Cariama karyotype. Findings of Sagittarius chromosomes are essentially similar to those published by de Boer[2].

The Seriema, Cariama cristata, has approximately 94 chromosomes including numerous microchromosomes of which only the first 21 pairs are shown (figure 2). The karyotype consists of only acrocentric chromosomes with the first pair being easily separated because of its large size. There is a gradual decrease in the size of the chromosomes to the miniature size of the microchromosomes. No dimorphic sex chromosomes could be identified and the bird was, therefore, considered to be a male.

The karyotype of Cariama, composed of only acrocentrics is considerably more primitive than that of Sagittarius. This would suggest that the close relationship of these 2 species by Jollie[4] cannot be supported by karyological studies and that Cariamidae indeed should be considered a separate group.

New inversion of the pair no. 3 chromosome in a black rat

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Summary. A Japanese black rat (Rattus rattus tanezumi) with a subtelocentric pair no. 3 chromosome was found in Gotenba, Japan. By comparison of the length in both members of the chromosome pair, and from the G-band pattern, the subtelocentrics seemed to have developed from the original acrocentrics by the pericentric inversion.

Polymorphism of pair no. 1, 9 and 13 chromosomes, with respect to acrocentrics and subtelocentrics, has been found widely in black rats, Rattus rattus, collected in Japan and also in several other countries in East and Southeast Asia[2-6]. Based on measurment of the length of the acrocentrics and subtelocentrics and also on comparison of the G-banding patterns between them, it was assumed that the subtelocentrics had developed by periocentric inversion from the acrocentrics[2-4,6]. Pair no. 3 chromosomes in the black rats collected in several countries in the world, however, was usually characterized by having the acrocentric centromere, so far as the present author examined them. Recently a subtelocentric pair no. 3 chromosomes was found in a black rat collected in Gotenba, Shizuoka-ken, Japan. As this inversion is a new finding in the animal, detail of the karyotype will be reported.

The black rat (Rattus rattus tanezumi) was collected in the field of Gotenba, Shizuoka-ken, Japan. The chromosomes of the rat were observed in cultured cells of the tail tip of the animal by our routine procedure[3]. G-bands staining was used according to the tripsin treatment technique[7], and the C-band was stained by application of a slight modification of Sumner's technique[8].

Chromosome number of the black rat was 42 in the diploid cells, likewise in the other black rats captured in Japan. Basic karyotype of the black rat is generally characterized by having 13 acrocentric autosome pairs (nos 1–13) and 7 small metacentric autosome pairs (nos 14–20) and acrocentric X and Y chromosomes. The pairs no. 1, 9 and 13 of the black rats are remarkable by showing an acrocentric and a subtelocentric polymorphism as already reported[2-6]. The present material showed acrocentric pair no. 1 and 9, but acrocentric and subtelocentric heteromorphic pair no. 13. Out of the heterologors pair no. 13, the pair no. 3 was remarkable in having the acrocentric and subtelocentric heterologous pair (figure 1 A, B). As the lenght of the acrocentrics and subtelocentrics was almost similar, the subtelocentrics seem to have developed by pericentric inversion of the acrocentric chromosome.

The pair no. 3 is remarkable in having its characteristic G-banding pattern as already reported by the present author[9]. From the banding pattern analysis, it strongly suggests that pericentric inversion could have occurred in about one-third of the acrocentric pair no. 3 chromosomes (figure 2, A), and then the subtelocentrics developed.

C-band pattern of the Japanese black rats has been reported by Yosida and Sagai[8]. According to them, the

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Japanese black rats are remarkable by having no C-band pattern in many acrocentric pairs. The pair no. 3 chromosomes of the black rat concerned here were also characterized by deficiency of C-bands in the acrocentrics and in its subtelocentric partner. C-bands of the other pairs in the rat are as follows; pairs no 1, 5 and 13 were heteromorphic; pairs nos 2, 3, 4, 6, 7, 8, 10, 11 had no bands and only pairs nos 9 and 12 showed the homomorphic bands. In the previous paper, the present author[8] pointed out that the presence and absence of C-bands in the pair no. 1 is closely related to its polymorphic character; namely the band was observed in only the acrocentrics, but not in the subtelocentrics. The black rat in the present study, however, is an exceptional case, because heteromorphic C-band was observed in the pair no. 1, although the pair is characterized by both acrocentrics. A noticeable fact is that the length of 1 member of the pair no. 1, which has no C-band, was usually shorter than that of the other partner. It seems that a deletion occurred in the short arm of the subtelocentric pair no. 1 and then the acrocentric no. 1 chromosome without the C-band could have developed (figure 2B).

The supposition that the original form of the pair no. 3 in the black rat is the acrocentrics is reasonable, because it was usually observed by many investigators[2–9]. Therefore, the subtelocentric pair no. 3 observed in the present material leads me to conclude that it developed by the pericentric inversion from the acrocentrics. The present author have observed already about 1000 black rats from Japan and the other countries, but the subtelocentric pair no. 3 could not be found, except in 1 rat reported in this paper. This inversion seems to have developed recently in Gotenba area of Japan. The animal is now breeding in the author's laboratory and further study will be reported in the future.

