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The karyotype and taxonomic status of *Cryptomys hottentotus darlingi* (Rodentia: Bathyergidae)

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Cytogenetic analyses were performed on twenty specimens referable to *Cryptomys hottentotus darlingi* from north eastern Zimbabwe. In comparison to the southern subspecies *C. h. hottentotus* (aFN = 102) and *C. h. natalensis* (aFN = 100), *C. h. darlingi* showed the same diploid number (2n = 54), but a striking reduction in the fundamental number (aFN = 80). C-banding analysis suggests that chromosome differentiation arose most probably by pericentric inversions. The magnitude of the karyotypic differences is assumed to represent reproductive isolation and consequently the specific status for the *darlingi* cytotype is recommended.

Sitogenetiese ontleding is uitgevoer op 20 individue van *Cryptomys hottentotus darlingi* van noord-oostelike Zimbabwe. In vergelyking met die suidelike subspesies *C. h. hottentotus* (aNF = 102) en *C. h. natalensis* (aNF = 100) vertoon *C. h. darlingi* dieselfde diploïde getal (2n = 54), en 'n verbasende vermindering in die *nombre fondamentale* (aNF = 80). C-band-analise impliseer dat chromosoomdifferensiering heel waarskynlik ontstaan het deur middel van perisentriese inversies. Daar word aangeneem dat die grootte van die kariotiepverskille reprodutiewe isolasie verteenwoordig, en gevolglik word spesifieke status vir die *darlingi* sitotipe aanbeveel.

Mole-rats of the genus *Cryptomys* are a group of subterranean rodents (Family Bathyergidae), endemic to central and southern Africa. Systematic relationships and taxonomic delimitations among most of the taxa within the genus

remain obscure. The common mole-rat, *Cryptomys hottentotus*, is a geographically variable species which occurs from the western part of central Tanzania southwards into Zambia, Malawi, Zimbabwe, Mozambique and South Africa. At present, five subspecies are recognized within its distributional range (Honeycutt, Allard, Edwards & Shluter 1991). *Cryptomys h. hottentotus* inhabits the south and west of South Africa, *C. h. natalensis* occurs in the east and north of South Africa, *C. h. darlingi* occurs in eastern Zimbabwe and western parts of Mozambique, *C. h. amatus* and *C. h. whytei* occur in the northern part of the distributional range, being reported from eastern Zambia, northern Malawi and south-western Tanzania (De Graaff 1981; Ansell 1978; Ansell & Dowsett 1988).

Although there is some literature on the systematics of the genus *Cryptomys*, most of the information concerns those taxa living in the southern part of its distributional range (Allard & Honeycutt 1992; Honeycutt, Edwards, Nelson & Nevo 1987; Nevo, Shlomo, Beiles, Jarvis, & Hickman

Table 1 Mean relative length, arm ratio, centromeric index and type of metaphase chromosomes of *Cryptomys h. darlingi* from Goromonzi, north-eastern Zimbabwe

Chromosome pair	Mean relative length \pm SE	Arm ^b ratio	Centromeric ^c index	Type ^d
1	6,85 \pm 0,27	–	0,00	t
2	6,36 \pm 0,23	2,9	0,26	sm
3	5,76 \pm 0,45	1,5	0,40	m
4	4,89 \pm 0,22	–	0,00	t
5	4,71 \pm 0,22	–	0,00	t
6	4,40 \pm 0,30	1,9	0,34	sm
7	4,23 \pm 0,07	1,7	0,37	sm
8	4,13 \pm 0,22	1,4	0,42	m
9	4,00 \pm 0,29	–	0,00	t
10	3,80 \pm 0,22	1,3	0,43	m
11	3,40 \pm 0,19	1,3	0,43	m
12	3,38 \pm 0,13	–	0,00	t
13	3,30 \pm 0,20	1,4	0,42	m
14	3,22 \pm 0,08	–	0,00	t
15	3,13 \pm 0,14	–	0,00	t
16	3,09 \pm 0,08	1,3	0,44	m
17	2,89 \pm 0,09	–	0,00	t
18	2,80 \pm 0,09	–	0,00	t
19	2,80 \pm 0,12	1,5	0,40	m
20	2,79 \pm 0,11	1,4	0,42	m
21	2,50 \pm 0,12	1,2	0,45	m
22	2,41 \pm 0,12	–	0,00	t
23	2,40 \pm 0,16	1,5	0,40	m
24	2,30 \pm 0,19	–	0,00	t
25	2,15 \pm 0,15	–	0,00	t
26	1,97 \pm 0,32	1,2	0,45	m
X	3,95 \pm 0,62	1,6	0,39	m
Y	2,36 \pm 0,46	1,4	0,41	m

Karyotypical descriptors based on 12 metaphase chromosome plates:

^a Mean relative length as a percentage of the haploid genome length with its standard error. ^b Arm ratio is the proportion between the short and the long arm of the chromosome. ^c Centromeric index determined by dividing the length of the short arm by the total length of the chromosome. ^d Type of chromosome determined by the position of the centromere: (t) telocentric/acrocentric, (sm) submetacentric and (m) metacentric chromosome.

