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CHROMOSOMAL STUDIES OF THE AFRICAN GIANT RAT AND THE HAIRY-SOLED GERBILS *(RODENTIA, CRICETIDAE)*

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Abstract

The chromosomal complements of two species of mammals, the African giant rat, *Cricetomys emini* (Wroughton) and the hairy-soled Gerbils, *Gerbillus agag* (Thomas) from two localities in South Western Nigeria were analysed. A diploid chromosome number (2n) of 76 with a fundamental number (FN) of 77 was got for *C. emini. G. agag* had a diploid chromosome complement and fundamental number of 30 and 53 respectively. The sex chromosomes in the two species were well differentiated.

Keywords: *Cricetomys emini, Gerbillus agag,* Chromosome, Karyotype, Idiogram.

1. Introduction

The cricetidae is a vast rodent family found not only throughout Africa but over much of Europe, Asia and as well as America. The cricetids are overwhelmingly the majority of the New World rodents (Rosevear, 1969).

Improvements in cytological techniques have made the examination of chromosome complement easier, so that investigation of chromosome characteristics have become routine. The Committee on Standardised Genetic Nomenclature for mice (1972) produced a standard karyotype of the mouse and this has made it easier to investigate critical taxonomic groups. Karyotypic studies have been used to properly classify some species of rats (Capanna and Civitelli, 1990; Yüksel and Gülkaç, 2001; Mattevi, *et al.*, 2002).

The studies of mammalian chromosomes have constituted an effective area of investigation to explain their relationship. Karyotypic studies of mole rats in Turkey were initiated by Savic and Soldatovic (1977, 1979a and 1979b) and Soldatovic and Savic (1978). The karyotype of *Arvicanthis dembeensis* was reported to be indentical to that of *Arvicanthis niloticus* from *terra typical* by Corti *et al.* (1996). Attempts were also made to assess the phytogenetic relationships among the taxa of the genus *Arvicanthis* by Corti *et al.* (1996) on the basis of chromosomal rearrangements, by Capula *et al.* (1997) through multi-locus protein electrophoresis, and by Ducroz, *et al.* (1998) on the basis of the sequence of mitochondrial gene for the cytochrome b. All the different sets of data support the major pattern of subdivision which depict two main clades: one included ANI-2, ANI-3, ANI-4 from Central and West Africa, and the other included ANI-1 and Ethiopian and Tanzanian species. The present study was undertaken to provide information on the karyotype of the African giant rat, *Cricetomys emini* and the hairy-soled Gerbils, *Gerbillus agag.*

2. Materials and Methods

The animals used for this study were collected live, using locally made traps constructed with wire mesh, from Osogbo (7° 50' N, 4° 35' E) and Alakowe – a surbub of Ile-Ife (7°35' N, 4° 35'E). The animals were identified from the collection at the Natural History Museum of the Obafemi Awolowo University, Ile-Ife, Nigeria and by the identification key prepared by Rosevear (1969). Four cricetid rodents made up of three males of *Cricetomys emini* and one male *Gerbillus agag* were examined.

Chromosome Preparation

Chromosome spreads from the bone marrow tissue were prepared on slides following the technique described by Adegoke (1988). The cricetids were injected with 1.0-1.5ml 0.2% colchicine depending on their size and left for two hours before being sacrificed. The femur and humerus were cut off and the bone marrow were flushed out into a 15ml centrifuge tube containing about 10ml of freshly prepared warm (37 °C), 0.55 % potassium chloride (hypotonic buffer). The cells were left in the hypotonic solution for 10-15 minutes and then fixed in 1:3 glacial acetic acid:methanol. The cells were then kept in the refrigerator overnight. The cells were subsequently resuspended in 1:1 glacial acetic acid:methanol and then spread on clean, cold wet

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slides. The slides were dried at 60°C on a slide warmer for about 24 hours and thereafter stained with 6% Giemsa stain solution for 20-25 minutes. The stained slides were dried and observed directly under X40 of a compound microscope. Well spread cells were observed under oil immersion for counting and photographing. The chromosome karyotypes were prepared from such photographs. The evaluation of the chromosome morphology and centromere position terminologies were made using the system proposed by Abraham and Prasad (1983).

Chromosome measurements were made in millimetres from photomicrograph of good somatic cells which were enlarged at 2240X. The establishment of karyotype for each species was based on the mean of the measurements of at least four to ten well spread metaphase cells at approximately the same level of condensation. The measurements were later converted into microns as described by Faluyi (1992). Idiograms were constructed from the measurement of the total length of each chromosome for each species.

The determination of the diploid chromosome number for each species was carried out by counting the number of chromosomes in at least 150 well spread metaphase cells. The total number of arms of the diploid set of chromosomes, which is the fundamental number (FN) was also calculated.

3. Results

(a) Analyses of the chromosomes of male, (Wroughton)

Plate 1 shows the mitotic metaphase chromosomes of male *Cricetomys emini* with a diploid chromosome number of 76 and a fundamental number (FN) of 77. The karyotype is shown in Plate 2. The chromosome measurements given in Table 1 show that there are 37 terminal autosome pairs. The X chromosome is nearly median and the Y chromosome is terminal.

