COMPARATIVE ANALYSIS OF GENETIC MAPS OF *Bos taurus* L. AND *Capra hircus* L.

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S u m m a r y

With the use of data base of genetic maps of animals and developed software the authors have made comparative analysis of gene orders in two representatives of *Bovidae* family, *Bos taurus* L. and *Capra hircus* L. It was shown the high similarity of gene orders of homeological chromosomes in compared species, with the exception of 9th and 14th chromosome pairs.

Keywords: divergence, genome, genetic maps, homology, karyotype, chromosome, chromosome maps.

Today, phylogenetic research is supported by achievements of modern biology, such as the knowledge of structure and functioning of chromosome apparatus. Cytogenetic techniques are an important tool in systematics and phylogeny of mammals (1-3). In recent decades, the study of chromosome sets is a part of applied studies (4, 5), including the works on conservation and rational use of animal gene pools (6-10). Analysis of the fine structure of chromosomes is widely used in evolutionary genetics. One of approaches in the study of homology of chromosomes and chromosomal regions in various mammalian species is the comparison of differences in their striation.

The analysis of cytogenetic similarities and karyotype evolution are described in number of scientific works (11-13). According to A.S. Grafodatsky and L.S. Bitueva (12), homeologous chromosomal regions can be identified from the nature of striation more often and exactly the less the compared karyotypes are rearranged relative to each other. With a few exceptions, homology is clearly seen in compared species within one genus or related genera. Sometimes it can be more or less reliably identified within a family.

Recent works on assessment of genomic similarity often use molecular genetic markers (14-19). However, the most accurate measure of similarity (identity) of genomes is only the fact that chromosomes or chromosomal regions contain similar nucleotide sequences arranged in the similar order, regardless of their alleles.

The comparison of genetic composition of individual chromosomes in different species was the subject of many studies (20-28), as well as phylogenetic analysis based on comparison of gene maps (29-32). The comparison of chromosomal structure revealed divergent pathways in cytogenetic evolution of sheep species (33-37). The study of gene orders of *Bos taurus* L. and *Ovis aries* L. allowed a detailed analysis of their karyotypic divergence (32). However, in all these studies the subjects were species with pronounced cytogenetic differences.

In this work the authors compared gene maps of two closely relative species – members of the family *Bovidae* with similar chromosome sets – *Bos taurus* L. and *Capra hircus* L., in order to find differences in organization of their genomes at the level of gene orders.

Technique. The study was conducted using the own databank of chromosomal location of markers in *B. taurus* L. and *C. hircus* L. that included generalized information from databases NAGRP (National Animal Genome Research Program, USA) (38) and INRA (39, 40) with the data about location of 28 282 and 708 markers, respectively. Chromosomal location of 249 these markers was known in both species. Along with it, the authors used the data of A. Eggen and R. Fries (41), J.J. Lauvergne et al. (42), J. Maurico et al. (43), and Bovine genome DataBase (44). Analysis of gene maps was performed according to the algorithms described previously (28, 29).

Cytogenetic characteristics of the compared species were studied in chromosome preparations of a 72-hour culture of peripheral lymphocytes stimulated with Concanavalin A ("Paneco", Russia) at a dose of 10 ug/ml. Culturing of the lymphocytes, preparation and staining of chromosomes were carried out by conventional methods (45) with own modifications (46).

Results of the study were documented with a digital video camera KC-583C ("Digital", Tawan) and Windows-compatible software. Image processing and karyotyping were conducted following the earlier reported method (46).

Results. Species of the family *Bovidae* show high cytogenetic variability. It is believed that initial karyotype of bovids was a set of 60 chromosomes with 29 pairs of uni-armed autosomes. The divergence of phylogenetic branches occurred 15-20 million years ago and gave rise to modern representatives of this family. According to comparison of chromosome sets of various bovids, it is accepted that evolution of karyotypes in this family occurred mainly through centric fusions (47). Changes in morphology of sex chromosomes of bovids are assumed as result of pericentric inversions.

The modern genus *Capra* is considered as karyologically closest to the ancestral bovids by monomorphic structure of chromosomes (3, 45, 48, 49). Karyotype of *C. hircus* is the most well studied in the genus (50-53). Domestic goat has a diploid set of 60 chromosomes, where 29 pairs are acrocentric autosomes. X-chromosome is a large acrocentric, while Y-chromosome is metacentric and one of the smallest in the set (Figure 1, A). Accurate identification of chromosomes except Y-chromosome is only possible with the use of differential staining. *B. taurus* is another domestic bovid the most close to *C. hircus* in number and morphology of chromosomes (Fig. 1, B).

Diploid set of the both species is 60, and the number of arms in autosomes – 58; the species have identical patterns of homologous chromosomes, except the 9th and 14th pairs (4, 5). Most of the chromosomes of *B. taurus* and *C. hircus* show relatively

uniform alternation of light and dark bands across the length. These species differ in morphological organization of female sex chromosomes: X chromosome of *B. taurus* is a large metacentric. This fact is associated with pericentric inversion (54)

Fig. 1. Karyotypes of *Capra hircus* L. (male) (A) and *Bos taurus* L. (male) (B). Giemsa stained, magnification $\times 100$.

В таблице представлены данные о соответствии генного состава хромосом *B. taurus* и *C. hircus*., в частности сведения 95 маркеров первого и 154 маркеров второго типа. Для 22 пар хромосом у анализируемых видов отмечалось полное совпадение их генного состава. В эту группу входят хромосомы 2-5-й, 9-13-й, 15-19-й, 21-25-й, 28-й, 29-й пар и половые хромосомы. В качестве примера на рисунке 2, А приведены генные карты 2-й и 5-й пар хромосом крупного рогатого скота и козы.

