The corpus luteum (CL) is a gland present in the ovary of mature females during the estrous cycle and pregnancy. The primary hormone secreted by this structure is progesterone (P_4) which is necessary for a proper course of the estrous cycle, the embryo development, its implantation and maintenance of pregnancy. Besides P_4, the CL produces 17β-estradiol (E_2) and prostaglandins (PG) E_2 and $F_{2\alpha}$, involved in the CL formation and degradation respectively.

Our earlier studies suggested a relationship between the secretory function of the corpus luteum and the peroxisome proliferator-activated receptors. They act as transcription factors and they can be activated by both endogenous and exogenous substances. All PPAR isoforms (-α, -β and -γ) have been identified in the ovary of many species including the rat, mouse, pig, sheep, cow and human. Available results indicate that PPARs participate in the regulation of ovarian processes such as steroidogenesis, tissue remodeling, formation of blood vessels and lipid metabolism. There is evidence indicating that the expression of PPARγ in the bovine corpus luteum is variable and depends on the phase of the estrous cycle. In addition, our results have shown the involvement of PPARγ in the regulation of P_4 and PGE_2 and $PGF_2\alpha$ release by the porcine corpus luteum. The participation of PPARγ in the synthesis of enzymes involved in the production of steroids has been also suggested.

Taking into account the above observations, a research hypothesis has been formulated: PPARγ regulates various metabolic pathways in the porcine corpus luteum depending on the physiological status of animals. To verify the hypothesis, the studies were planned to determine the impact of PPARγ ligands (synthetic agonist and antagonist) on the transcriptome and proteome profile of the porcine corpus luteum during the luteal phase of the estrous cycle (days 10-12 and 14-16 represent respectively, mid- and late-luteal phase of the estrous cycle). The research will be carried out *in vitro* on the slices of the porcine corpus luteum. It should be emphasized that the pig is a good experimental model for testing various physiological processes due to the high similarity with the human body in terms of many anatomical features and the course of various physiological processes. For ethical reasons, it is often not possible to conduct experiments on human and in such circumstances, the use of the pig model is a valid and good choice.

The impact of PPAR ligands on the transcriptome and proteome profile of the porcine corpus luteum was not the subject of scientists' interests so far. Planned studies are cognitive and using the RNA Seq (NGS) sequencing method for the analysis of the transcriptome and two-dimensional electrophoresis/mass spectrometry for the proteome analysis will provide valuable information on: 1) gene and proteins expression associated with PPARγ in the corpus luteum and 2) dependent on physiological status changes in gene and proteins expression modulated by PPARγ ligands. In addition, the applied research techniques will be useful to identify new, undescribed yet, PPARγ-dependent factors present in the porcine corpus luteum.