Figure 1 shows that there are at least five groups of chromosomes denoting a rather heterogeneous group 1 consisting of large chromosomes numbered 1 to 9 which are always clearly visible and identifiable in all metaphase spreads. This is followed by four other groups, in order of size, 10 to 17, 18 to 23, 24 to 27, and 28 to 37 having the following lengths, 1.56µm, 1.34µm, 1.12µm and 0.89µm respectively. The chromosome measurements in table 1 clearly indicated the sharp demarcations shown between the groups that were not quite apparent in plate 2.

The chromosome morphology for the male *C. emini* is shown in Figure 2 and they are all terminal with the exception of the X chromosome. The X chromosome is the largest chromosome in the complement while the Y chromosome is the smallest.

(b) Analyses of the chromosomes of the male (Thomas)

The mitotic metaphase chromosome spread of the male *Gerbillus agag* is shown in Plate 3. After the examination of 220 well spread metaphase cells from the only specimen caught, a diploid chromosome number of 30 was obtained for the male *Gerbillus agag* with a fundamental number (FN) of 53. The karyotype is shown in Plate 4 while the chromosome measurements and nomenclature are given in Table 2.

The size variation among the chromosomes and the idiogram for the chromosome morphology are shown in Figures 3 and 4 respectively. The karyotype may be divided into three main groups. Group one consists of the large chromosomes numbered 1 to 6. These are always clearly visible and identifiable in all metaphase spreads. This group morphologically comprises five nearly submedian (-) chromosomes (1,2,3,4 and 6), and one nearly submedian (+), chromosome (5). The second group comprises the medium sized chromosomes numbered 7 to 12, which are also always clearly visible and identifiable like the large chromosomes. Group two consists of two median chromosomes, (7 and 9), two nearly median chromosomes (8 and 12), one nearly submedian (-) chromosome, (10), and one terminal chromosome, (11). Group three consists of the small chromosomes which are not very clear morphologically in all metaphase spreads. These are chromosomes having approximately the same length. The X chromosome is nearly median and the Y chromosome is terminal.

The lengths of the chromosomes as shown in Figure 3 reveal that chromosomes 2 and 3 have approximately the same length. There is a sharp break in chromosome length between chromosomes 6 and 7 followed by a gradual decrease in size and then a sharp break between chromosomes 12 and 13. The X chromosome is the largest of all the chromosomes while the Y chromosome has approximately the same length with chromosome 5.

4. Discussion

(a) The chromosomes of *Cricetomys emini*

The genus *Cricetomys* was classified into two defined species, *C. gambianus* and *C. emini* by Rosevear (1969). A number of reports on the ecology and taxonomy of the species within the genus were provided by Rosevear (1969), however, there is paucity of reports in literature on the karyotype of the genus Cricetomys. Hence, this paper will most probably be the first report on the karyotype of the genus Cricetomys.

In this study, a diploid chromosome number of 76 was obtained for *C. emini* with all the 37 autosome

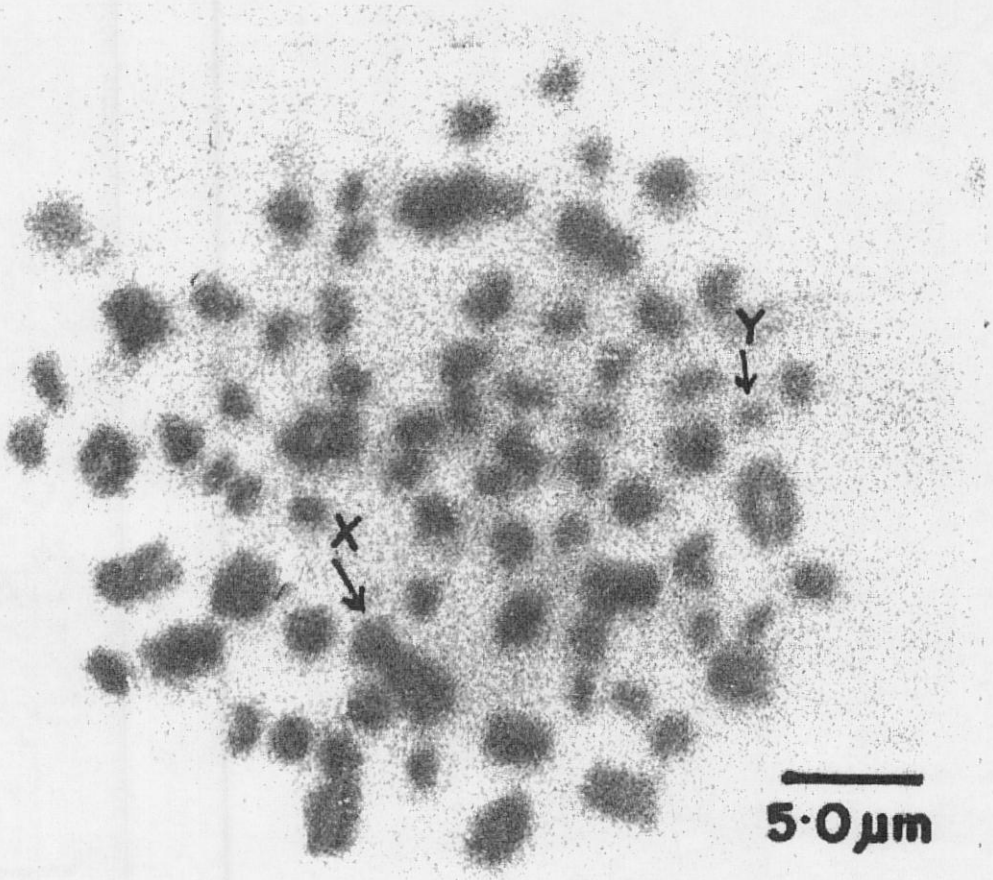

Plate 1: Mitotic metaphase chromosomes of male *Cricetomys emini*, 2n of 76. The arrows show the X and Y chromosomes.

