The relationship between metabolic status and reproductive success in animal has been known for a long time. One may assume the existence of hormonal links, creating a network controlling both, the metabolic and reproductive processes. Based on sparse literature data we hypothesize, that obestatin also belongs to the group of such hormones. This 23-amino acid peptide is a product of obestatin and ghrelin precursor gene (*GHRL*). The protein product of the *GHRL* gene is preproghrelin, which is conversed into proghrelin, and then, as a result of post-translational modifications, into ghrelin (acetylation) and/or obestatin (amidation). Obestatin secretion occurs mainly in the stomach and intestines, but its presence and pleiotropic properties have been reported in various tissues, among others: hypothalamus, pituitary gland, salivary glands, liver, pancreas, and reproductive system organs and adipocytes. It is suggested that this hormone may influence food intake, stomach and intestinal function in a manner opposite to ghrelin. Obestatin is involved in the regulation of insulin metabolism. The hormone stimulates the proliferation and differentiation of preadipocytes and may inhibit their apoptosis. More and more reports refer to its effect on the reproductive system of both, females (impact on oocyte maturation, secretion of tropic and steroid hormones and apoptosis of granulosa cells), as well as males (presence in Leydig cells, vas deferens and testes). It is suggested that obestatin has a regulatory function in the reproductive system, but its role has not yet been thoroughly understood and described. One of the reasons may be its chimeric nature, depending on experimental conditions.

As a part of this project, we plan to examine the expression of obestatin in the porcine uterus during the oestrous cycle and early pregnancy as well as in conceptuses and trophoblasts. Another aim of the presented project is to determine the impact of the obestatin on the secretion of steroid hormones by the porcine endometrium expression of steroidogenic enzymes as well as proteins involved in the process of steroidogenesis in this tissue. We are particularly interested in analyzing the effect of obestatin on the proteome and transcriptome of porcine endometrial luminal epithelial cell.

The obtained results will allow to determine the expression of obestatin in the porcine uterus and its dependence on the physiological status of the animal (oestrous cycle/pregnancy). The results will also help to explain the impact of the adipokine on the process of steroidogenesis in the porcine endometrium. The use of advanced high-throughput methods (NGS, LC-MS) will permit to detect all genes and proteins (also new, not yet associated with the impact of obestatin), whose expression changes under the influence of this hormone, and as a result, to describe new, unknown so far functions of obestatin in the porcine uterus. The obtained results will provide information about the role of obestatin in the porcine uterine physiology. In addition to their purely scientific value, the obtained results may allow, in the future, for the development of effective methods of intervention in these processes in farm animals.