<u>Streszczenie rozprawy doktorskiej pt.</u> "Analiza profilu ekspresji wybranych genów regulujących procesy wzrostu, różnicowania i apoptozy w komórkach ziarnistych jajnika świni podczas ich krótkoterminowej pierwotnej hodowli *in vitro*".

<u>Summary of the dissertation entitled:</u> "Expression profile analysis of selected genes regulating growth, differentiation and apoptosis processes in porcine ovarian granulosa cells during their short-term primary *in vitro* culture".

Granulosa cells, forming the ovarian follicle, are closely involved in the folliculogenesis and oogenesis processes. By interacting with the oocyte and other ovarian follicle cells, they are essential for the physiology of the ovary and the entire reproductive system. The processes taking place in the female gonad are generally well known, but their molecular background requires more detailed research. The multiple interactions between ovarian cells make these processes highly sophisticated and dependent on a specific intercellular "dialogue". In recent years, it has been discovered that granulosa cells show stem-like potential and can differentiate towards other cell lineages. This knowledge presents new possibilities of using these cells in veterinary, as well as in human medicine. A thorough analysis of the regulation mechanisms of these processes is necessary for further stages of research. Furthermore, the data obtained may complement the basic knowledge of the processes taking place in the ovary. In this paper, expression profile analysis of selected genes regulating growth, differentiation, and apoptotic processes in porcine granulosa cells during their short-term primary *in vitro* culture was performed. Thanks to the use of expressive microarrays, transcripts of cells from particular time intervals (0 h, 48 h, 96 h and 144 h) were analyzed, and genes with the highest differential expression levels were selected. Then, we have further extracted genes coming from ontological groups related to cell development, differentiation and morphogenesis, as well as genes participating in growth, aging and apoptosis, and cell cycle regulation. The published results of the first stage of the study showed that, out of the 20 analyzed genes, as many as 19 belong to the "*cell differentiation*" ontological group, expression of which in granulosa cells may confirm their ability to differentiate into other cell types. Additionally, genes with no apparent role in folliculogenesis have also been identified, although previous studies indicate their expression in porcine granulosa cells. Therefore, these genes may be candidates for genetic markers of critical processes occurring within granulosa cells under *in vitro* culture conditions. It should be noted that the presented results also indicate several genes that have shown a connection with apoptosis and follicular atresia, and the significant expression of genes from ontological groups responsible for programmed cell death confirms their influence on the

course of these processes. The last stage of the study was devoted to the analysis of the level of expression of genes from ontological groups associated with cell cycle regulation.

To conclude, the obtained data referring to the molecular background of the processes mentioned above may complement the existing knowledge about the regulatory mechanisms and signal pathways within the ovarian follicle. Additionally, recently discovered stem-like properties of granulosa cells, partially confirmed in this paper, may indicate new research directions and possibilities of their use in modern regenerative medicine.