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A female Bukhara deer *Cervus elaphus bactrianus* Lydekker, 1900 with 68 chromosomes

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A previously unknown karyotype numbering 68 chromosomes is described for Bukhara deer *Cervus elaphus bactrianus*. A single pair of autosomes being metacentric, N.F. numbered 70.

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Introduction

Comprising merely 32 contemporary species, cervids display an extreme extent of chromosomal differentiation. Diploid chromosome numbers vary from 2n = 6 (females) / 7 (males) in the Indian muntjac *Muntiacus muntjac* to 2n = 80 in Siberian roe deer *Capreolus pygargus* (Neitzel 1987). In the genus *Cervus* (*sensu stricto*) which consists of two species, sika deer *C. nippon* and red deer *C. elaphus* (Groves and Grubb 1987), diploid complements range from 62–68 chromosomes (Neitzel 1987, Herzog 1988). This numeric diversity does not affect the N.F. value which is 70 throughout but is entirely associated with Robertsonian rearrangements. Sika is the more ancestral species whose subspecies and distinct populations are in need taxonomic revision; most karyotyped sika deer belonged to captive populations kept outside their native ranges and probably contain racial hybrids. Gustavsson and Sundt (1969) reported on polymorphism ranging from 62 to 68 chromosomes within a herd of sika deer kept at Woburn Abbey, England. However, most reports on sika populations found less extensive polymorphism within the range between 62 and 68 chromosomes (review: Herzog 1988). Holarctic red deer *Cervus elaphus* evolved from sika-like ancestors in Asia and comprises many populations classified in three subspecies groups. In the nominate *elaphus*--group from Europe, an invariant complement of 68 chromosomes has been reported in at least 13 published investigations (review: Herzog 1988), as has been found for the wapiti-group (Wurster and Benirschke 1967, Koulischer *et al.* 1972). Distributed geographically between the *elaphus*-group and the east Asiatic and

Nearctic wapitis, a third semispecies, the acoronate or *wallichi*-group (with *C. e. bactrianus*, *C. e. yarkandensis*, *C. e. hanglu*, *C. e. wallichi*, *C. e. macneilli*, and *C. e. kansuensis*) inhabits central Asia in isolated populations which remain badly known even as museum specimens (Groves and Grubb 1987). These taxa of phylogenetically primitive deer connect morphologically the derived red deer with sika. Bukhara deer *C. e. bactrianus* from the Amu Darya and Syr Darya river basins of Turan represents a particularly small, light-coloured form adapted to life in gallery vegetation of arid lands. Wang and Du (1981) investigated the karyotypes of four central Asiatic deer classified as *C. e. bactrianus* kept at Beijing Zoo, and found complements of 2n = 67 in three offspring of a stag containing 2n = 66. The only other deer from the *wallichi*-group whose karyotype is known is *C. e. macneilli* from Sichuan and Yunnan, with 2n = 68 chromosomes (Wang and Du 1981, 1983). This article reports on a previously unknown karyotype of a female Bukhara deer.

Material and methods

Heparinized whole blood was obtained from a Bukhara deer kept at Cologne Zoo, Germany. Three-day lymphocyte cultures were grown in Chromosomen-Medium B (Seromed, Berlin), and karyotypes prepared as described previously (Schreiber *et al.* 1993). Twenty metaphase patterns of the Giemsa-stained chromosomes were photographed and analyzed.

Results and discussion

The karyotype of a Bukhara deer hind imported from the formerly Soviet part of this subspecies's range comprised 68 chromosomes, including one metacentric and 33 acrocentric pairs. N. F. amounted to 70. The G-stained karyotype (Fig. 1) does not show differences in chromosomal morphology from red deer of the *elaphus*-group from central and north-west Europe, and accordingly the longest telocentric pair will represent the female gonosomes. Although our lack of banding patterns prohibit individual identification of most chromosomes, the present result complements the findings of Wang and Du (1981) to demonstrate a Robertsonian translocation system of 2n = 66 to 2n = 68 in this taxon. The reduced chromosome numbers described by Wang and Du (1981) correlate with the appearance of one (2n = 67) or two (2n = 66) additional (sub)metacentrics. Interpreted as a Robertsonian polymorphism, the karyotype added in this report would represent the homozygous pattern lacking the translocation metacentrics.

Numerous red deer of the derived *elaphus*-group have been karyotyped, with invariant patterns of 2n = 68 encountered throughout which is also the pattern found in American wapiti *C. e. canadensis* (review: Herzog 1988). Belonging to a supposed ancestral population stratum of *C. elaphus*, Bukhara deer with their cytogenetic variation nearly fit into the model of chromosome evolution detailed by Neitzel (1982, 1987) which suggests that Robertsonian translocations are the predominant if not exclusive mode of cytogenetic evolution within *Cervus*, leading

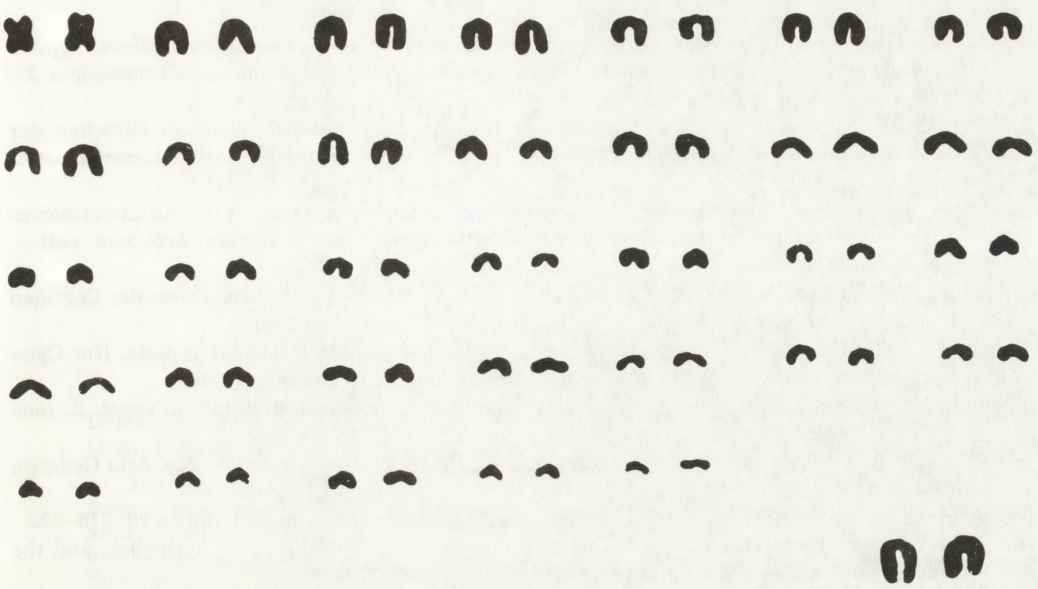

Fig. 1. Karyotype of a female Bukhara deer *Cervus elaphus bactrianus*. The X-chromosomes have been identified in analogy to *C. e. elaphus*.

from an insufficiently understood Robertsonian variation between and within sika deer populations to the supposedly monomorphic pattern of derived red deer from either Europe of America.

Having recovered from an all-time low of 3–400 individuals in the 1960s to some 900 animals in the late 1970s, Bukhara deer is a threatened taxon confined to ecologically fragile riverine tugai thickets within the semidesert of Turan, and will remain a rare deer even if conservation measures are effective (Bannikov 1978, Flint *et al.* 1989). Therefore, cytogenetic analysis of all zoo-living Buchara deer is suggested as a prerequisite to conserve possible chromosomal polymorphism in the small captive herd.

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