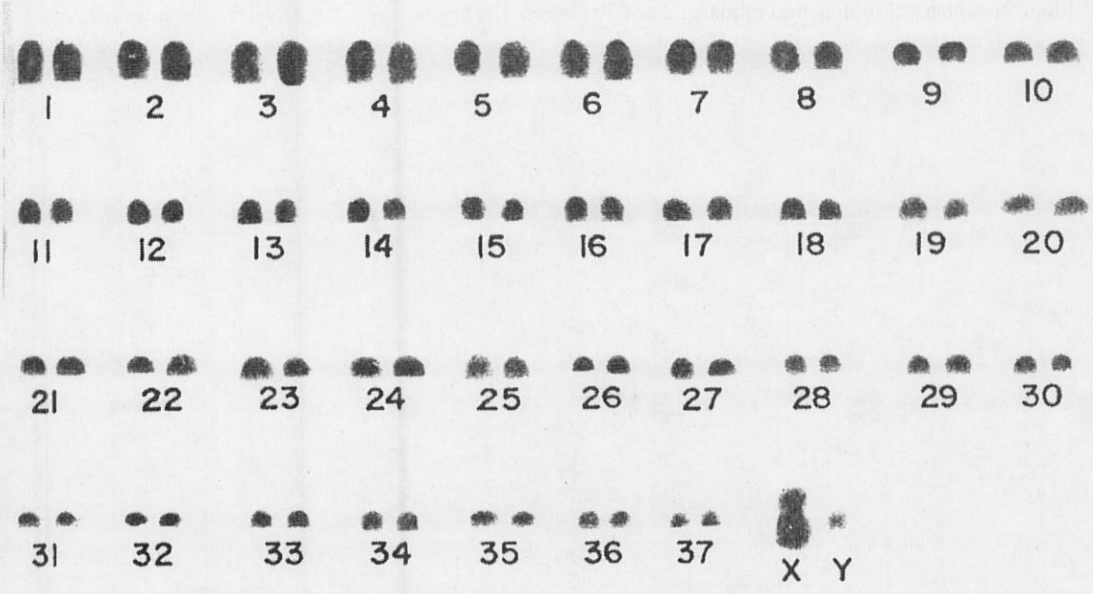

Plate 2: Karyotype of male *Cricetomys emini*

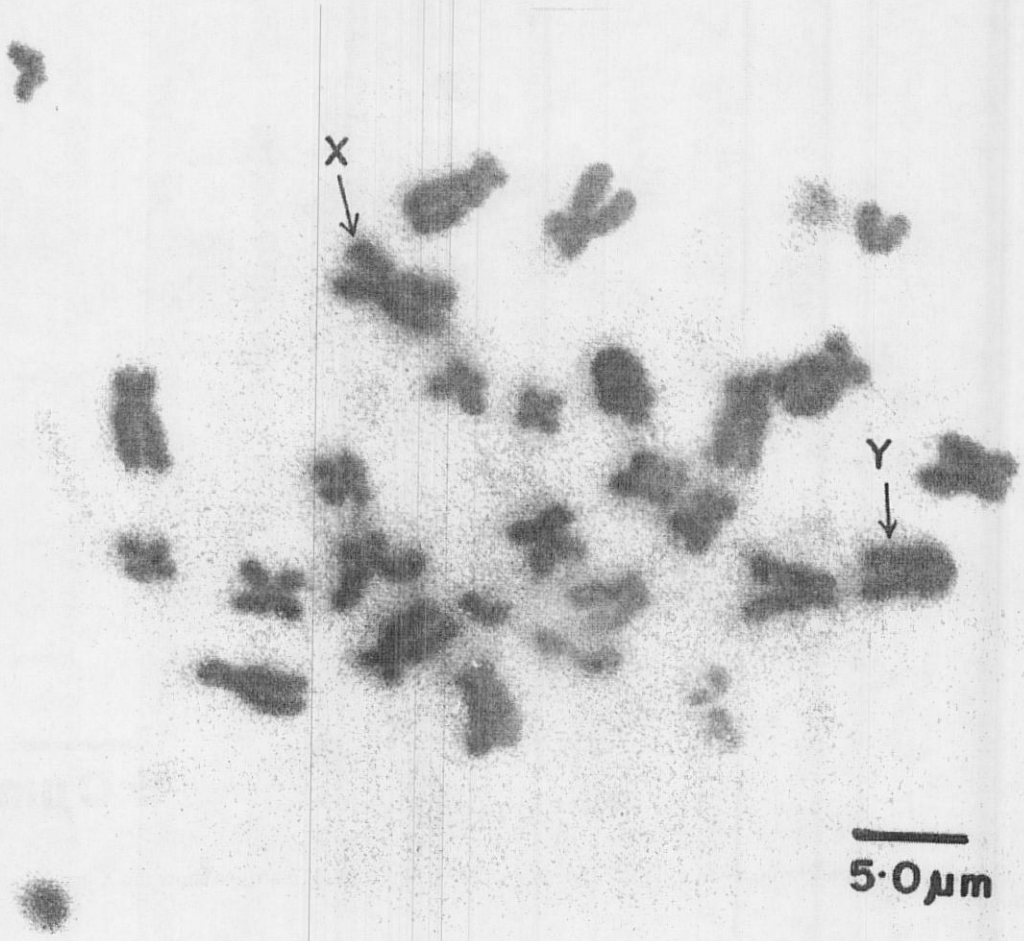

Plate 3: Mitotic metaphase chromosomes of male , 2n of 30 *Gerbil.* The arrows show the X and Y chromosomes.

