on a world scale and the probable adaptative value of traits having a polygenic determinism[17–20].

Résumé. Chez *Drosophila melanogaster*, les souches provenant d'Afrique tropicale sont plus légères et ont moins de tubes ovariens que les souches françaises. Des mouches provenant de latitudes intermédiaires présentent des caractéristiques génétiques intermédiaires pour les deux caractères. Des clines latitudinaux existent donc entre l'Europe et la région éthiopienne. Un phénomène semblable est retrouvé sur le continent américain. La régularité de ces variations prouve qu'elles correspondent très probablement à une adaptation climatique.

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[17] M. J. KEARSEY and K. I. KOJIMA, Genetics *56*, 23 (1967).
[18] M. THOMAS-ORILLARD, Annls Génét. *10*, 207 (1967).
[19] M. DE SCHEEMAKER-LOUIS, Archs Biol. *81*, 495 (1971).
[20] We thank R. GRANTHAM for help with the manuscript and M. F. ARENS, M. DE SCHEEMAKER-LOUIS and P. FOUILLET for technical assistance.

Chromosomes of Three Species of Asian Tree Squirrels, *Callosciurus* (Rodentia: Sciuridae)

Tree squirrels of the genus *Callosciurus* occur widely in southeastern Asia, from Nepal eastward through southern China to Formosa, and southward through Malaysia and Indonesia to the Celebes and the Philippine Islands. 13 species are recognized[1], and according to ELLERMAN[2], 'This genus is second in number of named forms to *Rattus* only in the order'. Moreover, the tribe Callosciurini[3,4], to which the genus belongs, along with 11 or 12 other genera, is a very diverse one morphologically and ecologically, and relationships to other squirrel tribes within the family Sciuridae are not well understood[4].

The chromosomes of 3 species in the tribe have been described[5]. *Menetes berdmorei* had a diploid number ($2n$) of 62, the largest $2n$f any sq ouirrel so far described. *Dremomys rufigenis* possessed $2n = 38$, and *Callosciurus flavimanus*, $2n = 40$; *Dremomys* was further characterized by possession of a pair of acrocentric chromosomes with prominent satellites.

Fig. 1. Karyotype of a male *Callosciurus notatus* ($2n = 40$) from Malaysia ($2n = 40$). The sex chromosomes are the pair at the far right, bottom row, and the satellited acrocentric pair is in the middle of the bottom row.

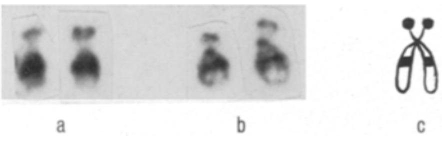

Fig. 2. Giemsa band patterns of satellited acrocentric autosomes from a) *Callosciurus notatus* compared with those of b) *Xerus rutilus* and c) an ideogram derived from both species.

The present paper reports a new specimen of *C. flavimanus* and specimens of previously unreported *C. finlaysoni* and *C. notatus*, and compares Giemsa (G-band) patterns of satellited acrocentrics with those found in *Xerus rutilus* from Africa.

Materials and methods. The following specimens were studied: *Callosciurus notatus* (Boddaert), Malaysia, Kuala Lampur, 2 males; Indonesia, Djakarta, 1 female and 1 male; *Callosciurus flavimanus* (I. Geoffroy), Thailand, 1 male; South Viet Nam: 1 male[5]; *Callosciurus finlaysoni* (Horsfield), Thailand, 1 male. Mitotic chromosomes were examined from marrow cell suspensions[6], or from skin biopsies through the courtesy of Dr. T. C. HSU, Anderson Hospital, Houston, Texas. G-band preparations were made using the method of SEABRIGHT[7]. Voucher specimens are presently in the possession of Dr. W. PRYCHODKO, Wayne State University, Detroit, Michigan.

