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This is the author's manuscript

Original Citation:

Availability:

This version is available http://hdl.handle.net/2318/1507158 since 2018-03-18T15:54:03Z

Published version:

DOI:10.1007/s10577-008-1922-2

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14 October 2026

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This is the author's final version of the contribution published as:

D. Nicodemo, A. Pauciullo, A. Castello, G. Cosenza, V. Peretti, A. Perucatt, G.P. Di Meo, G. Ficco, L. Ramunno, L. Iannuzzi, J. Rubes and D. Di Berardino. A cytogenetic investigation on the yak (Bos grunniens) reared in central Italy. Chromosome Research (2008) 16:1027-1071
DOI: 10.1007/s10577-008-1922-2

The publisher's version is available at:
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A cytogenetic investigation on the yak (Bos grunniens) reared in central Italy

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The domestic yak (Bos grunniens) is an important Bovidae species which in Asia plays a remarkable role for the economy of the Tibetan highlands (over 4000 m above sea level.). Despite its strategic and economical importance, this species has been almost neglected, from a cytogenetic point of view, as demonstrated by the few papers present in the literature. To fill this gap, we undertook a cytogenetic investigation by using blood samples of eight yak bulls recently imported into central Italy. CGR-banding, silver staining and FISH-techniques were applied. The preliminary results were as follows: (a) the chromosomal make-up of the yak was 2n=60,XY, (b) the animals investigated showed normal karyotype, (c) the frequency of chromosome/chromatid breaks was similar to that of cattle (3.7 vs 3.0 %, respectively), (d) the mean rate of SCE/cell at 10 2g/ml (f.c.) was significantly ($P<0.001$) lower compared to that of cattle (5.2 vs 8.3, respectively), (e) the GTG-RBA-RBG banding patterns Y at the 400 bands level of resolution Y did not reveal structural differences compared to cattle, (f) the CBA-banding pattern was also similar to cattle, i.e. no C-bands on the subcentromeric X, while the Y- chromosome showed heterochromatic tips in the short arms.
Zoo-FISH with bovine painting probes derived from microdissected chromosomes 5-X-Xcen and Y- upon yak metaphase chromosomes showed complete hybridization, thus confirming the close homology between the two species. In addition, FISH-mapping with bovine BAC-clones containing ZFY and SRY genes to the yak Y-chromosome also revealed the same localization as reported in cattle (Yp12.2 and Yq23dist, respectively).
However, the fact that Bos taurus x Bos grunniens F1 male hybrids are sterile, while the females are normally fertile, suggests that the main difference between yak and cattle might be in the X-Y pseudoautosomal (PAR) region of the two species. Further investigation, therefore, is necessary with more effective cytogenetic techniques, such as high resolution banding, fine gene mapping analysis and DNA sequencing.