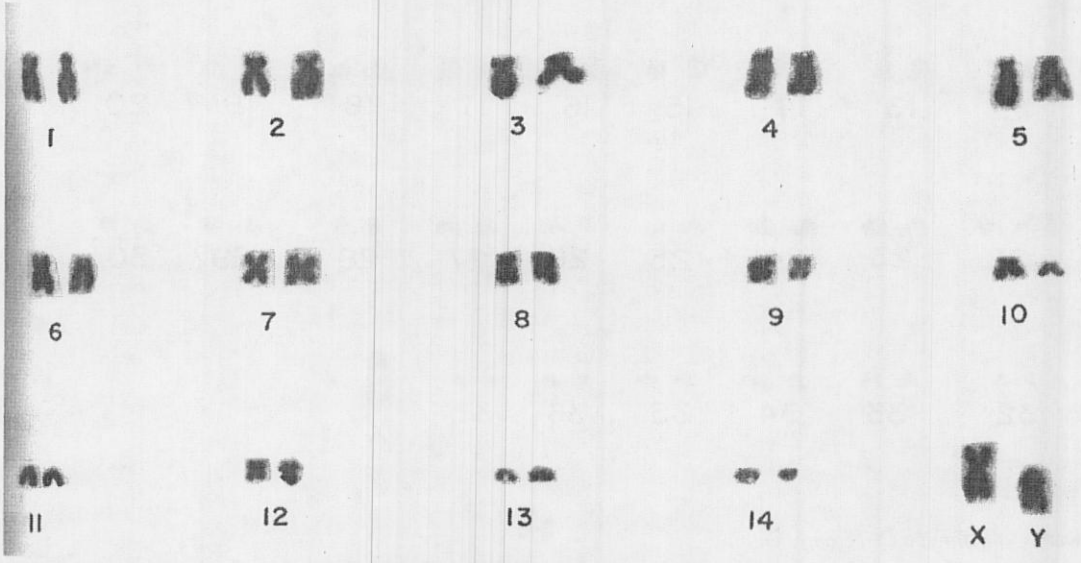

Plate 4: Karyotype of male *Gerbillus agag.*

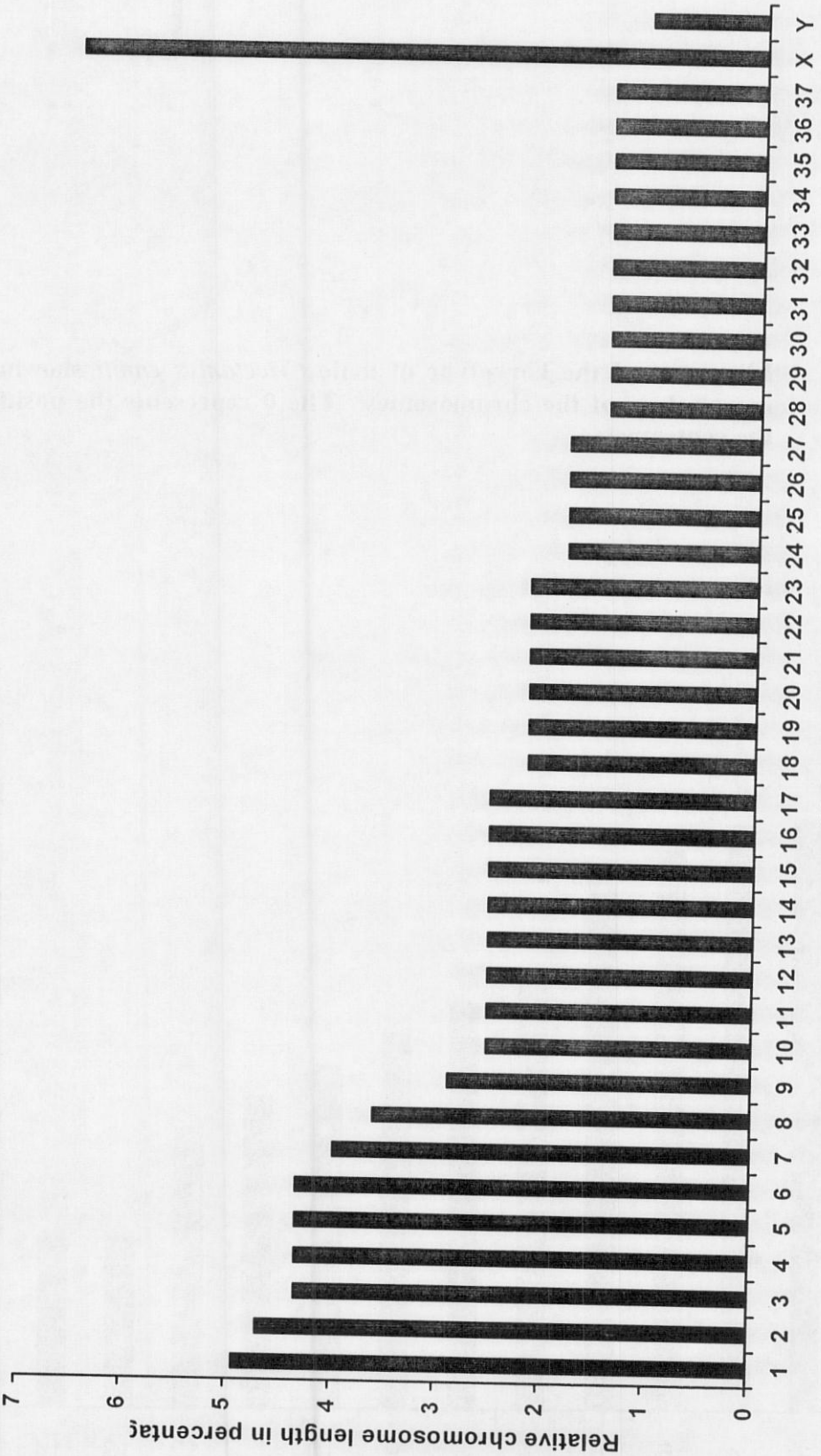

Figure 1: Relative length of the chromosomes of male *Cricetomys emini* showing the size of variation.