1987). Chromosomal information for the different taxa within the genus *Cryptomys* is minimal (Nevo, Capanna, Corti, Jarvis & Hickman 1986; Williams, Shlitter & Robbins 1983). The systematics and phylogenetic relationships at the specific and infraspecific levels of those taxa in the northern part of the range remain poorly understood. Herein, the karyotype of 20 specimens referable to *C. h. darlingi* (Thomas 1895) is reported, and its taxonomic status discussed. The present report forms part of a research program on the behaviour, ecophysiology and evolutionary biology of the genus *Cryptomys* in sub-Saharan Africa.

Twelve males and eight females from six different colonies were collected at Goromonzi (reference grid 1731Cd), in north-eastern Zimbabwe. Standard karyotypes were prepared by the direct bone marrow technique (Hsu & Patton 1969) using $0,075 \text{ mol dm}^{-3}$ potassium chloride as a hypotonic solution. The animals were injected subcutaneously with yeast for three consecutive days before colchicine injection to increase the mitotic rate in the bone marrow cells (Lee & Elder 1980). C-banded karyotypes were prepared by the barium hydroxide technique of Sumner (1972). Nomenclature for centromeric position on

the chromosomes follows that of Levan, Fredga & Sandberg (1964).

The diploid number ($2n = 54$) and fundamental number, defined here as the total number of visible autosomal arms (aFN = 80), of *C. h. darlingi* were constant for the specimens analysed. The autosome complement of this taxon showed 12 pairs of acrocentric/telocentric, three pairs of submetacentric and 11 pairs of metacentric chromosomes (Table 1, Figure 1a). The sex chromosome pair consists of a medium sized subtelocentric X and a small metacentric Y chromosome. The differentially stained karyotype of *C. h. darlingi* is presented in Figure 1b. Assignment of chromosomes to pair numbers is based on their relative lengths (Table 1). The analysis of constitutive heterochromatin distribution (indicated by C-banding) reveals, in addition to small centric C-blocks present on all the autosomes and Y chromosome, distal telomeric blocks on chromosomes 2-7, 9, 12-26, an interstitial block on chromosome 4, and a large C-band on the short arm of the X chromosome. Marked heteromorphism in the amount of telomeric heterochromatin was evident between the homologues of pairs 3, 4, 6, 9, 23 and 26.

