

## Comparison of the Lowland and Lowland-Caucasian lines of the European bison (*Bison bonasus*)

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**Aim of the study:** The European Bison (*Bison bonasus* L.) is the only wild species of the subfamily Bovinae which has survived to the present day in Europe. The last wild populations of the species were destroyed at the beginning of the 20th century. Currently, Belovezian Forest is the habitat of the largest population of the European Bison. Geographically, the population is divided into 2 parts – Belarusian (Lowland-Caucasian line) and Polish (Lowland line). Did the different principles of breeding affect the overall survival of animals, the effective numbers and the level of inbreeding? The purpose of this study is to compare the genetic markers of two populations of the Bison.

**Material and Methods:** We studied polymorphism of nine microsatellite loci of both studied populations of bison (30 individuals of Belarusian and 17 Polish individuals). Based on the allele frequencies of microsatellite loci we calculated the main indices of genetic variability for each population -  $F_{is}$ ,  $H_e$ ,  $N_e$ . Unique allelic variants were identified in the Belarusian population of bison. We also analyzed the polymorphism of the second exon of the DRB3 gene and the second exon of the DQB gene of the Major Histocompatibility Complex (MHC). Four allele variants of the DRB3 MHC gene are described for the European bison. In the Belarusian population, three ones were found: Bibo-0101, Bibo-0201, Bibo-0301. The allele variant of Bibo-0401 is rare for the Polish population. Its frequency of occurrence is 2%. It was not identified in the samples of analyzed Belarusian animals. In the studied fragment of the DQB gene of MHC there were 5 allelic variants - 2 found in Belarusian, 2 - in Polish and 1 in the both populations.

**Results:** Variations of the nucleotide sequences of the studied allelic variants of the MHC genes are in the 2nd exon of the genes. This fragment encodes the peptide sequence of the so-called "antigen-binding site" - the sites where antigens of intracellular or extracellular pathogens are bound. It is believed that a high difference in the available allelic variants of genes is maintained by natural selection. Individuals with a large allelic diversity of MHC genes have a selective advantage, as they can form an immune response against a wider range of antigens. The obtained results show that, despite the uniform origin, the high similarity of the two populations of the European bison studied, the different principles of breeding led to obvious differences in the genetic structure. The presence of unique alleles of microsatellite loci can indicate the hybrid origin of the Belarusian livestock - a mixture of the Lowland and the Caucasian bison lines. Also, Belarusian individuals show the worst indicators of effective size and inbreeding levels than Polish ones. The presence in the Polish population of unique allelic variants of the DQB gene (Bibo-DQB-Pol2 and Bibo-DQB-Pol3) makes it a valuable source of genetic diversity for the Belarusian population.

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