Robertsonian translocation, pericentric inversion and heterochromatin block in the evolution of the Tailless Fruit Bat[1]

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Summary. The karyotype of *Megaerops ecaudatus* from Peninsular Malaysia consists of 24 chromosomes as compared to 2n = 26 for specimens from Thailand. The difference in diploid number is the result of Robertsonian translocation. The Peninsular Malaysian specimens also exhibit pericentric inversion in the smallest pair of autosomes, and the presence of a totally heterochromatic short arm in the second longest metacentric pair. There is 1 pair of Ag-NOR, located on the secondary constriction of the longest metacentric autosome.

The Tailless Fruit Bat, *Megaerops ecaudatus* (Temminck) (Mammalia, Chiroptera) is a monotypic species. It is distributed from Thailand and the Indochinese region southwards to Peninsular Malaysia, Sumatra and Borneo[2]. Although it has a wide geographical distribution, no subspecies has been described. The bats from Thailand have been found to possess a diploid number of 26[3,4]. It comprises 4 pairs of metacentric, 5 pairs of subacrocentric and 3 pairs of acrocentric autosomes, and subacrocentric X and acrocentric Y sex chromosomes. Recently, 2 female specimens of *Megaerops ecaudatus* (one collected in November 1981 and the other in April 1983) from the Cameron Highlands, Peninsular Malaysia, were available for chromosomal studies. The diploid number and the detailed karyotype of these Peninsular Malaysian bats differ from those reported for the sepcimens from Thailand.

The karyotype of the Peninsular Malaysian *Megaerops ecaudatus* consists of 24 chromosomes (fig. 1). This is the second example of the lowest diploid number for the fruit bats; the other example with 2n = 24 is *Balionycteris maculata*[5]. Only biarmed chromosomes are found in the present materials. Comparisons with the karyotype of the Thailand materials show that the difference in chromosome number is the result of Robertsonian translocation, involving the 2 larger pairs of acrocentric autosomes in the Thailand karyotype with 2n = 26. This mechanism of Robertsonian translocation has been reported in the flat-headed bats (*Tylonycteris* spp.) from Peninsular Malaysia[6]. The smallest pair of autosomes in the Peninsular Malaysian bats is metacentric in contrast to acrocentric in the Thailand specimens. This difference in the morphology of the smallest pair of autosomes most probably results from pericentric inversion. In the present materials, the karyotype consists of 5 pairs of large, distinctly metacentric chromosomes as compared to 4 pairs in the Thailand materials. This indicates that another pericentric inversion might have taken place in the course of evolution. As no G-banded karyotype of the Thailand taxon is available for comparison, it cannot be determined at this stage whether other chromsomal rearrangements occur. The longest pair of autosomes in both the Peninsular Malaysian and Thailand *Megaerops ecaudatus* is characterized by the presence of a secondary constriction. This secondary constriction is shown by silver staining in the present material to be the nucleolus organizer region (fig. 2).

In the present study, C-banding reveals that the short arm of the 2nd longest metacentric chromosome is totally hetero-

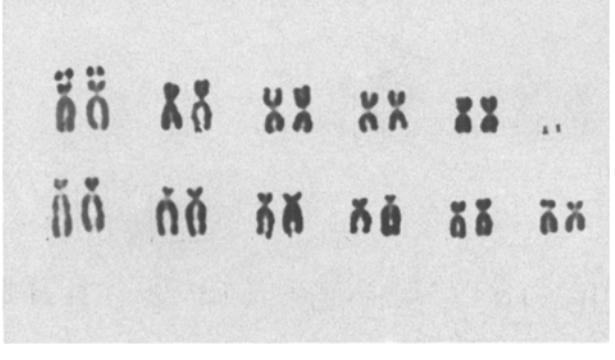

Figure 1. Conventional karyotype of a female *Megaerops ecaudatus* from Peninsular Malaysia.

