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Tentative chromosomal assignment of the glucose phosphate isomerase gene in cattle, sheep and goat by *in situ* hybridization

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INTRODUCTION

Cattle, sheep and goat are evolutionarily closely related species belonging to the family Bovidae. Karyologically, on the basis of GTG- and RBA-bands, the three species are quite similar except for the sex chromosomes and minor differences between some autosomes (ISCNDA, 1989). Much data have accumulated in the past decade which suggest that, in the majority of the cases, chromosome-banding homologies correspond to similarities in the gene content. This conclusion is based on the results of the comparative banding and gene mapping studies carried out in human, big apes and New World monkeys (Dutrillaux *et al*, 1981; Lalley *et al*, 1989), along with comparisons made between man and mouse (Sawyer and Hozier, 1986), within the group of Cricetidae and Muridae (Yoshida, 1984; Levan *et al*, 1987), between cat and human (O'Brien *et al*, 1985), and cat and mink (Graphodatsky, 1989). In phylogenetically distant species, however, comparative banding and gene mapping homologies are less evident. In domestic animals, very few studies involving such comparisons have yet been made. The assignment of the major histocompatibility complex (MHC), cytokeratin A (KRTA) and cytokeratin B (KRTB) genes in cattle and sheep (Hediger, 1988; Mahdy *et al*, 1989) support the similar banding–similar gene concept.

MATERIALS AND METHODS

A porcine genomic glucose phosphate isomerase (GPI) DNA (GPI8R) was used for *in situ* hybridization in cattle, sheep and goat. Hybridization of GPI8R and a GPI

cDNA to genomic blots from the same species indicated that the porcine genomic probe binds to the GPI locus in these species (results not shown). The probe was tritium labeled using the random-priming method (Feinberg and Vogelstein, 1983; Lin *et al*, 1985). The specific activity of the probe was 5×10^8 dpm/μg of DNA. Lymphocytes from two Swedish *Red and White* bulls, two Swedish *Landrace* ewes and two Finnish *Landrace* bucks were cultured using standard techniques. The chromosome preparation method and the technique of *in situ* hybridization have been described elsewhere (Mäkinen *et al*, 1989). The chromosomes were GTG-banded after hybridization using the technique described by Popescu *et al* (1985). The idiograms of G-banded chromosomes of cattle were adapted for sheep and goat chromosomes and the grains were plotted on these idiograms (ISCNDA, 1989). The χ^2-test was used for statistical analysis.

RESULTS

Cattle

A total of 113 metaphases from two experiments were analyzed and the grains scored were plotted on the idiogram of G-banded cattle chromosomes (fig 1a). In all, 363 grains were counted, of which 80 (22%) were located on chromosome 18. Furthermore, of the total number of grains on this chromosome, 75 (94%) were located on the distal half of the chromosome with the peak on segment q22→ proximal part of q24, where approximately 73% (58) of the total number of grains on chromosome 18 were located.

Sheep

A total of 118 metaphases from two experiments were analyzed and the grains scored were plotted on the idiogram of G-banded sheep chromosomes (fig 1b). In all, 495 grains were counted, of which 93 (19%) were located on chromosome 14. Furthermore, of the total number of grains on this chromosome, 81 (87%) were located on the distal half of the chromosome with the peak on the segment q22→proximal part of q24, where approximately 62% (58) of the total grains on chromosome 14 were located.

Goat

A total of 121 metaphases from two experiments were analyzed and the grains scored were plotted on the idiogram of G-banded goat chromosomes (fig 1c). The sex chromosomes were drawn on the basis of the photographs of G-banded X and Y chromosomes. In all, 479 grains were counted, of which 61 (13%) were located on chromosome 18. Of the total number of grains on this chromosome, about 56 (92%) were localized on the distal half of the chromosome. A close examination revealed that the peak clustered in the q22→proximal part of q24 with about 69% (42) of the total grains on chromosome 18.

