Possible ways for manipulating the gene expression in Ixodes ricinus ticks

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Ticks *Ixodes ricinus* are blood-feeding parasites that can transmit various viruses, bacteria, protozoa, and, thus, are vectors of various diseases, such as tick-borne encephalitis, Lyme disease, anaplasmosis, and others. Extensive knowledge of the genome and transcriptome of *Ixodes* ticks has opened up the possibility of studying these ticks at the level of molecular biology. Therefore, in our work, we aimed to find ways to manipulate the expression of the *I. ricinus* genes. One of them may be epigenetic regulation, in particular, DNA methylation. We identified DNA methyltransferases in the *I. ricinus* transcriptome, namely DNA methyltransferase 1 (DNMT1), DNMT3, and DNA adenine methyltransferase (DAMT) (Previously published in: Kotsarenko K et al. (2020) Ticks Tick Borne Dis 11, doi: 10.1016/j.ttbdis.2019.101348). We found the differences in the expression level and DNA methylation at the different life stages: egg, larvae, nymph, and an adult female. These results suggest that DNA methylation is essential for the physiology and transstadial development of tick. Tick cell lines might serve as a model system of tick *I. ricinus* for studying the genome manipulation. Thus, we analyzed the highly-passaged IRE/CTVM19 and IRE/CTVM20 cell lines (provided by Tick Cell Biobank) and found that, despite some changes in the karyotype, they still retain the similarity of the 16S rRNA sequence to the parental tick. We have also optimized the transfection procedure for these tick cell lines, and they successfully expressed some reporter genes. Thus, our findings opened up the possibility of editing the gene expression in *I. ricinus* cells using epigenetic regulation or CRISPR/Cas9 technology, as well as to obtain recombinant proteins in tick cell lines.