The table presents the composition of genes in chromosomes of *B. taurus* and *C. hircus* in respect to 95 markers of the first type and 154 markers of the second type. In these species, 22 pairs of their chromosomes have identical genetic composition: the pairs 2-5th, 9-13th, 15-19th, 21-25th, 28th, 29th, and sex chromosomes. For example, Figure 2, A shows gene maps for the 2nd and 5th pairs of chromosomes in cattle and goat.

Composition of genes in chromosomes of *Capra hircus* L. (male) and *Bos taurus* L. (male)

<i>C. hircus</i> L.		<i>B. taurus</i> L.
№ pair of chromosomes	arm	№ pairs of chromosomes and number of genes
1 st	q	1q (23: 9, 14); 16q (1: 0, 1)
2 nd	q	2q (14: 6, 8)
3 rd	q	3q (10: 2, 8)
4 th	q	4q (9: 3, 6)
5 th	q	5q (11: 4, 7)
6 th	q	6q (5: 3, 2)
7 th	q	7q (5: 3, 2)
8 th	q	8q (7: 2, 5); 11q (1: 0, 1)
9 th	q	9q (6: 1, 5)
10 th	q	10q (10: 4, 6)
11 th	q	11q (16: 5, 11)
12 th	q	12q (9: 3, 6)
13 th	q	13q (6: 3, 3)
14 th	q	9q (3: 0, 3); 14q (8: 3, 5)
15 th	q	15q (7: 3, 4)
16 th	q	16q (9: 1, 8)
17 th	q	17q (7: 2, 5)
18 th	q	18q (10: 6, 4)
19 th	q	19q (4: 1, 3)
20 th	q	1q (1: 1, 0); 9q (1: 0, 1); 20 (6: 0, 6)
21 st	q	21q (6: 2, 4)
22 nd	q	7q (1: 0, 1); 22q (7: 3, 4)
23 rd	q	23q (5: 2, 3)
24 th	q	24q (6: 0, 6)
25 th	q	25q (8: 2, 6)
26 th	q	14q (1: 0, 1); 26q (4: 1, 3)
27 th	q	17q (1: 1, 0); 26q (1: 0, 1); 27q (4: 0, 4)
28 th	q	28q (5: 0, 5)
29 th	q	29q (4: 0, 4)
X		X (5: 3, 2)
Y		Y (1: 1, 0)

N o t e . In brackets – total number of loci identified in *C. hircus* L., including, respectively, structural genes and DNA-markers.

It should be noted that for a part of genetic markers reviewed in this work and common for cattle and goat there's yet no data on exact location on chromosomes.

7 chromosomal pairs of *C. hircus* and *B. taurus* showed a partial mismatch of gene composition. The most significant differences in order of genes were found in the 14th pair (Fig., B).

Fig. 2. Comparison of gene maps for the 2nd and 5th pairs of chromosomes of *Capra hircus* L. (CHI2, CHI5) and *Bos taurus* L. (BTA2, BTA5) (A); 9th and 14th pairs of *C. hircus* (CHI9, CHI14) and *B. taurus* (BTA9, BTA14) (B); 1st pair of *C. hircus* (CHI1) and *B. taurus* (BTA1) (C). In square – symbols of genes with indefinite location. Gene C9 and marker INRA36 are located on the 20th chromosome of goat.

On the 14th chromosome of *C. hircus* there were located 11 genetic markers peculiar to cattle chromosomes BTA14 (8 markers) and BTA9 (3 markers). On the 9th chromosome of *B. taurus* there were located 10 genetic markers whose localization is known in goat on CHI9 (9 markers), HI14 (3 markers), and CHI20 (1 marker). Unfortunately, exact localization of genetic markers on BTA9 is indefinite, which doesn't allow revealing the nature of changes in genetic composition of these chromosomes. Another obstacle is the absence of data about reaper genes of BTA14 localized outside CHI14.

Goat chromosome of the 1st pair was similar to BTA1 in composition of genes. But along with markers located on CHI1, BTA1 contained the gene for the 9th component of complement (C9) that in goat is located on the 20th pair (Fig. 2, B).

In cattle, the 8th and 22nd pairs of chromosomes corresponded to CHI8 and CHI22 for the most of markers. But on CHI8 there was also found DNA-marker HEL13 known in cattle chromosome BTA11, and on CHI22 – a microsatellite marker BM7160 peculiar to BTA7.

Comparison of the 26th chromosomal pair of these species revealed 4 similar markers on CHI26 and BTA26. In addition, on BTA26 there was the marker CSSM43 associated with CHI27, and on CHI26 – the marker BM4305 also found on BTA14.

On the 20th pair of goat chromosomes it was found 8 markers, 6 of which were present on BTA20, and the markers C9 and INRA36 located on, respectively, BTA1 and BTA9. The 27th pair of goat chromosomes contained 6 markers, 4 of which were associated with BTA27 in *B. taurus*, as well as the gene for coagulation factor 11-F11 and microsatellite CSSM43 – with chromosomes of the 17th and 26th pairs, respectively.

Thus, the compared bovid species showed high similarity of genetic composition. However, evolutionary divergence of their

karyotypes was associated with exchange of genetic material between non-homologous chromosomes. All peculiarities of this process not revealed by classical cytogenetic analysis necessitate the analysis of genomes at the level of gene maps even in closely related species.

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