

lating mechanisms against unsettling gene flow from other closely-related species (Dobzhansky 1937, Mayr 1942). Many criticisms of the BSC have focused on this problem of demonstrating the existence of reproductive isolation mechanisms (reviewed in King 1993, Sbordoni 1993, Mallet 1995, among others). This problem is more acute in the case of allopatric populations, which are unable to interbreed by virtue of their geographic separation. In such cases, captive-breeding provides a means of testing for the presence or absence of reproductive barriers between populations. However, even under these conditions, conclusions drawn are equivocal: an absence of reproductive success in captivity does not necessarily imply an inability to breed in nature; and successful inter-breeding does not definitely prove conspecificity, as shown for mammals by the impressive list of interspecies hybrids produced in captivity (Gray 1971), and even by the known cases of hybrid fertility (Short 1976). Partly based on these criticisms, a number of alternative concepts integrating new methodological approaches have been developed (see for instance the multidimensional species concept of Sbordoni (1993) and the genotypic cluster definition of Mallet (1995)). In these new frameworks, reproductive data remain of value in the understanding and interpretation of evolution at the species level, but only as a complement to other data sets.

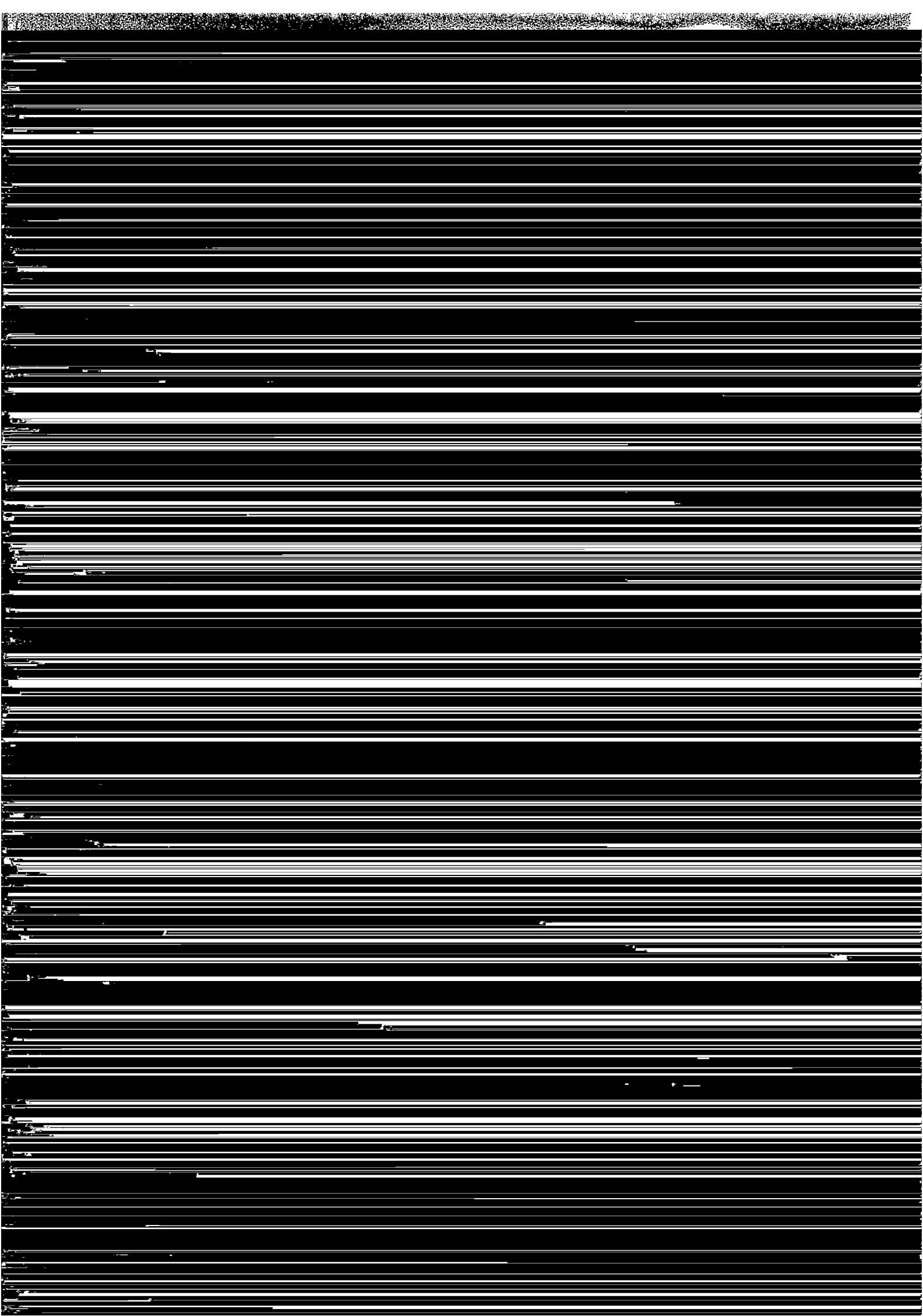
Our knowledge of the systematics and evolutionary history of the murid rodent genus *Mastomys* has improved considerably of late, thanks to the integration of different methodological approaches (see Britton-Davidian *et al.* 1995, for review). In this genus, the best tool for unambiguous species characterization remains chromosomal analysis, as each species seems to be characterized by a specific karyotype. As described in Britton-Davidian *et al.* (1995), the one of *M. natalensis* is typically composed of 32 chromosomes, with an autosomal fundamental number of 54. Nevertheless, intraspecific variation already identified in this species as well as in *M. coucha*, *M. erythroleucus* and *M. huberti* (Hallett 1977, Duplantier *et al.* 1990, Lavrenchenko *et al.* 1992, Britton-Davidian *et al.* 1995) raises the question of the potential polytypism in these species.

