

its peak at the breakpoint and the outer turbulent zone is characterized by high diversity and biomass. In the King's Beach transect *Callianassa* were first recorded around the outer limit of the transition zone (4 m) and were abundant in the outer turbulent zone which started at 5 m. The absence of *Callianassa* from the outer turbulent zone at Sundays River is not explained by our data and must be related to a factor other than substrate. Forbes (1973a) postulated that water movement and sediment transport limited the distribution of *C. kraussi*. The stronger longshore currents in the exposed eastern side of the bay and the possible increase in sediment transport may preclude *Callianassa* from this area.

Using the mean *Callianassa* spp. biomass ($10,04 \pm 8,9$ g m⁻²) for the 15 stations sampled in the transition and outer turbulent zones of King's and Hobie Beaches (area ca 2 km²) a conservative biomass estimate of 20 000 kg is obtained for this sheltered section of Algoa Bay. The total standing biomass for the Swartkops estuary was estimated at ca 12 000 kg by Hanekom (1980). This population of prawns is a major food source for fish, and is important in bioturbation and ventilation of the sediment.

Further study is required to establish factors influencing competition/co-existence between the two *Callianassa* species found in the King's Beach transect.

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The chromosomes of the tsessebe *Damaliscus lunatus*

H J van der Veen*

Department of Zootechnology, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110

B.L. Penzhorn

Department of Parasitology, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110

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Mitotic chromosome studies in five male tsessebe are described. The diploid chromosome number of 36 (NF = 61) is reported for the first time.

'n Onderzoek is na die mitotiese chromosome van vyf tsessebebulle uitgevoer. Die diploïede chromosoomgetal van 36 (NF = 61) word vir die eerste keer beskryf.

*To whom correspondence should be addressed at: South African Institute for Medical Research, P.O.Box 1038, Johannesburg, 2000.

The mitotic chromosome complement of tsessebe *Damaliscus lunatus* is reported here for the first time. Chromosome analyses of free-ranging large mammals have been carried out by various researchers in Southern Africa. Prominent among these are the investigation into chromosomes of the Perissodactyla by Heinichen (1970), and the extensive survey of chromosomes of Artiodactyla, Carnivora, Proboscidea and Perissodactyla in the Kruger National Park by Wallace (1976).

Tsessebe are rare in South Africa and study material is not readily available. Wallace (1976) attempted bone marrow chromosome analysis from a male and female tsessebe in the Kruger National Park, but this was not

successful. An opportunity to study the mitotic chromosomes of tsessebe arose when surplus tsessebe males in the Nylsvley Nature Reserve, Central Transvaal (24°29'S / 28°42'E), were shot during a parasite survey between May 1985 and March 1986. Tsessebe were introduced to Nylsvley in 1977 from the Percy Fyfe Nature Reserve, which had been stocked with tsessebe captured in the Waterberg District, Transvaal (Parris & Smith 1980).

Tsessebe belong to the subfamily Alcelaphinae of the family Bovidae (Smithers 1983). The other Southern

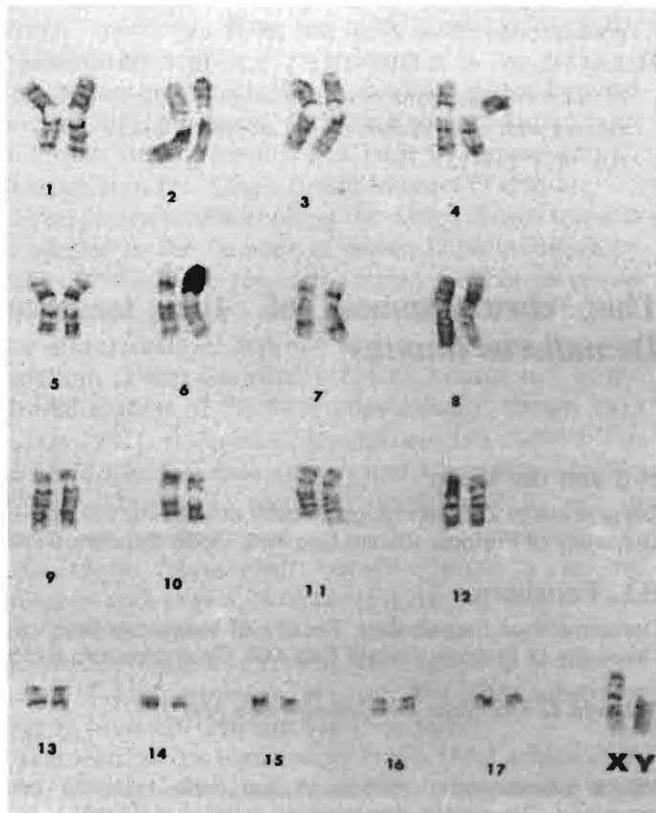


Figure 1 G-banded karyotype of a male tsessebe from Nylsvley Nature Reserve, Central Transvaal.

African members of the subfamily are: bontebok *Damaliscus dorcas dorcas*, blesbok *D.d. phillipsi*, Lichtenstein's hartebeest *Sigmocerus lichtensteini*, red hartebeest *Alcelaphus buselaphus*, black wildebeest *Connochaetes gnou* and blue wildebeest *C. taurinus* (Meester, Rautenbach, Dippenaar & Baker 1986).