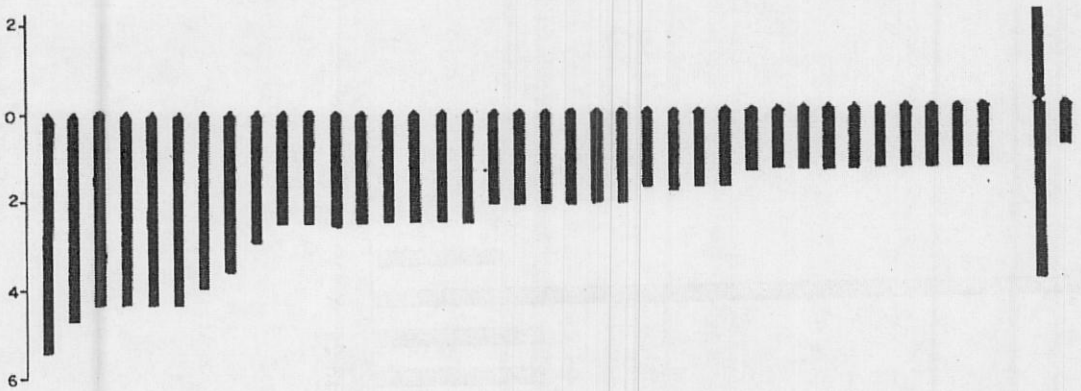

Figure 2: **Idiograms of the karyotype of male *Cricetomys emini* showing the morphology of the chromosomes. The 0 represents the position of the centrometre.**

