Identification of the metabolomic and proteomic molecular components associated with neoplastic disease by mass spectrometry techniques

Despite the progress made in oncological diagnostics, it is not always possible to properly predict the course of the disease, and therefore to undertake appropriate treatment. For this reason, molecular prognostic factors are beginning to play an increasingly important role as a prognostic supplement filling the gap left by imprecise prognostic clinical factors. The search for new potential cancer biomarkers, including proteins, metabolites, and lipids, is increasingly carried out with the use of modern multi-omics tools. In recent years, there has also been increased interest in the possibility of using exosomes as a source of cancer biomarkers.

The main goal of my research was the identification of the metabolomic and proteomic components specific to the studied neoplasms with the use of mass spectrometry (MS) techniques. I have carried out this research as part of two projects. The first was focused on searching for metabolites and proteins specific for particular types of thyroid cancer in formalin-fixed and paraffin-embedded (FFPE) tissues. The developed methodology for conducting proteomic and metabolomic research with the use of retrospective clinical material, enabled the identification of compounds present in the FFPE tissues of thyroid carcinomas, differing in the histological type in relation to benign neoplastic lesions and healthy tissue. Thus, I showed that profiling proteins and metabolites by mass spectrometry techniques can serve as an auxiliary diagnostic tool supporting the classification of thyroid neoplasms.

As part of the next project, I was looking for molecular components (including proteins, metabolites, and lipids) related to the progression of cancer and the response to treatment, with particular emphasis on the participation of exosomes modulating these processes. The developed methodology for conducting comprehensive proteomic and metabolomic analyzes of exosomes isolated from serum, using MS techniques, made it possible to conduct appropriate experiments on serum samples of patients diagnosed with head and neck cancer and locally advanced rectal cancer treated with ionizing radiation. I have shown that the metabolomic profile of exosomes isolated from serum in relation to whole serum is different in head and neck cancer after radiotherapy. However, cancer-specific features of energy metabolism could be detected in both types of samples. Moreover, I have shown that the molecular composition of exosomes isolated from serum can be used to predict the response to neoadjuvant radiotherapy in rectal cancer. Integration of metabolomic and proteomic data, which enables the identification of disrupted metabolic pathways and signaling processes connected with neoplastic disease and response to radiation therapy, presents a modern look at the analysis of the global response to cancer treatment from the level of systems biology.