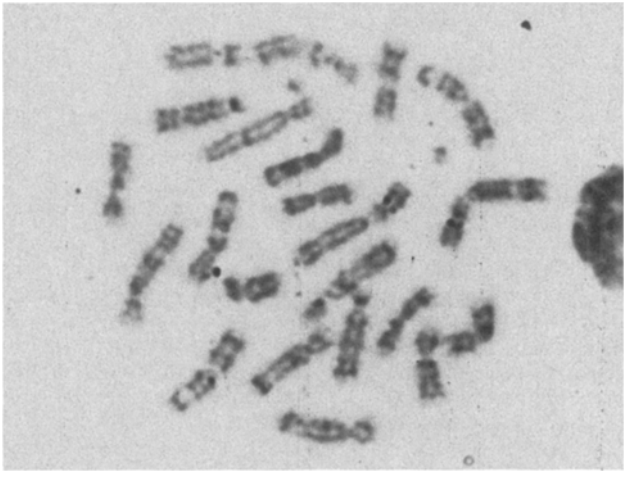

Figure 2. A metaphase plate showing the nucleolus organizer region of a female *Megaerops ecaudatus* from Peninsular Malaysia. The Ag-NORs (arrowed) are revealed by incubating the chromosomal preparation in 7 parts 50% $AgNO_3$ and 3 parts 0.02% formic acid for 2 h at 60 °C. After the $AgNO_3$-formic acid treatment, the slide was treated with 0.025% trypsin for about 8 min and stained for 1 h in 4% Giemsa solution.

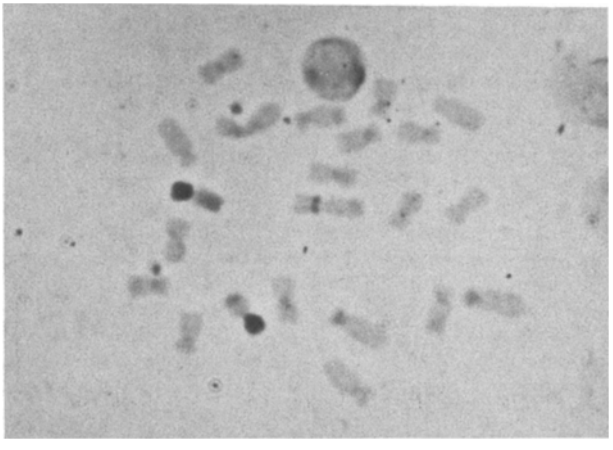

Figure 3. A C-banded metaphase plate of a female *Megaerops ecaudatus* from Peninsular Malaysia. C-bands were obtained by $Ba(OH)_2$ treatment.

chromatic (fig. 3). One arm of the smallest chromosome is also highly heterochromatic. The present finding poses the question whether the Peninsular Malaysian and Thailand populations of *Megaerops ecaudatus* are conspecific. To answer this, more specimens, collected throughout the distribution range of this bat, need to be studied. Meanwhile, on the basis of large chromosomal differentiation, the 2 populations may be accorded subspecific status, viz. *Megaerops ecaudatus malayanus* for the Peninsular Malaysian taxon and *Megaerops ecaudatus siamensis* for the Thailand taxon.

1 This work is supported by a University of Malaya research grant.
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Hybridization between Robertsonian karyotypic races of the common shrew *Sorex araneus*

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Summary. British common shrews of the Aberdeen, Oxford and Hermitage Robertsonian karyotypic races were hybridized successfully in captivity. Hybrids, both simple Robertsonian heterozygotes and double Robertsonian heterozygotes with monobrachial homology, have been identified in an area of contact between the Oxford and Hermitage races. The relative fertility of these two types of hybrid is considered.

Many closely related taxa, classified as separate species or races, differ by karyotypic rearrangements. Of interest is the extent to which such taxa may interbreed, and in particular the contribution of the karyotypic rearrangements to any reproductive isolation. Such a contribution may be direct, through reduction of fertility in hybrids (e.g. due to nondisjunction at anaphase I of meiosis associated with karyotypic heterozygosity) or indirect, as in the case of assortative mating which has arisen as a consequence of selection against karyotypic heterozygotes because of their reduced fertility.