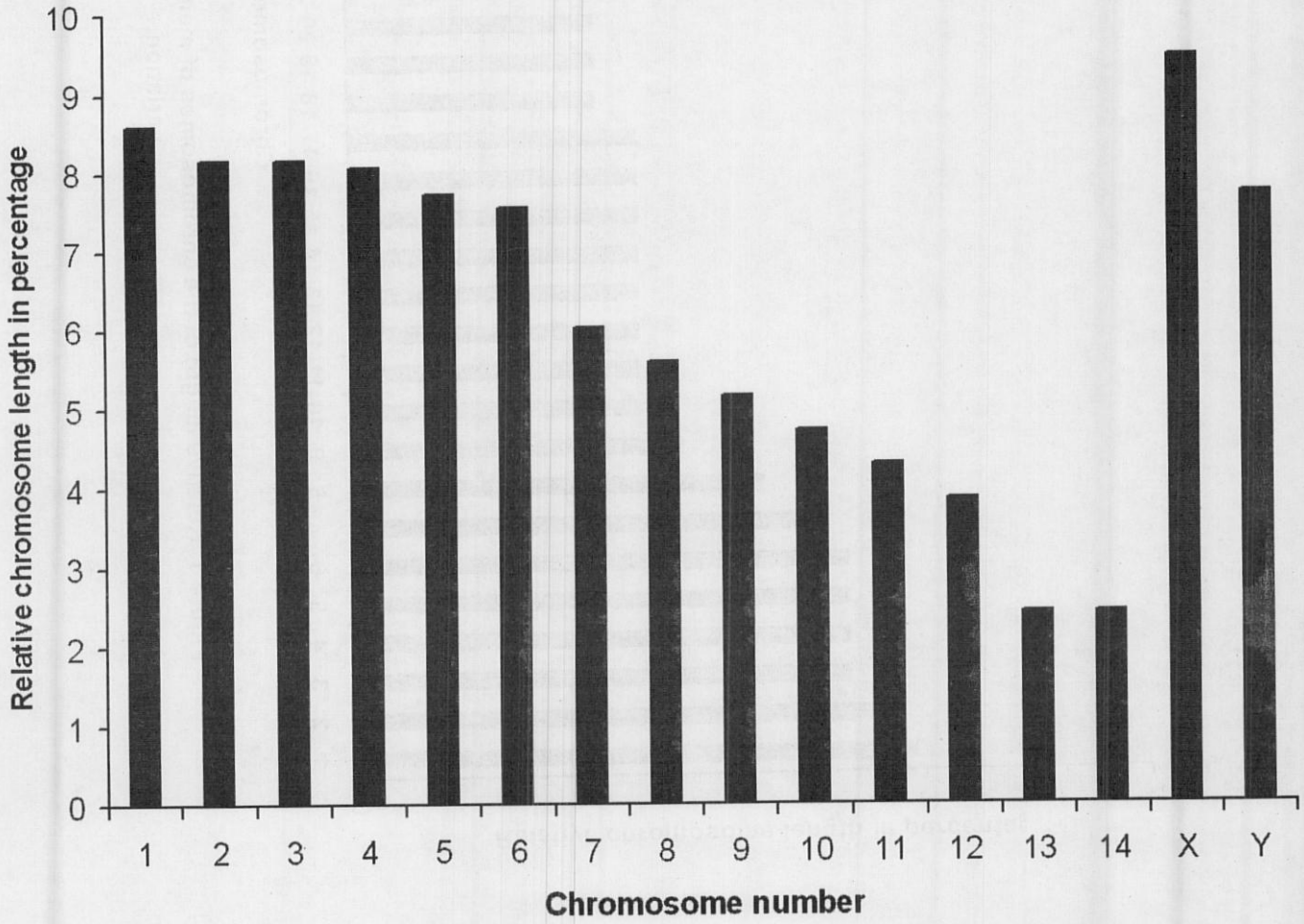

Figure 3: Relative length of the chromosomes of male *Gerbillus agag* showing the size variation

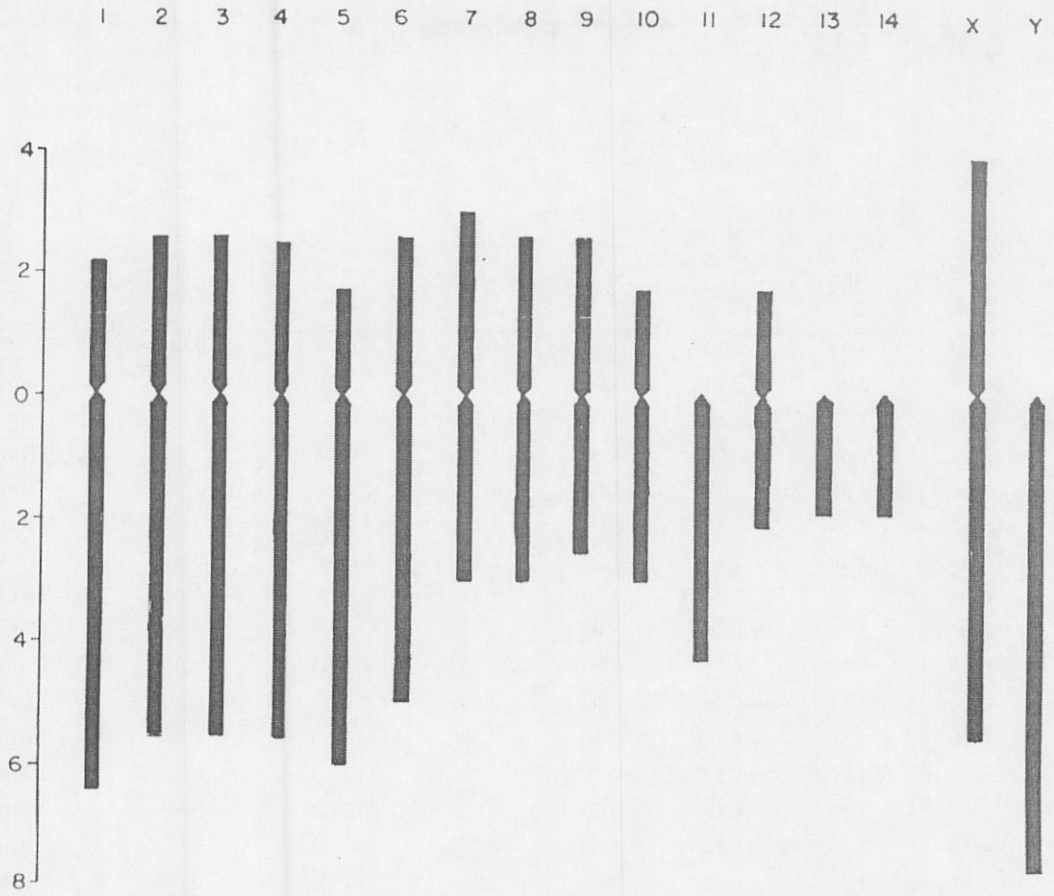

Figure 4: Idiograms of the karyotype of male *Gerbillus agag* showing the morphology of the chromosomes. The 0 represents the position of the centrometre.

pairs and the Y chromosome being terminal while the X chromosome was nearly median.

