the neocortex in the circumscribed area. The uptake of radiochemical by some limbic cortical structures was in agreement with the findings of PFAFF[4,5] as far as the olfactory tubercle and piriform cortex are concerned. However, no incorporation into the hippocampal archicortex has been found at one with ANDERSON and GREENWALD[6].

A repeatedly established excitatory action exerted by estrogens in the central nervous system as shown by a decrease in threshold for electrically induced seizures (reviewed by WOODBURY and VERNADAKIS[7]) causes an impression of a rather diffuse effect of estrogens on the cerebral cortex. We speculate about the possible relationship between the demonstrated preferential localization of tritiated estradiol in the neocortex and the efferent cortico-hypothalamic connections.

Zusammenfassung. Durch autoradiographische Untersuchung wurde die Einlagerung von Radioaktivität in ein begrenztes Gebiet des Neocortex der Rattenweibchen nach einmaliger Verabreichung von ^{3}H-Östradiol im Alter von 5 bis 50 Tagen nachgewiesen. Die reduzierten Silberkörner zeigen eine vorwiegend perinukleare Akkumulation, was für die Zellen der Östrogen-Zielgewebe typisch ist.

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Centric Fusion in the Malayan House Rat, *Rattus rattus diardii* (Rodentia, Muridae)

The Malayan house rat is currently recognized as a form of *Rattus rattus* viz. *R. r. diardii* (CHASEN[1], MEDWAY[2], YONG[3]). Its karyotype has been reported by YONG[3] to consist of 11 pairs of acrocentric, 2 pairs of subtelocentric, and 7 pairs of metacentric autosomes, acrocentric *X* and acrocentric *Y* sex chromosomes, with $2n = 42$. The longest autosomal pair has been found to be heteromorphic giving rise to 3 karyotypic classes viz. homozygous acrocentric, homozygous subtelocentric, and heterozygous individuals (YONG and DHALIWAL[4]). A high proportion of the Malayan house rat has also been reported to possess chromosome numbers differing from the normal diploid number of 42 (YONG and DHALIWAL[4], YONG[5]). The present report deals with a case of structural aberration due to Robertsonian-type translocation.

In the course of a population cytogenetic study of the Malayan house rat, a single male was found to possess 41 chromosomes and characterized by an extremely large biarmed (submetacentric) chromosome (Figure 1) which is not present in the normal karyotype (Figure 2).

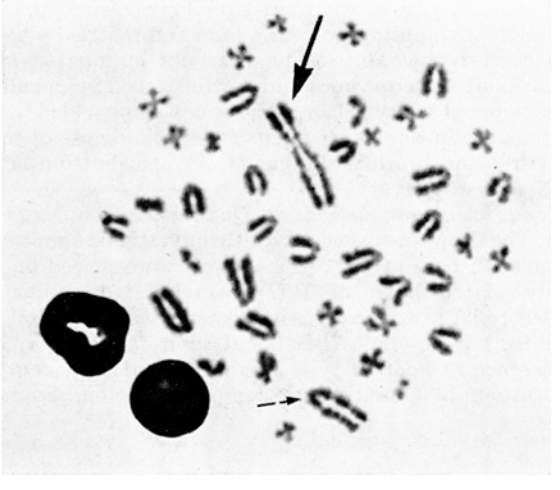

Fig. 1. Metaphase of *Rattus rattus diardii* with 41 chromosomes due to Robertsonian-type translocation. Thick arrow, translocated chromosome; thin, broken arrow, longest autosome.

Detailed karyotype study shows that this biarmed chromosome is most probably the result of centric fusion between the longest autosome and the third longest acrocentric autosome in the complement. There is, however, no means of ascertaining whether the *X* chromosome (the fourth longest acrocentric in the complement, YONG[3]) is involved instead of the third longest autosome.

This case of centric fusion in *Rattus rattus diardii* substantiates 3 earlier reports (BIANCHI et al.[6], CAPANNA et al.[7], YOSIDA et al.[8]) of $2n = 38$ in 3 widely separated populations of *R. rattus* (viz. Italy, South America and Oceania). All 3 populations are characterized by the presence of 2 pairs of large metacentric (one larger than the other), 7 pairs of acrocentric and 2 pairs of subtelocentric (1 larger than the other) autosomes. BIANCHI et al.[6] and YOSIDA et al.[8] reported 7 pairs of small metacentric autosomes, while CAPANNA et al.[7] reported 6 pairs of small metacentric and a pair of small submetacentric. The 2 pairs of large metacentric autosomes were attributed to Robertsonian-type translocation between heterologous chromosomes resulting in the reduction of $2n = 42$ to $2n = 38$. The autosomes involved in centric fusion were medium-sized and small acrocentrics. In all three instances only homozygous animals were reported.