Material and methods

Venous blood from five male tsessebe was collected into 10 ml evacuated heparinized tubes. The blood specimens were cooled by placing them next to a frozen commercial cold-pack in a styrofoam container, which was sealed with masking tape. Specimens were delivered to the laboratory within 6 h and kept at 4°C until processed. Whole blood was used for leucocyte culture. Chromosome preparations were made according to the technique of Moorhead, Nowell, Mellman, Bottips & Hungerford (1960). The slides were pretreated with trypsin before staining with Giemsa (Seabright 1971). G-banding was performed to facilitate the matching of chromosome pairs.

Results and discussion

Chromosome preparations of all five tsessebe were of rather poor technical quality. In 30 dividing leucocytes a modal diploid number of 36 was found. The autosomal complement comprised eight pairs of metacentric chromosomes, four pairs of submetacentric chromosomes and five pairs of acrocentric chromosomes (Figure 1). The X-chromosome is of submetacentric morphology, while the Y-chromosome is the largest acrocentric in the complement. The chromosome arm number or fundamental number (NF) was 61.

The results of this study are compared to data from other Southern African members of the subfamily Alcelaphinae (Table 1). The chromosomes of Lichtenstein's hartebeest have not been described. Although the diploid chromosome number of members of the superfamily Bovoidea varies from 30 to 60, the NF varies only (with but three exceptions) from 58 to 62, which indicates an almost exclusive use of the Robertsonian fusion mechanism of karyotype evolution

Table 1 Summary of chromosome findings of Southern African members of the subfamily Alcelaphinae

Species	♂:♀	2n	NF	M+SM	A+SA	X	Y	Reference
<i>Damaliscus lunatus</i>	5:0	36	61	24	10	SM	A	This study
<i>D. dorcas</i>	1:1	38	60	22	14	A	A	Wurster & Benirschke 1968
<i>Alcelaphus buselaphus</i>	0:2	39/40	58/60	21/22	16/18	A	?	"
<i>Connochaetes gnou</i>	0:1	58	60	2	56	?	?	"
<i>C. taurinus</i>	1:1	58	60	2	56	A	A	Gerneke 1967; Wallace 1978

2n = diploid chromosome number; NF = fundamental number (chromosome arm number); M = metacentric; SM = submetacentric; A = acrocentric; SA = subacrocentric.

in this group (Wurster & Benirschke 1968). In speculating about karyological evolution in the Bovidae, Wallace (1979) postulated that the common ancestral bovid had a diploid chromosome number of 60.

The poor technical quality of our G-banded specimens preclude comparison with other species. Buckland & Evans (1978a,b), using both G-banding and C-banding techniques on various bovids (including a female red hartebeest from Uganda), concluded that the conservation of banding patterns in chromosome arms strongly indicated that Robertsonian translocation type rearrangements had provided the major source of interspecies karyotype differences, with inversions and reciprocal and tandem translocations providing relatively minor contributions.

Wallace (1976) pointed out that chromosome analyses of free-ranging wild animals could be more representative of the naturally occurring situation than would analyses of the chromosomes of zoo-bred animals. Sampling errors owing to the usually small sample sizes obtainable from zoos may lead to errors in establishing karyotypes. Breeding between different subspecies or even species is not uncommon in captive animals housed together, which could be a source of mistyping. Owing to the sheltered environment and absence of natural competition in zoos, chromosome changes associated with harmful effects would not necessarily be eliminated, nor would chromosome changes attended by beneficial effects necessarily be selected for, although these factors are probably minor, compared to small sample size and possible hybridization.

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Observations on the attachment of a piscine gill parasitic ergasilid (Crustacea : Copepoda)

W.H. Oldewage and J.G. van As*

Research Unit for Fish Biology, Rand Afrikaans University, P.O.Box 524, Johannesburg, 2000 Republic of South Africa

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The attachment of the piscine gill parasite, *Ergasilus mirabilis* Oldewage & van As, 1987 is described by means of scanning electron microscopy and light microscopy. A variety of sensory structures occur on and around the host contact surface of the parasite and proliferation of gill tissue occurs at the site of attachment. It would appear that this proliferation of host tissue results from the feeding behaviour of the parasite rather than the actual attachment thereof.

Die vashegting van die vis-kieuparasiet, *Ergasilus mirabilis* Oldewage & Van As, 1987 word beskryf aan die hand van skandeerelektronmikroskopie en ligmikroskopie. 'n Verskeidenheid sensoriese strukture kom op en in die omgewing van die gasheerkontakvlak van die parasiet voor en proliferasie van die kieuepiteel vind plaas op die plek van vashegting. Dit blyk dat die proliferasie van gasheerweefsel eerder die gevolg van die voedingsgedrag van die parasiet is as van die vashegting daarvan.

*To whom correspondence should be addressed

It has been suggested, and available information supports this view, that parasitic copepods are phylogenetically derived from free-living cyclopoids (Fryer 1956; Kabata 1970a). A number of instances are reviewed by Kabata (1970b) of free-living cyclopoids displaying micropredatory behaviour, i.e. preying on fish eggs and larvae, suggesting a possible starting point