

POTENTIAL OF BOVINE SNP50 BEADCHIP FOR ANALYSIS OF GENETIC DIVERSITY OF WILD ANIMALS

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Phylogenetic analysis shows that for cows (*Bos taurus*), bison (*Bison bonasus*), moose (*Alces alces*), elk (*Cervus elaphus nelson*), sika deer (*Cervus nippon*) and fallow deer (*Dama dama*) there is a common ancestor. Bovine genome decoded in 2009 (Zimin et al.). The genomes of these wild animals have not sequenced or assembled. However, can transfer genetic markers (SNP, STR) from cows on wild animals. This is based on the principle of cross-amplification. In several researches has been shown that STR loci are mostly well tolerated by wild animals. But the allelic diversity is usually less. In relation to SNP markers research a little. Most of these researches made use of the Bovine SNP50 Beadchip (Illumina). Pertoldi et al. (2010) investigated the polymorphism of SNP markers from the Bovine SNP50 Beadchip on *Bison bonasus*. The total number of analyzed markers was 52 978, 97,6% of them were amplified, and only 1,8% were polymorphic. Decker et al. (2009) investigated the polymorphism of SNP markers from the Bovine SNP50 Beadchip on *Alces alces*, *Cervus elaphus nelson*, *Cervus nippon*, *Dama dama*. The total number of analyzed markers was 40 843, 62,0-66,1% of them were amplified, and only 0,1-0,3% were polymorphic. These studies show that evaluation of genetic diversity among wild animals is not enough to use only those SNP, which are part of the commercial panels. For these tasks the analysis of the genomes of wild animals. The transfer they in this case is better to produce from wild animals to wild animals.