In this paper, we examine this question in *M. natalensis*. This species has recently been shown to occur in Senegal, where it is represented by exclusively synanthropic populations in the south-east of the country (Duplantier 1988, Duplantier and Granjon 1988, Granjon and Duplantier 1993). This suggests that its distribution probably covers almost all Africa south of the Sahelian zone. Cross-breeding experiments between specimens from the two extremes of this range (Senegal and South Africa) were conducted to evaluate inter-fertility between them. The results are compared with data from pairs between individuals from Senegal. Biometric and cytogenetic differences between samples from Senegal and South Africa are also presented, to quantify the level of differentiation reached by these geographically distant populations.

MATERIAL AND METHODS

Laboratory crosses

Reproductive data for *M. natalensis* from Senegal were generated using live-trapped individuals, which were paired and bred in captivity during three distinct periods: 1984-1986 (Dakar, N = 12 pairs), 1989 (Mbour, N = 4 pairs), 1990-1994 (Dakar, N = 20 pairs). Pairs were kept in cages with food (commercial pellets) and water provided *ad libitum*, and maintained at ambient conditions of temperature, humi-



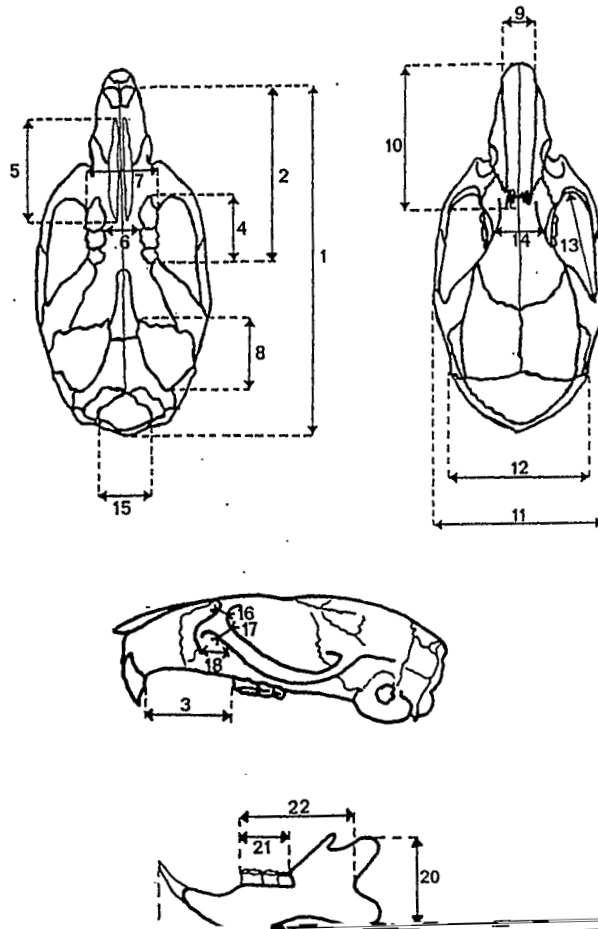


Fig. 1. — Measurements taken on skulls and mandibles of *M. natalensis*.

of 8 (75 %) F1 Senegal x South Africa pairs reproduced, whereas all backcrosses and F2 crosses were successful.

The results presented in Table 1 concern only those pairs that actually reproduced. No difference was found between the two types of backcrosses (F1 x Senegal or F1 x South Africa), so the results were pooled for statistical analyses. The same was done for the results of both combinations in bidirectional pairings. Backcrosses produced the smallest litters (5.35 young/litter), whereas F2 pairs gave birth to relatively large litters, with a mean size of 8.31 young/litter. Statistical analysis of the results of the

other chromosome member showed an additional segment near the centromere and in pair 12, a more intense staining of the centromeric region was observed. Both of these differences are present in the karyotype of *M. natalensis* from Zimbabwe published by Lyons *et al.* (1980). These results suggest that the karyotypes of *M. natalensis* from Zimbabwe and from Durban in South Africa share similar G-banding patterns and show only slight differences with those of *M. natalensis* from Senegal.

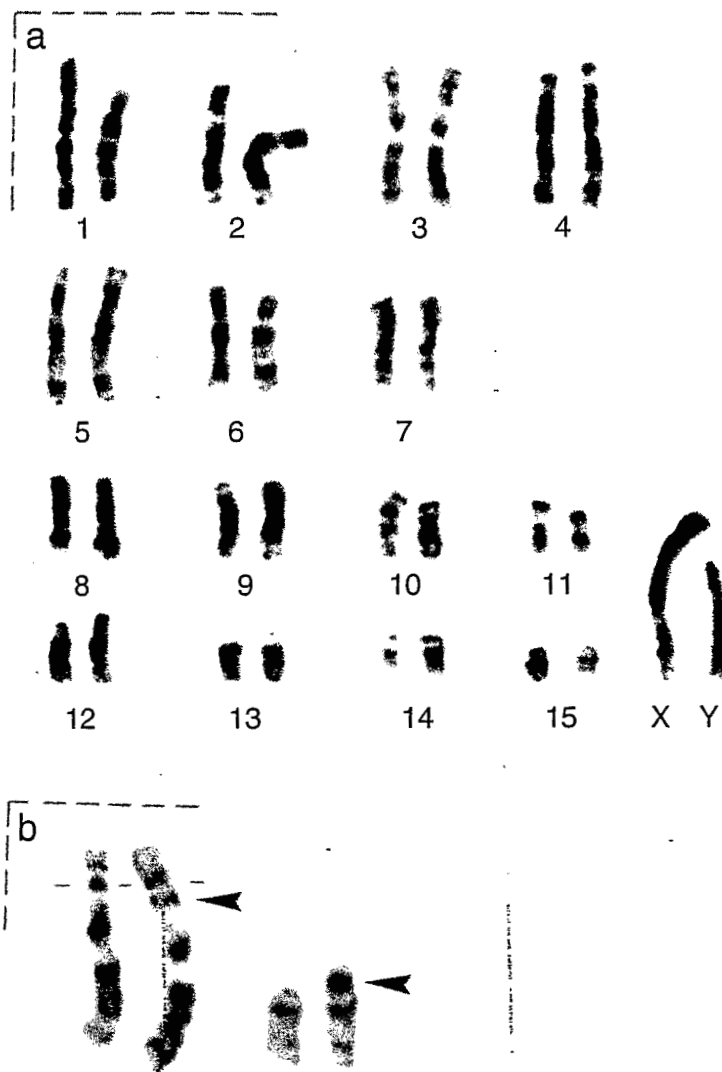
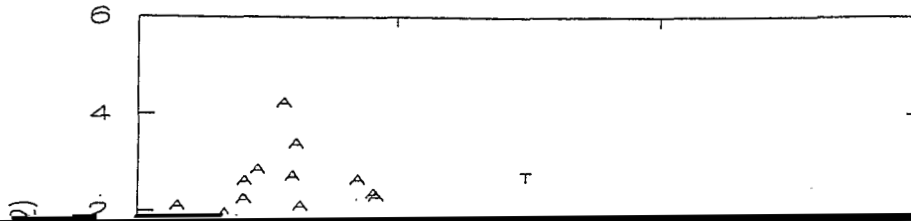


