

XX century went down in history as a period of huge progress in medicine. On the one hand, the pathomechanisms of number diseases have been identified, what on the other hand allowed to introduce a new targeted therapies. Despite such a visible progress, the pathogenesis and cure for type 2 diabetes remain a challenge of modern medicine for the future. Especially, that the number of diabetes is constantly increasing and the cost of diabetes itself and its complications treatment represents a huge economic challenge. It is known that type 2 diabetes is an inherited disease associated with disturbances in insulin secretion and / or action. The occurrence of type 2 diabetes promotes obesity, which is the cause of insulin resistance. Despite a variety of research methods are available, the mechanism responsible for type 2 diabetes development has not been fully explained. It appears that the development of diabetes is affected by both genetic and environmental factors. Some of these factors, such as diet or exercise can be controlled, while most of them (age, sex, genetic factors) are unmodified. Recently, a special interest of scientists enjoys the study of epigenetic changes, which are influenced by genetic and environmental factors. Epigenetic modifications has been found to control gene expression at various stages of developmental processes. Epigenetic modifications cover methylation of CpG islands, post-translational modifications of histones and microRNA. Numerous reports suggest that epigenetic changes may also be involved in the pathogenesis of many diseases. Therefore, the aim of this study is to determine the effect of hyperglycemia on epigenetic changes in p53 gene and its effectors in visceral adipose tissue. The p53 protein is a transcription factor that plays an important role in the control of many processes, including these related to the pathogenesis of diabetes, such as inflammation, apoptosis, metabolism and cell cycle. The study will be conducted on adipocytes isolated from visceral adipose tissue taken from patients with type 2 diabetes and those without diabetes, and on the human visceral adipocyte (undifferentiated and mature) grown in normo- and hyperglycaemia (in vitro model). The methylation pattern of promoter regions will be performed by MS-PCR. The analysis of the methylation/ acetylation profile of promoter regions ('promoter flanks', -3000 bp / + 1000 bp) of key genes will be performed using the chromatin immunoprecipitation (ChIP). The analysis of the expression of selected miRNA, p53 and its effectors at the mRNA level will be performed using real-time PCR, and at the protein level using ELISA or Western blotting.