Summary

Current research of treatment of oncological diseases is focused on the identification of changes that occur in the process of carcinogenesis and on the search for therapeutics that would make it possible to eliminate the manifestation of these changes. Early diagnosis, estimating prognosis, monitoring of the course of the disease and prediction of the effect of treatment are increasingly associated with the determination of appropriate biomarkers. The assessment of predictive biomarkers should become an integral part of treatment decisions and, as a result, help patients to prolong life and improve quality of life.

The aim of my thesis was to find prognostic and predictive biomarkers for more effective treatment of cancer patients. In cooperation with a number of clinical departments of the University Hospital in Pilsen, I focused on the research of these biomarkers at the Department of Biology, especially in non-small cell lung cancer, endometrial cancer, colorectal cancer, liver metastases of colorectal cancer, clear cell renal cell carcinoma and sarcomas.

We focused on the research of molecules that are involved in the process of carcinogenesis and whose levels in body fluids or directly in tumor tissue would be able to predict further disease development or therapeutic response. Using molecular biological methods, we detected molecules at the level of expression of RNA, protein or circulating tumor DNA (ctDNA).

We identified miRNA molecules with prognostic significance, both determined in formalin-fixed tissue samples and in blood plasma. We found the benefit of combining classical markers with miRNA molecules for estimation of prognosis. Some of our results support the so-called ceRNA hypothesis. We proposed how to use the OSNA method in the absence of the sentinel node concept in patients with NSCLC. We used the ddPCR method to show the prognostic significance of ctDNA in patients with colorectal cancer liver metastases. We found in certain cases, it may be more appropriate to determine the presence of a KRAS mutation based on plasma results instead of tissue sample results, if tissue samples are not available.

I present the results in the form of annotated published articles. The connection between each article is the purpose of the investigated markers and the methodological approach.