

Transcriptome analysis of liver in Polish Holstein-Friesian cows during ketosis using AMPLI-seq technique

The aim of this research is to expand current knowledge on the liver transcriptome of Polish Holstein-Friesian dairy cows. This research will focus particularly on the hepatic expression variations of the genes encoding enzymes involved in the maintenance of oxidative balance as well as recently identified candidate genes for ketosis by investigating the healthy Polish HF cows and those affected with ketosis.

Metabolic diseases and oxidative stress are constantly current threats to the health and welfare of dairy cows as well as the profitability of dairy farms and dairy industry. The breeding selection and the increasing intensification of milk production made the high-yielding dairy cow an animal with a huge metabolic burden and susceptibility to metabolic diseases such as ketosis. High-yielding animals due to the very high rate of number of metabolic processes are also more susceptible to oxidative balance disturbances and prone to oxidative stress. Both metabolic diseases and negative effects of oxidative stress contribute to shortening the life of animals or the need of culling them from the herd, and thus generate enormous economic losses in the dairy industry and decrease in animal welfare.

Implementation of the planned research will give answers to the following questions: 1) what is the physiological state of hepatic transcriptome of Polish Holstein-Friesian? 2) how does hepatic transcriptome of Polish Holstein-Friesian change during ketosis? 3) does ketosis significantly affect the gene expression variations of the GPx and SOD gene families involved in the maintenance of oxidative balance, as well as the gene expression variations of the recently identified candidate genes? The answers to the above-mentioned questions will allow to describe physiological state of liver transcriptome of Polish Holstein-Friesian cows and establish the relationship between metabolic diseases and susceptibility to oxidative stress, and other physiological metabolic functions. The results of this study will supplement the current knowledge on the *etiopathogenesis* of metabolic diseases and oxidative stress, and allow better understanding of interactions between those disorders. They will also come to the aid of determination of the patient's chances of developing oxidative stress and other physiological state and taking preventative measures, restoring production abilities, and thus help to reduce economic losses and increase the animal welfare and profitability of milk production.

Holstein-Friesian cows have been selected as experimental animals and they will be divided into two groups: clinically healthy animals and animals diagnosed with ketosis. The following tests will be carried out as part of this experiment: morphology and biochemistry of blood, ampli-seq targeted re-sequencing of liver transcriptome, bioinformatics analysis of liver transcriptome and analysis of gene expression levels using RT-PCR. Comparison of the results obtained in both groups will allow to describe the transcriptome of healthy cattle and affected with ketosis, determine the relationship between the occurrence of metabolic diseases and the susceptibility to oxidative stress and other physiological state.