

ABSTRACT

The broader purpose of the work is to find and interpret polymorphism in the genes of natural immunity of cattle to be used to improve disease resistance. The NGS method on the PacBio platform was applied for the resequencing of the gene for the key receptor of innate immunity TLR2 and two genes coding for the components of the downstream transcriptional factor NF- κ B. In the population of 149 bulls of the Czech Simmental breed, 22 polymorphisms were found in the gene *NFKB1* (5 new), while in the *NFKB2* gene 13 SNP were found (10 new). 21 SNP were found in the *TLR2* gene (3 new). Of the 56 found polymorphisms, 6 SNPs were nonsynonymous. One SNP leads to a change R474G in the *NFKB1* product and five to changes E63D, R152Q, I211V, R563H and H665Q in the protein TLR2. Knowledge of the haplotypes facilitated the development of individual genotyping reactions. In *TLR2*, a high number of haplotypes was detected, both from the PacBio reads and the statistical reconstruction. In addition, two clusters of haplotypes were distinguished in *TLR2*, possibly due to diversifying selection or introgression. The knowledge of genetic diversity in the population allows for the planned association studies with health data. Localization in functional domains allow to define the change with the greatest effect, in particular H665Q in the TLR2 TIR domain. The knowledge of diversity also allows to use the data on the value of individual variants from other studies.