The present observation of a single centric fusion involving the longest autosome and possibly a medium-sized acrocentric autosome is in direct contrast to the $2n = 38$ *Rattus rattus* where the longest autosome is

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homomorphic (subtelocentric). This seems to favour the hypothesis that the $2n = 38$ 'populations are interconnected by the same system that is responsible for the ubiquitous diffusion of the species, which is that associated with the black rat's condition as man's commensal' (CAPANNA et al.[7]). Moreover, the probability that 'centric fusion has occurred between the same pairs of autosomes independently' (CAPANNA et al.[7]) in 3 widely separated $2n = 38$ populations is rather remote.

Another interesting point is that the longest autosome in the Asian ($2n = 42$) populations of *Rattus rattus* seems to possess a readiness for aberration. Heteromorphism has been reported for the Japan and Korean taxa (YOSIDA et al.[9,10]), Malayan taxon (YONG and DHALIWAL[4]) and also the Vietnamese taxon (T. C. HSU, personal communication). In the present report, the longest autosome is involved in centric fusion. On the other hand, the longest autosome in the $2n = 38$ populations is homomorphic.

Fig. 2. Normal metaphase of *Rattus rattus diardii* with 42 chromosomes.

It is noteworthy that these 2 major populations exhibit different chromosomal polymorphism. This is probably not a result of environmental conditions as chromosomal polymorphism has been found in the Malayan house shrew, *Suncus murinus*, in which Robertsonian-type translocation is responsible for the existence of $2n = 38$, 39, and 40 individuals within the same population (YONG, Experientia, in press).

As stated by CAPANNA et al.[7] 'the study of the polymorphism of *Rattus rattus* appears highly promising'. It would be exciting if there should exist other populations in addition to the existing $2n = 42$ (Asian) and $2n = 38$ (European, S. American, Oceanian) populations.

Zusammenfassung. Bei einem Männchen von *Rattus rattus diardii* aus Kuala Lumpur (Malaysia) wurden 41 Chromosomen (normal $2n = 42$) gefunden, was mit der Robertson'schen Translokation in Zusammenhang stehen dürfte, welche die Fusion 2 einarmiger Autosomen in ein grosses, zweiarmiges Chromosom vollzieht.

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[10] T. H. YOSIDA, Y. MORIGUCHI, Y. S. KANG and K. SHIMAKURA, A. Rep. natn. Inst. Genet., Japan *17*, 61 (1967).

Studies on rII Region of T2L Phage

GANDHI, MEHTA and MODI[1] reported that rII region of phage T2L consists of one cistron and that in crosses between the mutants studied the maximal frequency of recombinants does not exceed 0.13%. In the course of the comparative genetic research of r-mutants of phages T2L and T4B, we obtained results contrary to that of GANDHI et al.[1]. It is evident from our results that rII region of phage T2L consists of two cistrons, the length of which corresponds to that of rII region of phage T4.

Materials and methods. Bacteria. Strain of *Escherichia coli* B was used as a host for the titrations of phages and for plating the progeny of crosses between rII mutants; *E. coli* BB was used to obtain rII mutants in high titer as on B cells the titres of r mutants are not as rule high. *E. coli* K12 (λ) and *E. coli* B (λ) were used as a plating indicator for assaying the revertants and recombinants and also in the experiments on complementation. Strain B (λ) was kindly supplied by Dr. ARBER.

Bacteriophages. Phage T2L of the wild type was obtained from laboratory of Dr. GOLDFARB (Institute of General Genetics, Moscow). Deletion mutants of rII region of phage T4B rII638, rII168, rIIW8-33 were obtained from Dr. BENZER. Mutant rII638 carries the deletion of the whole rIIB cistron, rII168 and rIIW8-33 contain the small deletions in rIIA and rIIB cistrons of phage T4B, respectively.

The phage T2L r^+ was treated with 0.2 M solution of HCl-hydroxylamine in the $^1/_{15}M$ Na-phosphate buffer pH = 6.0 at 4–10 h. Mutagenic reaction was stopped by dilution of sample in 2% solution of acetone in broth. Mutagenized phage was plated on Petri dishes and the selection of r-mutants from the pure and mottled plaques was carried out. The sample was not eliminated from mutational heterozygotes and thus the independent occurrence of every selected mutant was provided[2]. The media used in our experiments is tryptic digest of meat ('broth'), and broth with agar (1.2% agar-bottom layer, 0.7% agar-top layer).

Complementation methods. a) Qualitative complementation. The drops of suspension of the investigated mutants, taken with titre of 1×10^7 phages/ml were placed on the newly plated lawn of B (λ) bacteria (approximately 1×10^8 cells) in top layer with tester phage (multiplicity of infection is 0.1). After incubation for 18–20 h the occurrence of spot of lysis was estimated as a complementation. b) Quantitative complementation. Bacteria

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