(b) The chromosomes of *Gerbillus agag*

Rosevear (1969) reported that the taxonomy of this genus of Cricetids was in a confused state and that there was little doubt that seventy-seven species so far listed were in need of revision and probably drastic reduction. This was attributed to the slight evidence for the classification, which was sometimes based totally on inadequate material. Among these species, fourteen were Asiatic while the remaining sixty-three were African. However, only a few of these were found in West Africa.

The genus had commonly been regarded as comprising two subgenera, *Gerbillus* and *Dipodillus* (Rosevear, 1969) with the only distinction between them being the hind foot, the former being the hairy-soled Gerbils and the latter the Naked-soled Gerbils. In the reports of Rosevear (1969) *Gerbillus agag* was placed in the Sudan-woodland zone which was exactly the same vegetational belt as that of *Gerbillus nigeriae*. It was further noted that even though *G. agag* had been described as a species in its own right, it was nothing more than a race of *G. gerbillus*. Rosevear (1969) however, insisted that the locality of the species could not be fixed with complete certainty.

However, chromosome study of *Gerbillus pyramidum* which includes a number of allopatric forms that differ greatly in chromosome number was reported by White (1973). In the report the exact status of these as races or sibling species was uncertain and that a form from the Negev in Israel, had a diploid chromosome complement of 66 (6 pairs of metacentrics and 27 pairs of acrocentrics) while one from the coastal plains of Palestine had a diploid chromosome number of 52 (11 or 12 pairs of metacentrics, 14 or 15 pairs of acrocentrics) and one from Algeria with a diploid chromosome number of 40 (19 pairs of metacentrics and 1 pair of acrocentrics).

A comparison of the result of this study with that of the different forms of *Gerbillus pyramidum* shows that there is a wide range in chromosome number for the genus *Gerbillus*, which might have been one of the reasons for the uncertainty of the classification of this genus. Therefore, a lot has to be done on the

Table 1: Chromosome measurement and nomenclature of male *Cricetomys emini* using the centromeric index (CI) = 100s/c

	MEASUREMENT (µm)			RELATIVE LENGTH (%)				
Chromosome No.	Short arms s (µm)	Long arm l (µm)	Total length c (µm)	Short arm s'(%)	Long arm l'(%)	Total length c' (%)	Centromeric index (CI)	Nomenclature
1	0.00	3.04	3.04	0.00	4.92	4.92	0.00	Terminal
2	0.00	2.90	2.90	0.00	4.70	4.70	0.00	Terminal
3	0.00	2.68	2.68	0.00	4.34	4.34	0.00	Terminal
4	0.00	2.68	2.68	0.00	4.34	4.34	0.00	Terminal
5	0.00	2.68	2.68	0.00	4.34	4.34	0.00	Terminal
6	0.00	2.68	2.68	0.00	4.34	4.34	0.00	Terminal
7	0.00	2.46	2.46	0.00	3.99	3.99	0.00	Terminal
8	0.00	2.23	2.23	0.00	3.61	3.61	0.00	Terminal
9	0.00	1.79	1.79	0.00	2.90	2.90	0.00	Terminal
10	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
11	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
12	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
13	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
14	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
15	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
16	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
17	0.00	1.56	1.56	0.00	2.53	2.53	0.00	Terminal
18	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
19	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
20	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
21	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
22	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
23	0.00	1.34	1.34	0.00	2.17	2.17	0.00	Terminal
24	0.00	1.12	1.12	0.00	1.81	1.81	0.00	Terminal
25	0.00	1.12	1.12	0.00	1.81	1.81	0.00	Terminal
26	0.00	1.12	1.12	0.00	1.81	1.81	0.00	Terminal
27	0.00	1.12	1.12	0.00	1.81	1.81	0.00	Terminal
28	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
29	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
30	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
31	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
32	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
33	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
34	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
35	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
36	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
37	0.00	0.89	0.89	0.00	1.44	1.44	0.00	Terminal
X	1.56	2.46	4.02	2.53	3.99	6.52	38.81	Nearly median
Y	0.00	0.67	0.67	0.00	1.09	1.09	0.00	Terminal

The centromeric index (CI) for each chromosome was derived from the formula, CI = 100s/c. In the Table 1 and 2 the chromosome length was measured in micrometres (µm) as described under materials and methods and then individually converted to percentages of the total complement.