In the Norway rat, the telocentric (acrocentric) and subtelocentric polymorphism of the pair no. 3 chromosomes has been reported by the present author[10]. In this case, the short arm of the subtelocentrics was very small. In the black rat, however, the short arm of the subtelocentric pair no. 3 was very large and it is easily identified from the other acrocentric partner.

Karyotype of Asian type black rats with 2n = 42 are remarkable by having polymorphic pairs nos 1, 9 and 13 with respect to acrocentrics and subtelocentrics. Based on several karyological investigations on the black rats, the present author suggested that the original type of this pair is acrocentrics, and the subtelocentrics have developed by pericentric inversion[2–4]. Occurrence of the subtelocentric pair no. 3 seems to provide clear evidence in support of the above suggestion.

An acrocentric pair no. 1 without the C-band was the first observation so far as the present author is concerned. It might have occurred by deletion of a short arm of the

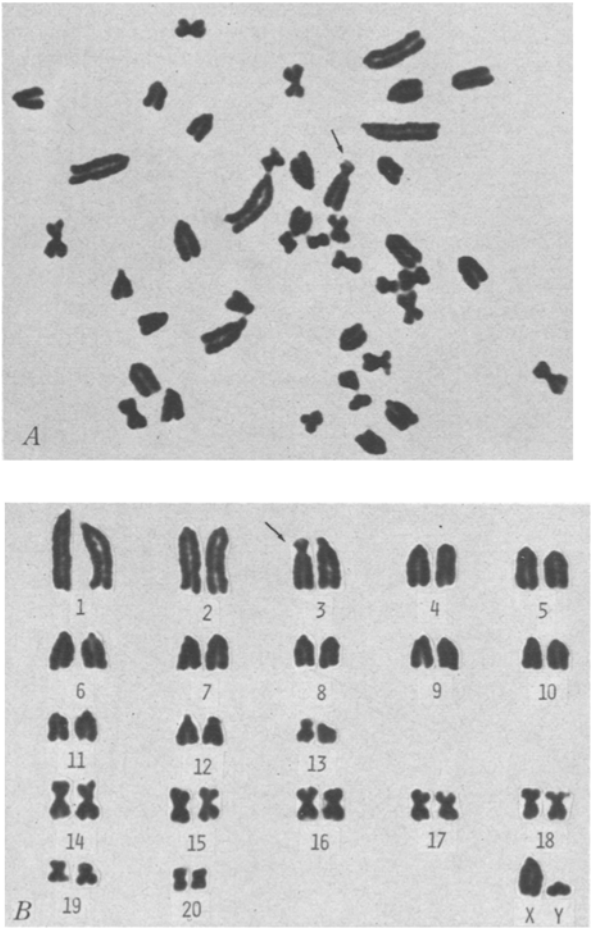

Fig. 1. Chromosomes in a Japanese black rat (Rattus rattus tanezumi) with the subtelocentric pair no. 3 chromosome (indicated by an arrow). *A* metaphase, *B* its karyotype.

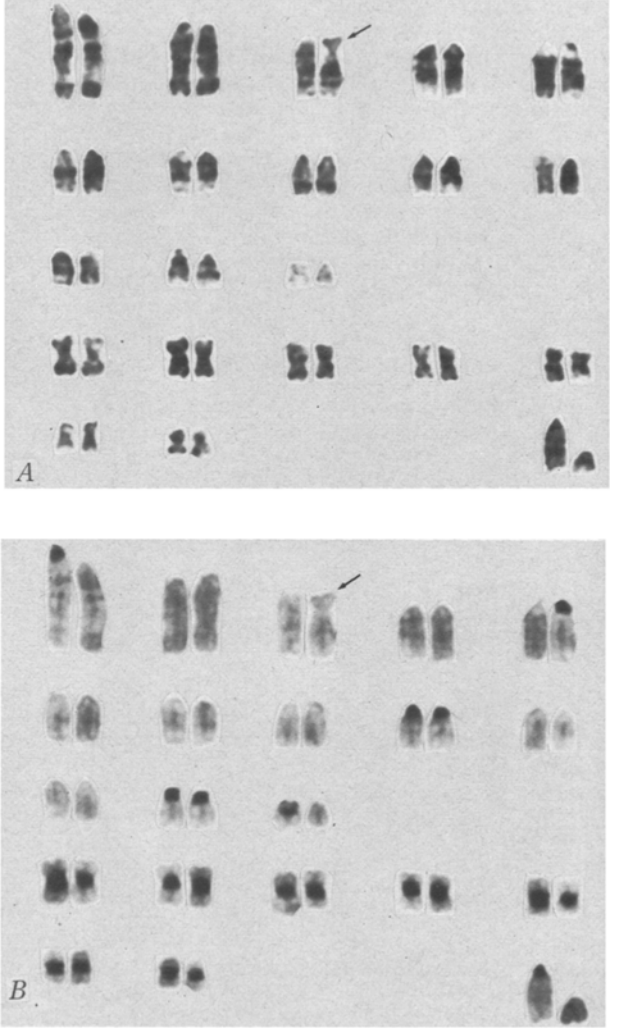

Fig. 2. Banding karyotypes in a Japanese black rat with the subtelocentric pair no 3 (indicated by an arrow). *A* G-bands, *B* C-bands.