Fig. 2. - a) G-banded karyotype of a male F1 hybrid. b) Insert showing dimorphism in chromosome pairs 3 and 12. Dashes indicate the position of the centromere; arrows highlight the additional segments corresponding to the G-band patterns of the karyotype of the South African parent.

Biometrical analysis

Principal component analysis (PCA) yielded no clear separation between the 3 samples studied (Senegal, South Africa, Tanzania). The use of discriminant analysis led to better separation between them (Fig. 3), but some overlap was still evident. The variables that participated the most to the overall discrimination between the three groups were n° 1, 4, 8, 9, 13, 14, 15, 16, 17, 21 and 22 (F tests, $p < 0.005$), indicating that both differences in size and shape were occurring. Three of the 35 individuals from Senegal were classified to the incorrect *a priori* groups (2 to the South African sample, 1 to the Tanzanian one), while 1 individual from Tanzania was classified into the South African sample.

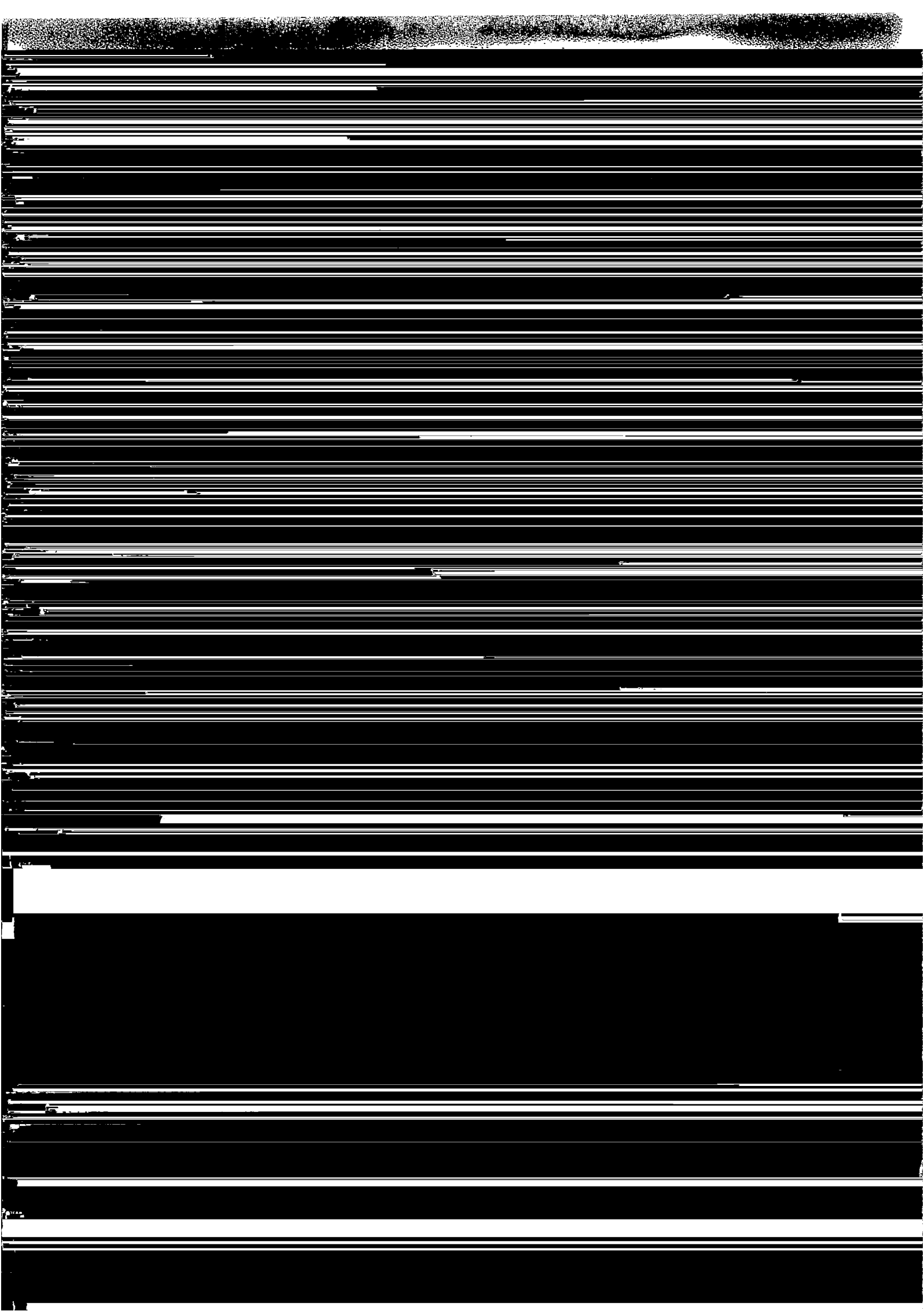


pairs were constituted from wild-caught individuals, whereas the Senegal x South Africa crosses were performed with captive-born animals. *N. natalensis* is known to be quite aggressive to conspecifics (Hallett 1977, Coetzee 1975, Granjon and Duplantier 1993), and this may be more the case in wild-caught than in captive-born individuals, thereby leading to a reduction in mating activity.

Conspicuity of M. natalensis from Senegal and South Africa

Intraspecific cross-breeding experiments between individuals from allopatric origins have seldom been conducted in African rodents. Petter *et al.* (1969) demonstrated complete interfertility between *Arvicanthis niloticus* from Ethiopia and Senegal, as well as between their progeny. Kaminski *et al.* (1984) described the same result between *A. niloticus* from Senegal and Egypt. Chromosomal studies on specimens from the latter two countries further demonstrated their karyotypic identity (Volobouev *et al.* 1988). The recent experiments of Pillay *et al.* (1992, 1995) concerned samples from different populations of *Otomys irroratus* that were not separated by a very large geographic distance, but had distinct karyotypes. This chromosomal differentiation resulted in a severe reduction of reproductive performances in interpopulation crosses, and of hybrid fitness.

In our case, only slight chromosomal differences have been evidenced by G-banding analyses between *M. natalensis* from Senegal and South Africa (see insert of Fig. 3). Similarly, our preliminary biometric results indicated no clearcut differentiation between samples of *M. natalensis* from Senegal and South Africa. While the level



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