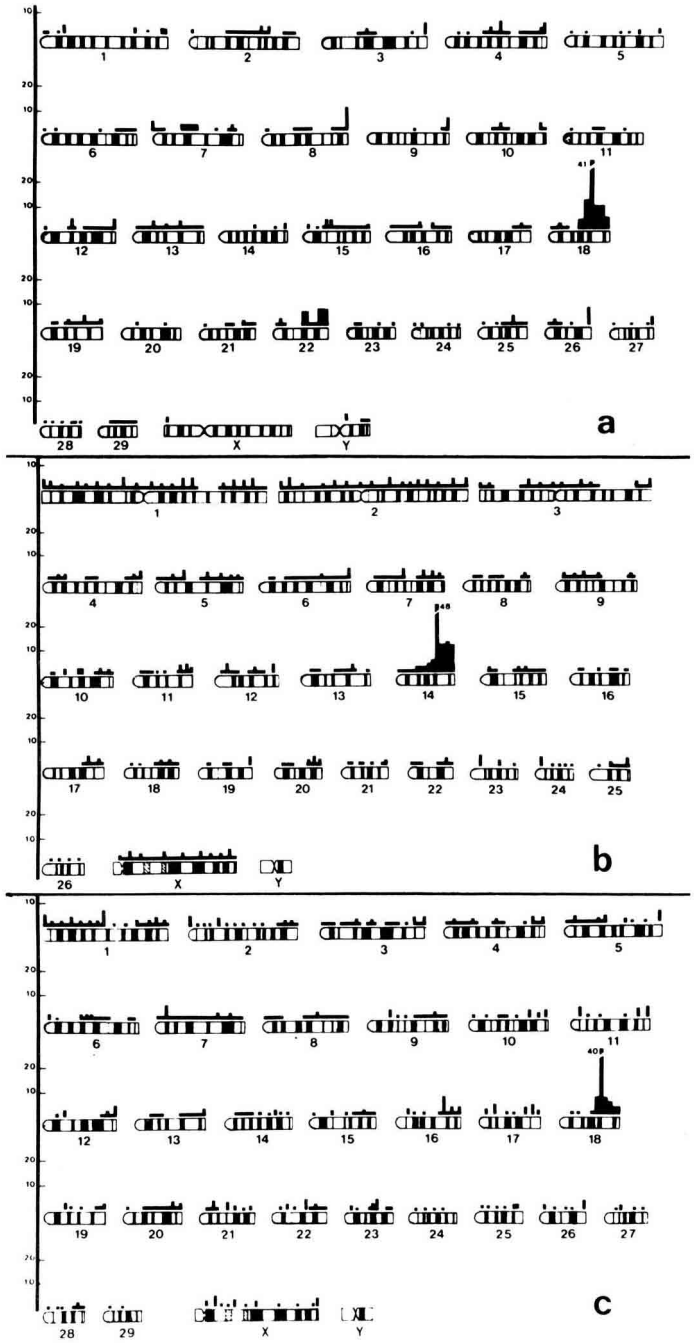

Fig 1. Grain distribution after *in situ* hybridization of the GPI8R DNA to (**a**) cattle, (**b**) sheep and (**c**) goat metaphase chromosomes.

Statistics

In all three species, the q22→proximal part of q24 constitutes less than 0.5% of the total genome. Statistical evaluation revealed that the probability of the presence of GPI8R DNA in this segment is highly significant ($P < 0.01$) in each species.

DISCUSSION

This study provides evidence that the glucose phosphate isomerase gene maps to chromosomes 18, 14 and 18 in cattle, sheep and goat, respectively. These three chromosomes have very similar banding patterns as well as hybridization signals using the GPI8R DNA probe. 87–94% of the grains on these chromosomes were located in the distal half with the peak on the same segment *viz* q22→proximal part of q24, where approximately 62–73% of the total number of grains on these chromosomes were located. The chromosomal region q24 is a relatively large region. Comparatively few grains were observed in the middle and distal parts of this region. Thus the GPI gene has tentatively been assigned to the q22→proximal part of q24 on chromosomes 18, 14 and 18 in cattle, sheep and goat, respectively, indicating the presence of similar genetic material in these regions which also appears to be similar after banding.

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