GENETIC CHARACTERIZATION OF
URUGUAYAN CREOLE CATTLE.
I. CYTOGENETIC CHARACTERIZATION OF A SAMPLE OF
URUGUAYAN CREOLE CATTLE

CARACTERIZACIÓN GENÉTICA DE LOS
BOVINOS CRIOLLOS DEL URUGUAY.
I. CARACTERIZACIÓN CITOGÉNÉTICA DE UNA MUESTRA DE
BOVINOS CRIOLLOS DEL URUGUAY

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Additional keywords
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SUMMARY

The high fitness of the American Creole breed cattle and degree of colours-coat variation have supported a genetic analysis to be compared to those ancestral Iberian races. To know the genetic value of Uruguayan creole breed cattle located at Southeast Uruguay, we have firstly carried out the searching of cytogenetic markers. Chromosome analysis was performed in 99 phenotypically normal Creole cattle (73 females, 26 males) among a population of 600. Peripheral blood was cultivated in a complete medium RPMI 1640. Among normal karyotypes (2n = 60, XX/XY), two relationship dams/sibs presented the chromosome formula 2n = 59/rob (1;29) confirmed it to chromosome banding RBG. C banding patterns (CBG) showed one block of constitutive heterochromatin (HC) in the proximal q-arm region of the rob(1;29). Fragil site expresion Xq 3.1 was determined in 6 p. cent of the analysed metaphases (N = 710). A Y metacentric chromosome was clearly found in the males, so the Bos indicus species was excluded.

RESUMEN

El alto grado de adaptabilidad fitness y la variación encontrada en el color del pelaje de los bovinos Criollos Americanos justifica realizar un análisis genético a efectos de ser comparados con sus razas ancestrales Ibéricas. Los estudios citogenéticos de la única reserva de bovinos Criollos del Uruguay han comenzado con la búsqueda de marcadores citogenéticos. La caracterización citogenética se realizó en 99 animales fenotípicamente normales (73 hembras, 26 machos) de una población de 600. Se cultivó sangre periférica en medio completo RPMI 1640. Entre los cariotipos normales (2n = 60,XX/XY) se encontraron dos relaciones madre/cría con la

fórmula cromosómica 2n=59/rob (1;29), confirmándose por bandeo cromosómico RBG. El modelo de bandeo C mostró un bloque de heterocromatina (HC) en la región proximal del brazo q de la rob (1;29). La expresión del sitio frágil Xq3.1 se determinó en un 6% de las metafases analizadas (N=710). Se observó un cromosoma Y metacentrico en todos los machos estudiados, excluyendo, por lo tanto la introducción de Bos indicus a esta reserva.

INTRODUCTION

Nowadays, Latin American Creole cattle reserves have been succeed to show high degree of fitness, as it has occupied diverse ecologic habitat since it has been brought to America by Spanish conquerors in the XVI century (Primo, 1992; Rabasa, 1976, 1993). Venezuelan Creole bulls is the only genetic research that concerned to cytogenetic analysis, as a low fertility rate was found, Robertsonian translocation was showed with an incidence of 21.6 p. cent (Muñoz et al. 1994).

Uruguayan Creole cattle has showed a diversity of colors-coat expression so, a genetic analysis should be done to compare to those ancestral Iberian races. The objective of this paper is to realize a cytogenetic characterization of the Uruguayan Creole cattle reserve where the presence of heterozygous centric fusion and an incidence of spontaneous fragile sites Xq3.1 are showed.

MATERIAL AND METHODS

Ninety-nine Uruguay creole cattle (73 females, 26 males) to the Natural Reserve of SEPAE (Servicio de Parques del Ejército) were submitted to cytogenetic analysis. Peripheral blood samples were cultured in a standard complete medium RPMI 1640 (GIBCO) supplemented with 20 p. cent fetal bovine serum (GIBCO) and phytohemagglutinin M (GIBCO). Cells were incubated for 72 h at 38°C in a Memmert bath.

Single synchronization of lymphocytes with fluorouracil (Sigma, 5 x 10^{-7} M) was applied after running 48 hours and bromodeoxyuridine (Sigma 1 x 10^{-4} M) was incorporated to the cells 6 h before harvesting. Slides were incubated with Hoechst 33258 (4 mg/l) in 0.9 NaCl during 30 min and stained with Hoechst 33258 15 min exposing them to UV light. After incubation in 2 x SSC for 1 h at 65°C the slides were washed and counterstained with Giemsa (pH 6.8) (Ronne, 1984). CBG banding (Summer, 1972) were used to determine chromosomes involved to centric fusion.

RESULTS AND DISCUSSION

Chromosome alterations like to robertsonian translocations, Fra Xq3.1, have been described in cattle (Gustavsson, 1969; Elridge, 1985; Randel-Figueiredo and Iannuzzi, 1991; Llambi and Postiglioni, 1994; Bashur, 1995). As centric fusion (1/29) should be involved in the karyotype evolution of Bovidae (Wurster and Benirschke, 1968), it would be presented in those bovines not submitted to rigorous artificial selection.

Uruguayan Creole cattle is a natural reserve of 600 animals where chromosome karyotype showed the normal formula 2n= 60,XX/XY in 96 of the examined animals. But two relationships dam/sibs determined the presence of a
large submetacentric chromosome (table I).

RBG replication banding showed a clearly telomeric band in the short arm while a medium R-band was found in the long arm (figure 1b,c). According to the

![Figure 1. Chromosomes metaphases from heterozygous carriers of centric fusion translocation. a, CBG technique. b and c RBG technique. Arrows indicate R-band and C-bands. The sex chromosomes are also indicated. The bars represent 5 μ. (Metafases cromosómicas de portadores heterocigotos de translocación de fusión céntrica. a, Técnica CBG. b y c, Técnica RBG. Las flechas indican la banda R y las bandas C. Los cromosomas sexuales están igualmente indicados. Las barras representan 5 μ).]

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ISCNDAMA (1989) this centric fusion had corresponded to chromosomes 1 and 29. The CBG technique (figure 1a) revealed only one pericentromeric constitutive heterochromatic (HC) block located in the proximal region of the q-arm. The presence of this noncentric fusion in Uruguayan and Venezuelan Creole cattle could be compared to those ancestral Iberian breeds (Arruga, 1982), so centric fusion (1/29) should be considered a chromosome marker of ancient origin. Otherwise, fragile site Xq3.1 alteration was firstly located in sex chromosomes of Holstein-Friesian with reproductive problems (Llambi and Postiglioni, 1994). Noe, we are showing a frequency of 6 p. cent besides a heterozygous condition expression (table I). Lately, we should not forget the rate of inbreeding resulting from the small population size (N=600) that could be a cause of these chromosome alterations expression.

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