Abstract

Regulatory T cells (Treg) play a key role in maintaining the immune tolerance. They suppress development of autoimmune diseases and contribute to maintaining the homeostasis of the immune system. Expansion and excessive ability of regulatory T cells to suppress the immune response is increasingly observed also at many types of cancer. Due to the active inhibition of the antitumor immune response Treg contribute to tumor progression. Specific phenotype based detection and analysis of Treg functional properties may contribute to the successful monitoring of Treg accounts and to the effective cancer immunotherapy itself.

Tumor cells express high amounts of so-called tumor antigens, which may play a key role in the antitumor immune response. Expression level of the tumor antigens gives the evidence about relevancy of each antigen in the specific immune response and efficiency of cancer immunotherapy. These data are obviously important to be obtained from the tumor cell lines as well as primary tumor cells.

In the first part of the thesis I was focusing on the quantitative analysis of regulatory T cells in tumor tissue and peripheral blood of patients with ovarian cancer. For this purpose I used the newly introduced methyl-sensitive quantitative PCR (MS-qPCR) method and compare the data with the widely used flow cytometry approach. I found significantly higher level of regulatory T cells in the tumor tissue if compared with the level of these cells in periphery. The ratio of regulatory T cells in peripheral blood of patients and healthy donors was almost identical. Moreover, frequency of regulatory T cells was positively correlating with the highly activated stage of these cells in periphery.

In the second part of the study I measured the expression of selected tumor antigens. Expression profiles were obtained for the ovarian cancer cell lines and also for cells isolated from the tumor tissue of selected ovarian cancer patients. I detected the significant difference of expression in case of five of the group of fifteen tumor antigens investigated in total. There was no difference of the antigens expression in case of the different stages of the disease. Therefore I can conclude that antigen expression is not affected during the course of ovarian cancer. In addition I observed large variability among tumor antigens expressed on patient's primary tumor cells and cancer cell lines OV-90 and SK-OV-3 and also even among the cell lines themselves.