Results. *Callosciurus notatus* (Figure 1), *C. flavimanus* from Thailand, and *C finlaysoni* all have $2n = 40$ and karyotypes comprized of 6 pairs of metacentric, 10 pairs of submetacentric, and 3 pairs of acrocentric autosomes, one of which bears satellites. A large submetacentric and a small submetacentric constitute the X and Y chromosomes respectively. *C. flavimanus* reported previously from South Viet Nam exhibited a karyotype similar to that of the specimen reported here from Thailand except for the fact that satellites were not recognized in the former and the otherwise comparable pair was classified within the submetacentric category.

Efforts to obtain G-band patterns in *C. notatus* from Kuala Lampur and Djakarta were only partially successful, but it was consistently possible to identify the pattern of the satellited acrocentrics. These chromosomes were

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[1] J. C. MOORE and G. H. H. TATE, Fieldiana Zool. *1965*, 48.
[2] J. R. ELLERMAN, *The Families and Genera of Living Rodents 1* (Brit. Mus. Nat. Hist., London 1940).
[3] G. G. SIMPSON, Bull. Am. Mus. Nat. Hist. *1945*, 85.
[4] J. C. MOORE, Bull. Am. Mus. Nat. Hist. *118*, 159 (1959).
[5] C. F. NADLER and R. S. HOFFMANN, Experientia *26*, 1383 (1970).
[6] C. F. NADLER and D. M. LAY, Z. Säugetierk. *32*, 285 (1967).
[7] M. SEABRIGHT, Chromosoma *36*, 204 (1972).

indistinguishable from the satellited acrocentric pair described in the African ground squirrel *Xerus rutilus*[8] (Figure 2). A single band located in the proximal half of the chromosome characterized the satellited pair from both *Callosciurus* and *Xerus*.

Discussion. Among the very few species of *Callosciurus* from scattered localities examined so far, no interspecific or geographic variation in karyotypes has been observed. Moreover, all possess a distinctive satellited pair of acrocentric chromosomes, similar to those found in the ground-dwelling callosciurine, *Dremomys rufigenis* ($2n = 38$). In addition, this satellited acrocentric pair appears to be morphologically identical, on the basis of Giemsa-band comparisons, with that of the satellited acrocentric chromosomal pair found in the African xerine ground squirrel, *Xerus rutilus* ($2n = 38$). This supports the suggestion[8] that xerines and callosciurines may be related. At the same time, the Asian palm squirrels, *Funambulus*, may also be related to callosciurines, according to immunological evidence[9]. However, neither *F. palmarum* ($2n = 46$)[10] nor *F. pennanti* ($2n = 54$)[11] appear to have satellited acrocentrics, and their karyotypes are quite different from those described for xerine and certain callosciurine squirrels.

Although the evolutionary history of *Calloscuirus* is poorly understood, fossil xerine ground squirrels are known from the late Oligocene of Europe (*Heteroxerus*), and the Miocene of Morocco and Spain (*Getuloxerus*)[12]. The satellited acrocentric autosomes of extant *X. rutilus* may have been retained within the xerine lineage since that time, a view that is supported by the appearance of seemingly identical chromosomes in *Callosciurus* and in the more recently evolved xerine genus *Spermophilopsis*[8].

Zusammenfassung. Die Karyotypen von *Callosciurus notatus*, *C. finlaysoni* und *C. flavimanus* besitzen alle $2n = 40$ Chromosomen: 6 metazentrisch, 10 submetazentrisch und 3 akrozentrisch. Eines der akrozentrischen Paare trägt einen auffälligen Satelliten; akrozentrische Satellitenchromosomen von *Callosciurus* und *Xerus rutilus* besitzen identische G-Bandmuster. Akrozentrische Chromosomen mit Satelliten wurden auch von den Callosciurinen *Dremomys rufigenis* und der Xerine *Spermophilopsis leptodactylus* beschrieben.

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7 October 1974.

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[8] C. F. Nadler and R. S. Hoffmann, Experientia, *30*, 889 (1974).