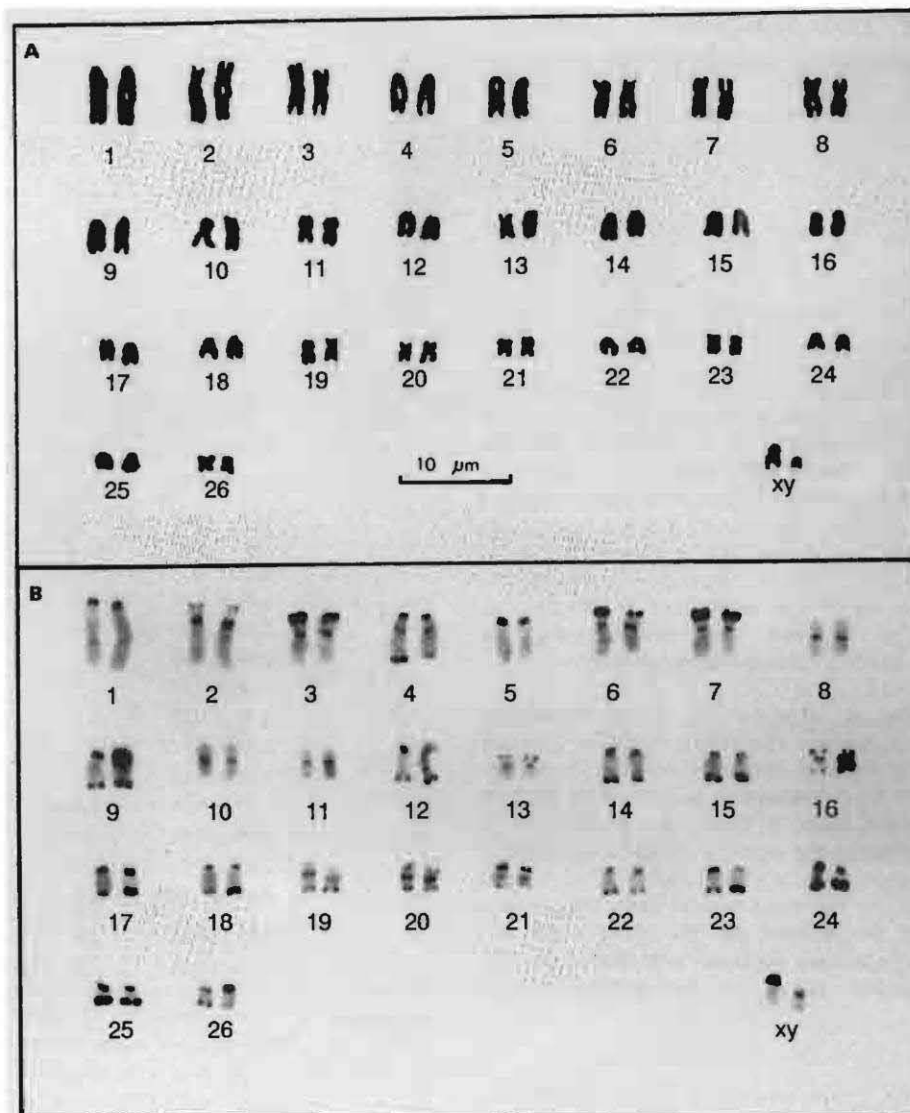


Figure 1 Standard karyotype (a), and C-bands (b), of a male *Cryptomys h. darlingi* from Goromonzi, north-eastern Zimbabwe. $2n = 54$, aFN = 84.

Nevo *et al.* (1986) described the karyotypes of the southern subspecies *C. h. hottentotus* and *C. h. natalensis* from South Africa. The chromosome complements of these two subspecies show similar characteristics: $2n = 54$ for both taxa; $aFN = 102$ and 100 for *hottentotus* and *natalensis* respectively, and a high predominance of biarmed elements. Differences in the number of arms between these cytotypes is interpreted as a result of pericentric inversions on pairs 3 and 15. Although the result on differential staining reported by these authors was not clear for the whole complement, the presence of large paracentric blocks of heterochromatin is evident for some of the biggest chromosomes in the karyotypes of these taxa (see Nevo *et al.* 1986, Figure 8). Interstitial or distal telomeric C-blocks were not recorded.

Differences in the chromosome complements of natural populations of rodents resulting from structural rearrangements are often associated with taxonomic differences (Patton & Sherwood 1983). Variation in the number of chromosome arms in a karyotype (FN), is usually the result of pericentric rearrangements (Mascarrello & Hsu 1976; Robbins & Baker 1981; Baker, Robbins, Stangel & Birney 1983; Nevo *et al.* 1986), or addition of whole heterochromatic arms (Duffy 1972; Patton & Smith 1990; Vidal-Rioja 1985; Massarini, Barros, Roig & Reig 1991). Heterochromatic arms in the karyotypes of *C. h. hottentotus* and *C. h. darlingi* were not detected and consequently pericentric inversions are the most probable rearrangements involved in the process of differentiation. Data about meiotic disturbances owing to structural heterozygosity of these inversions are not available for these taxa. However, it has been observed that individuals simultaneously heterozygous for several pericentric inversions show a drastic reduction in fecundity (Shaw 1976; Adkins, McBee, Porter & Baker 1991). A minimum of 12 pericentric rearrangements would be necessary to account for the difference in the chromosome arm number between *hottentotus* and *darlingi* cytotypes.

As in most of the taxa within the genus *Cryptomys*, the taxonomic status of *C. h. darlingi* has been ambiguous and unstable. Roberts (1951) and De Graaff (1964) regarded it as a distinct species, but Ellerman, Morrison-Scott & Hayman (1953), De Graaff (1971), and Meester, Rautenbach, Dippenaar & Baker (1986) considered it a race of *C. hottentotus*. Honeycutt *et al.* (1991) observed that the skull of the 'southern-eastern' African species *C. hottentotus* shows an elliptical infraorbital foramen with a thin external wall. Preliminary analysis of skull morphology shows some obvious differences between the two taxa. The infraorbital foramen in *C. h. darlingi* is small, with a triangular shape and a relatively wide wall, whereas that of *C. hottentotus* is bigger, elliptical and with a very thin wall. Furthermore, the rostrum of *C. h. darlingi* is shorter and wider with respect to that of *C. hottentotus*. Further investigation using a multivariate morphological approach might reveal discrete patterns of variation between the two taxa.

The chromosomal evidence presented here supports the recognition of *C. h. darlingi* as a separate species. Information about populational chromosome structure for the remaining *Cryptomys* taxa is currently being investigated, and any discussion about phylogenetic relationships within

the genus is premature. The magnitude, mode and role of chromosomal differentiation within the genus *Cryptomys* remains unknown.

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