

## **POPULAR SCIENCE PROJECT SUMMARY**

The pituitary is one of the most important endocrine glands in the mammalian organisms which maintains homeostasis and controls the function of other glands, including male and female gonads, and is, therefore, often described as ‘the master gland’. It can be stated that the hormonal milieu affects the expression profile of the pituitary gene and the course of alternative transcription regulation pathways. The secretory activity of the pituitary is in largely dependent on the phase of the oestrous cycle and the stage of pregnancy. The proposed study will verify the hypothesis that gene expression profiles and alternative transcription regulation pathways differ in the anterior pituitary of gilts in the luteal phase of the oestrous cycle and in early pregnancy period.

Gene expression and long non-coding RNA profiles will be examined, and the presence of correlations between them will be analysed. Moreover, alternative transcription control pathways, such as alternative splicing events and RNA editing sites, which can significantly modify the gene expression profiles will be detected.

The research will involve modern molecular biology methods, such as the next generation sequencing (NGS). Bioinformatics software and widely available biological databases will be used to analyse the data pertaining to the two selected physiological periods. The obtained results will be validated by quantitative reverse transcription PCR and the DNA sequencing with capillary array electrophoresis.

The project will aim to generate basic knowledge regarding the regulation of reproduction processes in the domestic pig as a model organism. Attempts will also be made to find previously unknown forms of transcription resulting from alternative splicing of transcripts and new RNA editing sites. The result will broaden our knowledge of the processes that accompany post-transcriptional modifications.

The existing research in this area is very limited. Most studies have focused on transcriptomic changes in the organs whose contribution to reproductive success is evident (the uterus, ovary and oviduct). However, the regulation of transcriptome processes taking place in the pituitary has never been explored.

The obtained data will expand our understanding of the influence of differences in the hormonal milieu related to the oestrous cycle and early stages of pregnancy on transcriptome processes in the anterior pituitary. Moreover, the results of the project could be a starting point for similar research into transcriptomic profiles of endocrine glands on other mammals, including other farm animals. Research findings will also contribute to the knowledge of human reproductive physiology.