The common shrew *Sorex araneus*, an insectivore with a Palaearctic distribution, is a spectacular example of a mammalian species that is multiplely subdivided into karyotypic races. Altogether 12 races have been described (reviewed by Searle[3]); each of these races differs by presence or absence of the products of Robertsonian fusion mutations. However, little is known of the extent to which these races may interbreed. The area of contact between the northern Swedish and central Swedish karyotypic races of common shrew has been fairly accurately delimited and 1 hybrid individual has been identified[4]. Hybrids have also been detected in recent studies of the area of contact between the Novosibirsk and Chaldejevo (Tomsk) races of common shrew in Siberia[5]. With regards laboratory studies, no attempts have been made to interbreed karyotypic races of common shrew in captivity.

Three karyotypic races of common shrew have been found in Britain. The Aberdeen race occurs in north-eastern Scotland, the Oxford race in southern Scotland and central and northern England and the Hermitage race in southern England[3]. In terms of the standard nomenclature[4], these races are characterized by the following arm combinations: Aberdeen 3*hi* 4*jl* 5*gm* 6*ko* 7*np* 8*qr*; Oxford 3*hi* 4*jl* 5*gm* 6*kq* 7*no* 8*pr*; Hermitage 3*hi* 4*jl* 5*gm* 6*ko* 7,8 *n/p/q/r*. Robertsonian polymorphism is found in all 3 races such that arm combinations *jl* (Aberdeen); *jl, kq, no* and *pr* (Oxford); and *jl* and *ko* (Hermitage) may occur as metacentrics or twin-acrocentrics.

This paper describes attempts to interbreed the British races in captivity, cases of hybridization between 2 of these races in nature and data on fertility of hybrids in nature.

Materials and methods. Common shrews were trapped in Grampian region (Aberdeen race shrews) and Oxfordshire, Berkshire and Hampshire (Oxford race, Hermitage race, Oxford-Hermitage hybrid shrews). For breeding, shrews were kept as single pairs in large enclosures and fed twice daily on a diet based on offal and cereal with a vitamin supplement[6]. Disturbance to breeding shrews was kept to a minimum until weaning, when young were counted and sacrificed. Direct, air-dried, mitotic chromosome preparations were made from bone marrow and G-banded by a composite method[7] in which the preparations are first treated as in the ASG method[8] but with a trypsinization step[9] included prior to staining. Meiotic chromosome preparations were made by a modification of the Evans method[10].

Results. Successful crosses in captivity between Oxford and Aberdeen race shrews, Oxford and Hermitage race shrews and

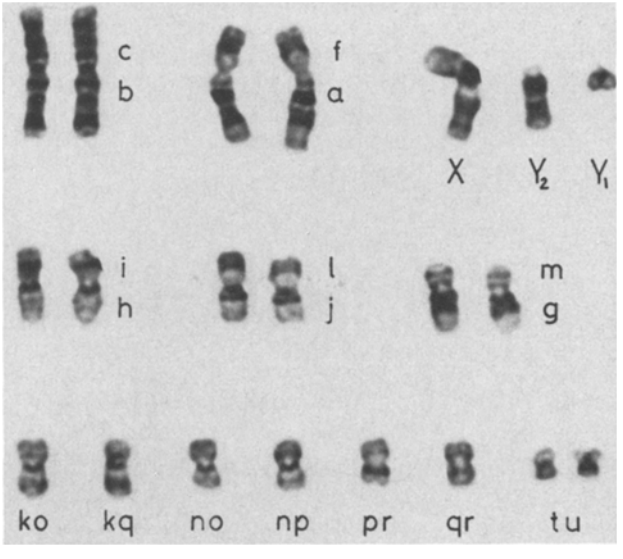

Figure 1. The karyotype of an Oxford-Aberdeen hybrid shrew reared in captivity. Note the 6 unpaired race-specific metacentrics.