ABSTRACT

The general aim of the work was to document the variation in the genes of the Toll signalling pathway in the innate immune system of cattle. This included the analysis of the potential of this variability in breeding for health traits. The population of Czech Red Pied (Czech Simmental, CRP) cattle has been chosen for this task as a model population. The genomic diversity of this breed has been characterised with whole-genome sequencing in a representative sample of bulls. The HiSeq technology was used at this step. Subsequently, the diversity in the set of genes of interest has been validated by hybrid sequencing with a different technology PacBio. The set of genes of interest included the genes for antibacterial Toll-like receptors, namely *TLR1*, *TLR2*, *TLR4*, *TLR5* and *TLR6*. The receptor genes were completed with genes for two key members of the Toll signalling pathway, *MYD88*, *NFKP1* and *NFKB2*. Occurence of unique forms with predicted effects was noted in the TLR genes, *MYD88* and *NFKB1*. Upon in silico characterization of a functional impact of the found variants, genotyping methods for the determination of single-nucleotide polymorphisms (SNP) in individual animals have been developed. The possibility of individual genotyping allowed to obtain population characteristics and performing association studies, including the association study of the variants of *TLR4* and *TLR5* with impact on the economic, udder health and reproductive traits in the CRP cattle population. The original findings suggesting the involvement of TLR variants in the reproductive trait formation were explainable in light of the already known effects of TLR4 activity in mice and human. The individual genotyping data also allowed for the reconstruction of the haplotype structure in the *TLR* genes for the given cattle population. Surprising bimodal distribution of haplotype clusters in the *TLR2*, *TLR5*, *TLR6* and partially *TLR4* genes indicates a long-term factor of balancing selection. Again, a parallel for this phenomenon can be found in the traditional models for the *TLR* population genetics, bank vole and human.