[9] M. E. Hight, M. Goodman and W. Prychodko, Syst. Zool. *23*, 12 (1974).

[10] K. L. Satya Prakash and N. V. Aswathanarayana, Mammal. Chromos. Newslett. *12*, 86 (1971).

[11] M. D. L. Srivastava and V. S. Bhatnagar, Mammal. Chromosomes Newslett. *12*, 51 (1971).

[12] C. C. Black, Evolut. Biol. *6*, 305 (1972).

[13] Supported by National Science Foundation Grants No. GB 32114X and 29131X. We thank Dr. T. C. Hsu, M. D. Anderson Hospital, Houston, Texas, for Giemsa-band chromosome preparations from skin biopsies. Dr. R. W. Turner and Dr. Illar Muul provided us with live specimens.

Cytotaxonomical Consideration of the Genus *Blennius* (Pisces-Perciformes)

Within the complicated suborder of the Blennioidea, in which various benthonic fish families are gathered[1,2], the Blenniidae comprise a large family whose ecological valence has allowed it to colonize the coastlines of all seas and to penetrate into brackish and even fresh waters. One of the problems of Blenniidae classification is the division into genera and subgenera[3,4].

The purpose of the present paper is to make some contribution to solving the above problem by means of the karyological data concerning several Mediterranean species of blenny of the genus *Blennius* L., 1758. As already demonstrated in one of our previous works[5], karyotype analysis can be useful if carried out on species belonging to taxonomically homogeneous groups whose classification is, however, complicated because of their great size and wealth of specialized forms.

One example of this is the genus *Blennius* L., a complicated and subdivided taxon including numerous species

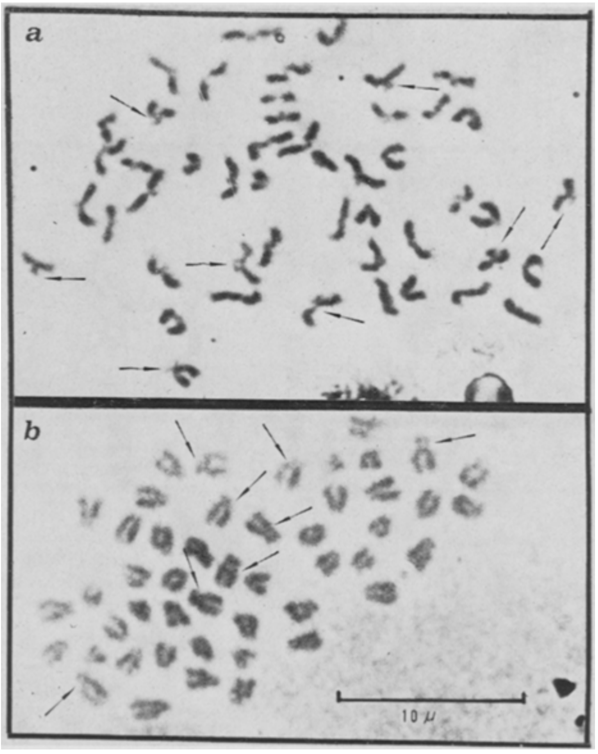

Fig. 1. Metaphase plate of *Blennius sanguinolentus* (a) and of *Blennius pavo* (b). Arrows indicate the subtelocentric chromosomes.

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[1] C. T. Regan, Ann. Mag. nat. Hist. Ser. 8, *10*, 256 (1912).

[2] L. S. Berg, Trudy Inst. Zool. Kyyiv *2*, 87 (1940).

[3] J. R. Norman, Ann. Mag. nat. Hist., Ser. 11, *10* (1943).

[4] V. G. Springer, Bull. Am. Mus. nat. Hist. *284*, 1 (1968).

[5] S. Cataudella, M. V. Civitelli and E. Capanna, Caryologia *27*, 93 (1974).

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