Table 2: Chromosome measurement and nomenclature of male *Gerbillus agag* using the centromeric index (CI) = 100s/c

	MEASUREMENT (μm)			RELATIVE LENGTH (%)				
Chromosome No.	Short arms s (μm)	Long arm l (μm)	Total length c (μm)	Short arm s'(%)	Long arm l'(%)	Total length c' (%)	Centromeric index (CI)	Nomenclature
1	1.12	3.35	4.47	2.16	6.45	8.61	25.06	Nearly submedian (-)
2	1.34	2.90	4.24	2.58	5.59	8.17	31.60	Nearly submedian (-)
3	1.34	2.90	4.24	2.58	5.59	8.17	31.60	Nearly submedian (-)
4	1.29	2.90	4.19	2.49	5.59	8.08	30.79	Nearly submedian (-)
5	0.89	3.13	4.02	1.71	6.03	7.74	22.14	Nearly submedian (+)
6	1.34	2.59	3.93	2.58	4.99	7.57	34.10	Nearly submedian (-)
7	1.56	1.56	3.12	3.01	3.01	6.02	50.00	Median
8	1.34	1.56	2.90	2.58	3.01	5.59	46.21	Nearly median
9	1.34	1.34	2.68	2.58	2.58	5.16	50.00	Median
10	0.89	1.56	2.45	1.71	3.01	4.72	36.33	Nearly submedian (-)
11	0.00	2.23	2.23	0.00	4.30	4.30	0.00	Terminal
12	0.89	1.12	2.01	1.71	2.16	3.87	44.28	Nearly median
13	0.00	1.25	1.25	0.00	2.41	2.41	0.00	Terminal
14	0.00	1.25	1.25	0.00	2.41	2.41	0.00	Terminal
X	2.01	2.90	4.91	3.87	5.59	9.46	40.94	Nearly median
Y	0.00	4.02	4.02	0.00	7.74	7.74	0.00	Terminal

cytogenetic studies of the genus *Gerbillus* before adequate classification of the genus could be arrived at.

5. Conclusion

The present study gives information on the cytogenetics of *Cricetomys emini* and *Gerbillus agag*. A diploid chromosome number of 76 was obtained for *Cricetomys emini* and 30 for *Gerbillus agag*.

The sex chromosomes observed from all the species were well differentiated. Consequently, there is a need for further systematic studies on the cytogenetics of African mammals based on the differences in chromosome number and morphology.

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REFERENCES

Abraham, Z. and Prasad, P.N., 1983. A system of chromosome classification and nomenclature. Cytologia, 48: 95-101.

Adegoke, J.A., 1988. Studies on the chromosome of the Rainbow Lizard, *Agama agama agama* (L.) with notes on polyploidy in the spermatocytes. *Cytologia*, 53: 233-239.

Capanna, E. and Civitelli, M.V., 1970. Chromosomal Mechanisms in the evolution of chiropteran karyotype chromosomal tables of chiroptera. *Caryologia*, 23: 79-111.

Capula, M., Civetilli, M.V., Corti, M., Bekele, A. and Capanna, E., 1997. Genetic divergence in the genus *Arvicanthis* (Rodentia: Murinae). *Biochem. Syst. Ecol.* 25(5): 403-409.

Committee on Standardized Genetic Nomenclature for Mice (Chairman P. Demant), 1972. Standard Karyotype of mouse, *Mus musculus*. *Journal of Heredity*, 63: 69-72.

Corti, M., Civitelli, M.V., Castiglia, R. Bekele, A. and Capanna, E., 1996. Cytogenetics of the genus *Arvicanthis* (Rodentia: Muridae). 2. The chromosomes of three species from Ethiopia: *A. abyssinicus, A. dembeensis* and *A. blicki. Z. Saugetierkd.* 61: 339-351.

Ducroz, J.F., Volobouev, V. and Granjon, I., 1998. A molecular perspective on the systematics and evolution of the genus *Arvicanthis* (Rodentia, Muridae): inferences from complete cytochrome b gene sequences. Mol. Phylogenet. Evol. 10(1): 104-117.

Faluyi, J.O., 1992. *Principles and Practice of Photomicrography*. Anchorprint Limited, Ile-Ife, Nigeria,102pp.

Mattevi M.S., Haag T., Nunes A.P., Oliveira L.F.B., Cordeiro J.L.P. and Andrades-Miranda J. 2002. Karyotypes of Brazilian Representatives of Genus Zygodontomys (Rodentia, Sigmodontinae). *Journal of Neotropical Mammals*. 9(1): 33-38.

Rosevear, D.R., 1969. *The Rodent of West-Africa*. Trustees of the British Museum (Natural History) London. Eyre and Spottiswoode Ltd., Great Britain, 603pp.

Savic, I. and Soldatovic, B., 1977. Contribution to the study Ecogeographic Distribution and Evolution of Chromosomal Forms of the Spalacidae from the Balkan Peninsula. *Arh. Biol. Nauka*. 29: 141-156.

Savic, I. and Soldatovic, B., 1979a. Distribution range and evolution of the chromosomal forms in the *spalacidae* from the Balkan peninsula and bordering regions. *Journal of Biogeography*, 6: 363-374.

Savic, I. and Soldatovic, B., 1979b. Contribution to knowledge of the genus *Spalax* (*Microspalax*) Karyotype from Asia Minor. *Arh. Biol. Nauka*, 31: 1-2.

Soldatovic, B. and Savic, I., 1978. Karyotype in some populations of the genus *spalax* (*Mesospalax*) in Bulgaria and Turkey. *Saugetierk. Mitt.*, 26:252-256.

White, M.J.D., 1973. Animal Cytology and evolution. Vikas Publishing House PVT Ltd., 961pp.

Yüksel E. and Gülkaç M.D., 2001. The Cytogenetical Comparison of spalax (Rodentia: Spalacidae) populations from middle Kizilirmak basin, Turkey. Turkey *Journal of Biology*, 25:17-24.