

Comparison of RBG-banded karyotypes of cattle, sheep and goat

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Based on natural taxonomic criteria, the 3 main domestic species of the Bovidae family belong to 2 different subfamilies: Bovinae (*Bos taurus*: domestic ox or cattle) and Caprinae (*Capra hircus*: goat, *Ovis aries*: domestic sheep).

Cattle, goat and sheep karyotypes show a high degree of similarity as far as their *nombre fondamental* $NF = 58$ (number of autosome arms) and the band patterns of most of their chromosome arms are concerned (Buckland and Evans, 1978; Di Berardino *et al*, 1987; Mensher *et al*, 1989).

Only small differences in the band patterns have been reported between goat and sheep, on the one hand, and cattle, on the other, for autosome 9 and for the sex chromosomes (Ford *et al*, 1980; ISCNDA, 1989).

In this study, we have investigated in greater detail these differences using synchronized cultures of primary embryo fibroblasts and the RBG-banding technique.

To obtain a high yield of metaphase and early metaphase cells, cultures of primary embryo fibroblasts were synchronized with a double thymidine block of S phase (Viegas-Pequignot and Dutrillaux, 1978, and personal communication).

Harvest, hypotonic treatment, fixation and spreading of cells and fluorescence plus Giemsa (FPG)-staining are described in Viegas-Pequignot *et al* 1989. Chromosomes were numbered according to ISCNDA 1989.

A band-by-band analysis of the RBG-banded chromosomes of sheep, goat and cattle clearly showed the high degree of conservation of their banding pattern; the only differences which we consistently observed concern autosome 9 and sex chromosomes.

Figure 1 shows sheep, goat and cattle autosomes 9 from different karyotypes chosen for their characteristic banding. Sheep and goat autosomes 9 appear identical at this level of resolution but differ from that of cattle. We found that the pale region

located in about the middle of this chromosome was lower in cattle than in goat and sheep and that the number of bands below this region was higher in goat and sheep than in cattle, while that above this region was smaller in goat and sheep than in cattle. This leads us to suggest that a paracentric inversion, as indicated in figure 1, may have occurred when Bovinae and Caprinae diverged. However, it will be necessary to obtain even finer banding patterns and/or to use specific probes of this region in *in situ* experiments to verify this hypothesis.

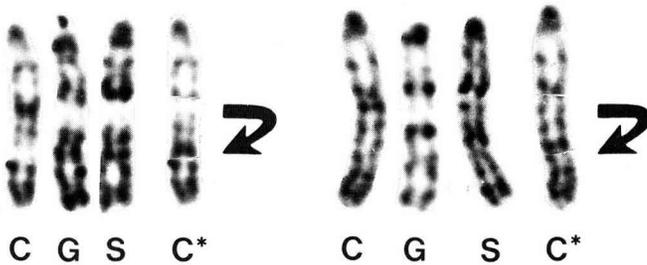


Fig 1. Comparison of goat (G), sheep (S) and cattle (C) RBG-banded autosomes 9. The proposed paracentric inversion leading to cattle autosome 9 is indicated by an arrow. C* is a montage of cattle autosome 9 with its central region inverted.

Figure 2 contains Y and X RBG-banded chromosomes. Figure 2a presents the Y chromosomes and, as previously reported, in sheep and goat they looked identical, very small, acrocentric with darkly stained p arms, while in cattle, they were larger, submetacentric and almost entirely pale except in the p arm.

Figure 2b shows X chromosomes for the 3 species from various karyotypes. As for Y chromosomes, we found that sheep and goat had identical X chromosomes while cattle were quite different. We did not observe the difference in the q terminal region that Mensher *et al* (1989) saw after G-banding.

However, as reported by Di Bernardino *et al* (1987) for goat and cattle, we also found that a large portion of the q arm of goat and sheep X chromosomes closely resembled the q arm of the cattle X chromosome, if the latter were turned upside down as shown in figure 2b. The remaining regions of this chromosome cannot be easily matched with those of goat and sheep X chromosomes, therefore it is probable that a complex series of events occurred between the ancestral form of the Bovidae X chromosome considered to be close to the goat type and the actual cattle type. Indeed, the fact that a large portion of the banding pattern was found to be common in all 3 species is in agreement with Ohno's (1969) hypothesis that the X chromosome has been preserved *in toto* from a common ancestor in many mammalian species.

ACKNOWLEDGMENTS

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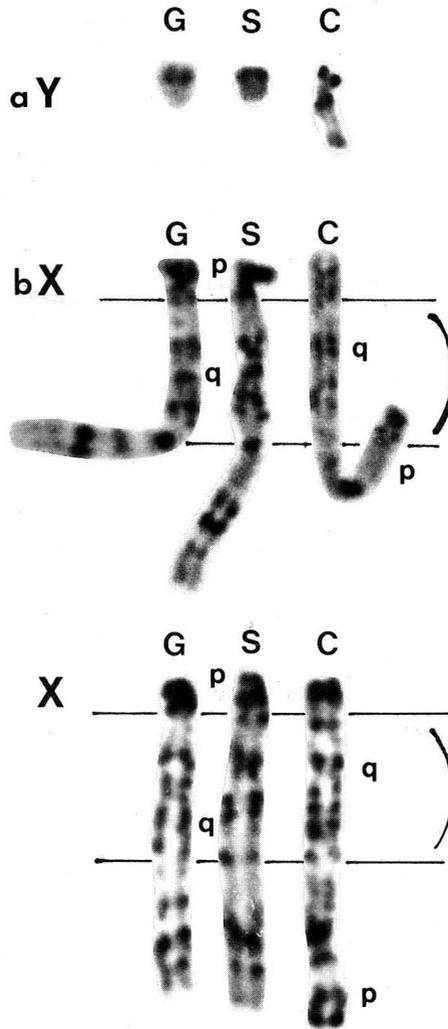


Fig 2. Comparison of goat (G), sheep (S) and cattle (C) RBG-banded Y (a) and X (b) chromosomes. The proposed common region in the X chromosome of these 3 species is indicated by a parenthesis.

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