Introduction and aims: Deep hypothermia is a medical method used in a variety of cardiological operations. Adipose tissue is one of the main endocrine organs and therefore its endocrine function significantly influences the state of a patient. The aim of this study was to explore the influence of deep hypothermia on the expression of selected proteins in adipose tissue, which has yet to be described in scientific literature.

Material and methods: Samples of subcutaneous and visceral fat were taken from 10 patients, who underwent planned surgery for pulmonary hypertension. The samples were taken at the beginning and the end of hypothermia, and at the end of the operation, respctively. Real-time PCR method was used to determine relative gene expression of selected adipocytokines (BCL-2, GLUT1, GPX1, HIF1- $\Box$, IL-6, IRS1, MCP1, MIF, MT3, TNF-$\Box$) from total fat and isolated adipocytes.

Results: Gene expression of GLUT1 (total subcutaneous fat), HIF1-$\Box$ (total subcutaneous and visceral fat) and IL-6 a MCP-1 (in all tissues) at the end of the operation was significantly higher compared to the gene expression at the beginning and end of hypothermia. Gene expression of TNF-$\Box$ in total subcutaneous fat increased significantly at the end of the operation compared to the beginning of hypothermia. Gene expressions of MIF, BCL-2, MT3, GPX1 and IRS1 did not differ between the samples. No differences between relative expressions of respective adipocytokines were found between subcutaneous and visceral adipose tissue depots.

Conclusion: Our results show that deep hypothermia suppresses the development of inflamatory response and consequences of anoxic period during surgery.