originally subtelocentrics pair no. 1. Although fate of the deleted piece of the short arm is still uncertain, it might have been eliminated from the chromosome complement. Another explanation of the fate of the arm, however, is that the deleted arm translocated to the pair no. 3, and then the subtelocentric no. 3 chromosome developed. To determine whether the subtelocentric no. 3 has occurred by pericentric inversion or by translocation is difficult at present. Based on the measurement of length of chromosomes and the G-band analysis, the former event seems to be more likely than the latter.

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Heritability as an indicator of genetical variation in fecundity

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Summary. Heritability is well known to be a poor indicator of genetical variation in fitness. We show here that it is also an inadequate measure of genetical variation in fecundity.

Ewens and Thomson[3] have recently shown, for a general multilocus system, that the additive genetic variance in fitness is zero at equilibrium. They point out that this implies (from the definition of heritability) that the heritability of fitness in such a system will also be zero. Haldane[4] showed, for a single autosomal locus, that parent-offspring correlation in fitness (and hence its heritability) would be zero, but not the sib correlation. He emphasized the strong contrast between Darwinian fitness and other metric traits, where detectable additive genetical variation leads to nonzero heritability estimates. Sex-linkage is a complication[5], and systems not in equilibrium will depart somewhat from zero heritabilities in fitness, but nonetheless Haldane's results have considerable evolutionary interest. We report here results of a simulation study of the heritability of fecundity, showing that this is a trait where genetical variability in fecundity may be masked by the form of the distribution of fecundity.

Following Gillespie[6], we can consider the following model, for variation in fecundity determined by a single locus:

Genotype	A_1A_1	A_1A_2	A_2A_2
Mean	$1+\mu_1$	$1+\mu_2$	$1+\mu_3$
Variance	$1+\sigma^2_1$	$1+\sigma^2_2$	$1+\sigma^2_3$

In general, selection can act on both mean and variance[6], and stability is unlikely for large values of σ^2 in large populations[6,7]. In small populations, fixation is generally more rapid than with neutral alleles starting at the same frequency with the same variance effective population number.

That genetical variability in fecundity is determined by a single locus is most unlikely. We have accordingly considered by simulation a 10 locus elaboration of Gillespie's model, such that for each locus, $\mu_j = (j-1)\ \varepsilon_\mu$, $j = 1,2,3$, $\sigma^2 = (j-1)\ \varepsilon_{\sigma 2}$, $j = 1,2,3$. Varying the values of ε_μ and $\varepsilon_{\sigma 2}$ allows the distribution to vary from under-dispersed to over-dispersed, in this case from binomial through Poisson to negative binomial, these being appropriate to fecundity in various organisms[8,9]. If the frequencies of the 3 genotypes at the i^{th} locus are P_{ij}, $j = 1,2,3$, then popula-

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The relationship between the form of the distribution of family size and estimated heritability of family size

Distribution	ε_μ	ε_σ^2	Initial Mean	Variance	Initial I Variance/(mean)^2	h^2	T	N_e	n
Negative	0.1	0.2	2	3	0.75	0.00 ± 0.02	319.0 ± 45.2	80.0	6
binomial	0.2	0.4	3	5	0.56	0.09 ± 0.05	195.8 ± 13.9	96.3	5
	0.5	1.0	6	11	0.31	0.36 ± 0.07	141.3 ± 21.4	124.7	6
	1.0	2.0	11	21	0.17	0.33 ± 0.10	93.0 ± 10.6	220.9	5
Poisson	0.01	0.01	1.1	1.1	0.91	0.00 ± 0.03	615.7 ± 80.1	55.0	3
	0.05	0.05	1.5	1.5	0.67	0.09 ± 0.08	253.2 ± 25.3	66.1	4
	0.1	0.1	2	2	0.5	0.03 ± 0.01	325.0 ± 51.6	95.7	4
	1.0	1.0	11	11	0.09	0.60 ± 0.15	67.0 ± 10.8	289.5	4
Binomial	0.1	0.08	2	1.8	0.45	0.30 ± 0.16	68.2 ± 9.9	73.8	4
	0.2	0.1	3	2	0.22	0.00 ± 0.06	163.0 ± 18.0	180.0	4
	0.5	0.1	6	2	0.02	0.20 ± 0.06	286.2 ± 51.7	391.3	5
	1.0	0.1	11	2	0.02	0.00 ± 0.06	324.2 ± 42.3	930.8	5

For explanation of symbols see text. n, Number of replicates.