SNP LOCUS FOR DIFFERENTIATION OF SOME WILD ANIMALS *(BISON BONASUS, RANGIFER TARANDUS, ALCES ALCES, CERVUS NIPPON, DAMA DAMA, CERVUS CANADENSIS)* FROM COW *(BOS TAURUS)*

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Holstein breed of cows is predominant in Belarus. It accounts for over 95% of all animals. A genetic difference of cows *(Bos taurus)* from wild animals *(Rangifer tarandus, Alces alces, Cervus nippon, Dama dama, Cervus canadensis)* shown in the study of Decker at al. (2009). In most cases, the sequenced samples include those that were genotyped with the BovineSNP50 BeadChip (Illumina). The aim of this research is to test the ability of the solution to this problem using the genomes of cows breed Holstein, *Cervus canadensis* and *Bison bonasus.* Analysis was performed using SRA Nucleotide BLAST algorithm and program BioEdit v.7.2.5. In analysis included SNP rs17871403 (Chr.18:48812014, Gene – ECH1, intron variant); the number of reads for whole genome *Bos taurus* – 10 (BioSample – SAMN02225734, SAMN02225735, SAMN02225736, SAMN02225737, SAMN02225738, SAMN02225739, SAMN02225740, SAMN02225741, SAMN02225742, SAMN02225743; https://www.ncbi.nlm.nih.gov/biosample), for whole genome *Cervus canadensis* – 8 (SAMN05859686, SAMN05859687, SAMN05859688, SAMN05859689, SAMN05859690, SAMN05859691, SAMN05859692, SAMN05859693), for whole genome *Bison bonasus* – 7 (SAMN05950802, SAMN05950803, SAMN05950804, SAMN05950805, SAMN05950806, SAMN05950807, SAMN05950808). The frequency of the allele T (rs17871403) for *Bos taurus* (Holstein breed) is 60,0%, the frequency of the allele A (rs17871403) for *Cervus canadensis* – 100%, the frequency of the allele G (rs17871403) for *Bison bonasus* – 100%. The analysis only one SNP is able with 100% efficiency to differentiate of wild animal *(Rangifer tarandus, Alces alces, Cervus nippon, Dama dama, Cervus canadensis)* from cows. For 100% accuracy of the differentiation of the cow from bison is necessary to search for additional SNP.