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Chromosome markers in cattle

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Summary. Giemsa banding in cattle chromosomes enables the demarcation of both centromeric areas as pale regions and banding patterns along the chromosome arms. These are valuable in identifying all the chromosomes of a given karyotype. A high degree of intra- and inter-individual variation in the size of the centromeres was observed. This variation is useful for the identification of each individual and provides a broad base of chromosome markers for cattle breeding.

Key words: Taurus cattle – Zebu cattle – Bali cattle – Chromosome polymorphisms – G-banding

Introduction

The elaboration of genetic markers is one of the major goals in animal breeding research. This applies also to cattle and related bovines. Regarding chromosomes, almost no markers are available yet in bovines. The only exceptions are a few translocation markers. However, the use of translocation markers for practical animal breeding is strongly restricted by the fertility depression of translocation heterozygotes (Gustavsson 1969; Mayr et al. 1983). Two facts are predominantly responsible for this remarkable lack of knowledge about chromosome markers in cattle. First, the general banding patterns along the chromosome arms appear rather conservative in the present banding techniques both within and between the investigated bovines (see Buckland et al. 1978 a). Second, the centrometric regions, which were recognized to be of variable size by C-banding (Buckland et al. 1978 b), have not been subjected to sequential banding procedures to allow chromosomes identification.

Based on this background we have started a careful evaluation of the centrometric regions by different staining methods. We found several sequential methods (e.g. combined fluorescence staining and C-banding, sequential fluorescence methods) well-suited for the provision of centrometric chromosome markers. The comparison between such step-by-step methods and G-banding made it obvious that the rapid, inexpensive and simple G-banding procedure can be recommended for the elaboration of centromeric markers in cattle. Our present report unequivocally documents the applicability of G-banding to this end in taurus cattle (*Bos taurus,* L.) zebu cattle (*Bos indicus,* L.) and bali cattle (*Bos sondaicus,* L.).

Material and methods

Chromosome preparations made from pokeweed stimulated peripheral blood lymphocyte cultures of 10 taurus cattle bulls (*Bos taurus,* L.; 2n=60), 3 zebu cattle (*Bos indicus,* L.; 2n=60; 1 male and 2 females) and 3 bali cattle (*Bos sondaicus,* L.; 2n=60; 1 male and 2 females) were G-banded following the method of Wang and Federoff (1972). The numbering of the chromosomes in the karyotype in taurus cattle followed the Reading recommendation for an international standard (Reading Conference 1980). The chromosome numbering in the zebu cattle and bali cattle was performed in accordance with the method used for the taurus cattle as far as possible.

Results

By G-banding, the centromeres of all autosomes of the 3 investigated species of cattle appear as pale dots or segments. Figure 1 demonstrates the G-band karyotypes of the 3 species. It has to be emphasized that the quantity of the centromeric heterochromatin has been

