

Abstract

The order *Cetartiodactyla* is currently one of the largest groups of mammals on Earth that includes 10 families of terrestrial and 12 families of aquatic mammals. The main hallmark of all today's ungulates is the limb axis passing between the third and fourth finger. The order *Cetartiodactyla* is a cytogenetically heterogeneous group of organisms, comprising families with slow karyotype evolution (*Cetacea* and *Hippopotamidae*) and families (e.g. *Bovidae*) whose representatives have distinct karyotypes ($2n = 30$ to 60). Comparative genomics, based on the analysis of chromosomes, gene mapping and DNA sequencing, greatly contributes to the clarification of evolutionary relationships between animals. One of the basic and abundantly used methods is ZOO-FISH, which is based on cross-hybridization of specific probes from one species on chromosomes of another species. Based on the knowledge of evolutionary chromosomal rearrangements, the process of organism speciation can be traced.

One of the aims of this study were comparative cytogenetics of selected mammals from the order *Cetartiodactyla*. For this purpose, whole chromosome and BAC FISH probes, prepared from pig and cow DNA, were used. Chromosomal DNA was obtained by flow cytometry of chromosomes or by laser microdissection. Using ZOO-FISH, comparative karyotype between pygmy hippo and common hippo was established for the first time. These karyotypes are almost identical. Detailed structure of the pygmy hippo X chromosome was defined and is very similar to the structure of the giraffe X chromosome. Within the family *Bovidae*, there is a considerable variability in the diploid number of chromosomes ($2n = 30$ to 60), but the number of autosomal arms remains almost constant and genomes of various species are highly homologous. It is believed that the ancestral karyotype, preserved in the genome of cows and goats, had a total of 58 acrocentric autosomes, an acrocentric X and a small submetacentric Y chromosome. The great variability in chromosome number and karyotype diversity in *Bovidae* is a very convenient feature for the study of meiotic division and recombination interference.

Another aim of this study was the comparison of recombination frequencies and their distribution between different species of *Bovidae*. We investigated if centric fusions and the process of domestication cause changes in recombination rates in the researched species. With the use of immunofluorescence detection of meiotic proteins (MLH1, SCP3) and subsequent FISH, we analysed the frequency and distribution of crossing-overs on

meiotic chromosomes in pachytene spermatocytes. A total of 112 individuals from 28 different *Bovidae* species were examined. In all investigated animals, significant individual and interspecies variability was found in the length of synaptonemal complexes and the number of recombination events per cell. A decrease in the number and a change in the distribution of crossing-overs on sheep metacentric chromosomes was demonstrated compared to their orthologues in cows and goats. These differences are probably caused by the metacentric state of chromosomes and by centromeric interference acting over the centromere.