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Cytogenetic characterization of the yak (*Bos grunniens*) and comparison with cattle (*Bos taurus*)

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ABSTRACT

The domestic yak (*Bos grunniens*) belongs to the family Bovidae and is one of the most important species for the economy of the Asian high lands. Recently, the interest for this species increased also in European countries, mainly because of its meat and milk characteristics. Furthermore, it is a species well adapted to marginal conditions and it could be used to preserve mountain territories economy. We carried out a detailed investigation on this species with the following main aims: 1) to perform a cytogenetic screening of a yak herd recently introduced in Italy; 36 out of 60 animals were analyzed by conventional and GTG-banding karyotype. All animals were $2n=60$ and no chromosomal abnormalities were found, confirming that the introduced herd is a good nucleus to start up with yak farming in Italy; 2) to determine the genetic stability of the animals reared under Italian conditions; two different tests were used: "Chromatid/chromosome breaks" and "Sister chromatid exchange (SCE)". Out of 400 analyzed cells, 3.75% showed one or more anomalies; the most represented were chromosome and chromatid breaks. The mean number of SCE/cells was 5.2%. Comparison with cattle revealed that the two species have the same percentage of chromosome anomalies, while SCE frequency is lower in yak compared to cattle; 3) to increase the cytogenetic knowledge about this species and compare *Bos taurus* and *Bos grunniens* in relation to male sterility of F1 hybrids; C-, R-, and G-banded karyotypes of yak were prepared and compared with the standard karyotypes of cattle. To identify Nucleolar Organizer Regions, sequential NOR's/R banded karyotypes were performed.

Despite the two species share a very high degree of banding homology, some differences can be pointed out; the most remarkable is on the centromeric region of chromosome 15, where a strong positive band is present in *Bos grunniens* while absent in *Bos taurus*. Molecular data indicate that in yak, unlike in cattle, the X chromosome has retained a homologous sequence (182 bp) to the Y chromosome. To verify if larger blocks of chromatin are involved, FISH analysis of yak metaphases using X and Y cattle painting probe was performed. The lack of unspecific signal indicated that no large blocks of chromatin are interested. Finally, we mapped two genes (SRY: sex-determining region Y gene and ZFY: zinc finger protein, Y-linked) on the yak Y chromosome to verify if this chromosome, like in other species, such as *Bos indicus*, underwent rearrangement during evolution. The two genes mapped at the same position compared to cattle, indicating that the sterility of F1 hybrids seems not to be due to Y chromosomal rearrangements relatively to the these two genes.