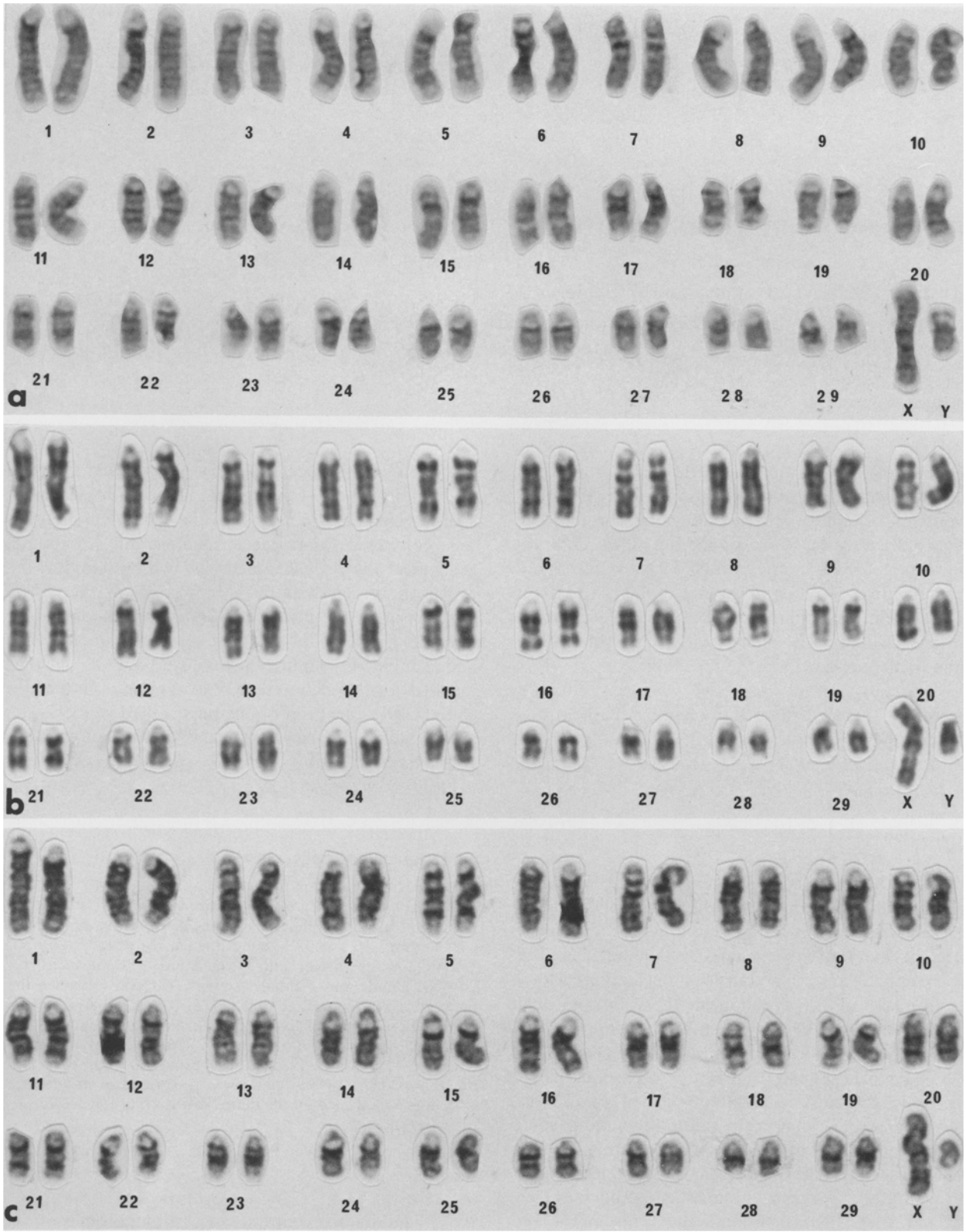

Fig. 1a–c. G-band karyotypes of taurus cattle (**a**), zebu cattle (**b**) and bali cattle (**c**). Note the size-polymorphisms of the centromeres in may chromsome pairs

Table 1. Size distribution of centromeres in taurus cattle, zebu cattle and bali cattle

Chromosome no.	1	2	3	4	5	6	7	8	9	10
Taurus C.	+ + / + + +	+ + / + + +	+ / + + +	+ / + + +	+ / + + +	+ + / + + +	+ / + + +	+ / + + +	+ / + + +	+ / + +
Zebu C.	+ + / + + +	+ + / + + +	+ +	+ / + + +	+ / + + +	+ / + + +	+ / + +	+ / + + +	+ / + + +	+ / + +
Bali C.	+ + / + + +	+ / + + +	+ / + + +	+ / + + +	+ / + + +	+ / + + +	+ + / + + +	+ / + +	+ + / + + +	+ / + + +
Chromosome no.	11	12	13	14	15	16	17	18	19	20
Taurus C.	+ / + + +	+ / + + +	+ + / + + +	+ / + + +	+ + / + + +	+ / + + +	+ / + + +	+ / + +	+ / + +	+ / + +
Zebu C.	+ / + + +	+ / + +	+	+ / + + +	+ / + + +	+ + / + + +	+ / + +	+	+ / + +	+
Bali C.	+ + / + + +	+ / + + +	+ / + +	+ + / + + +	+ / + + +	+ / + +	+ / + +	+ / + +	+ / + +	+ + / + + +
Chromosome no.	21	22	23	24	25	26	27	28	29	
Taurus C.	+ / + +	+ / + +	+ / + +	+ / + +	+ + / + + +	+ / + +	+ / + +	+ / + +	+ / + +	
Zebu C.	+ / + +	+ / + +	+	+ / + +	+ / + +	+	+ / + +	+ / + +	+	
Bali C.	+ / +	+ / + +	+ / +	+ / + +	+ / + +	+	+ / + +	+ / +	+ / +	

Relative size of centromeres is arbitrarily indicated by + (small) to + + + (large).
+ / + + means that all 3 size classes (+, + +, + + +) were observed

assessed from a careful examination of numerous metaphases from each individual chosen from each species. Despite the fact that we present only semiquantitative data, clear results could be delinated from our examinations in most cases. Striking centromeric heteromorphisms were encountered (Fig. 1 and Table 1): e.g. on chromosomes 4, 8, 17 and 23 in taurus cattle; on chromosomes 6 and 11 in zebu cattle; and on chromosomes 5, 6, 15 and 19 in bali cattle.

Exceptionally large centromeric blocks were observed on chromosomes 1, 2 and 15 in taurus cattle; on chromosomes 1 and 16 in zebu cattle; and on chromosomes 1, 7, 9, and 14 in bali cattle while especially small heterochromatin regions were observed on chromosomes 19 and 21 in taurus cattle; on chromosomes 10, 13 and 18 in zebu cattle; and on chromosomes 3, 8, 18 and 26 in bali cattle.

The heterochromatin pattern permits the characterization of each individual. We observed clearcut differences in the heterochromatin pattern of different individuals of each species. These intraspecies interindividual differences were in every case less pronounced than those between species.

Discussion

All our screened Bovinae possessed appreciable amounts of centromeric heterochromatin. The G-banding technique used by us proved to be easily practicable and reliable for both chromosome identification and detection of size polymorphisms in the heterochromatin regions of Bovidae. In all 3 investigated cattle species examined by G-banding, the autosomic centric regions remained weakly stained or unstained. Despite this similar staining behavior of the centromeric heterochromatin, no conclusions about biochemical resemblances may be drawn at present. Detailed molecular characterization of the satellites and other highly repeated DNA sequences is necessary for this end. At least eight different satellites have been distinguished in calf thymus DNA (Streek 1981; Singer 1982). It is presently unknown whether these different satellites are chromosomally organized as microscopically resolvable subregions of centromere C-bands such as are seen occasionally in elongated chromosomes, or whether they are arranged in a manner which would escape microscopic detection. In situ hybridization of highly repetitive DNAs will be necessary to resolve this problem.

Thus, many questions regarding knowledge about the basic biochemical nature of the bovine centromeric heterochromatin and its variants are yet open; nevertheless easily obtainable information about polymorphisms of many identified chromosomes in a

genome remains very worthwhile. It may provide valuable help, for example, in tracing certain chromosomes in controlled crossing programs. An especially important application will be the assignment of gene expression to one or the other partner homologue. This matter is normally unanswered in all claims of so-called "ribosomal RNA-expression heterozygotes" throughout domestic animals and other mammals. Furthermore, centric heterochromatin polymorphism data will provide a new impetus for the accomplishment of genetic linkage- and trait marker research in cattle breeding.

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