Female breast cancer is the most frequently diagnosed type of cancer and the leading cause of death in female oncological patients. In 2018 over 2 million new cases have been reported. Alarmingly, the mortality of breast cancer in Poland rises in recent years, despite an extensive prophylaxis programme. This highlights the need for novel therapeutic options in addition to development of new diagnostic strategies, as the survival rate is highly dependent on early diagnosis.

Over several decades of research a strong link between reprogramming of lipid metabolism and cancer have been established. These changes in metabolism allow cancer cells to gain an advantage to grow and spread. Lipids are a very large group of compounds of different structures but almost all of them contain a base-building block – a fatty acid chain or chains. These fatty acids can be supplied with diet or synthesised in human organism. In cancer cells fatty acids have many important functions: 1) in phospholipids they form lipid membranes which is necessary for rapidly proliferating cells and can also modify their susceptibility to stress, 2) in sphingolipids they can act as signalling molecules, 3) they can be incorporated into triacylglycerols, where they act as energy storage, and later are used for energy production. Many studies show that enzymes associated with fatty acid metabolism are dysregulated in breast cancer, for example fatty acid synthase, a main enzyme in fatty acids production or stearoyl-CoA desaturase 1, which introduces double bonds into saturated fatty acid chain. These changes contribute to further alterations when fatty acids are incorporated into more complex lipids, as the fatty acyl chain structure dictates molecule properties.

In our preliminary analysis of total fatty acids content in material form breast cancer patients we detected increased amount of polyunsaturated fatty acids, present abundantly in membrane phospholipids, and lowered amount of monounsaturated fatty acids, a main component of triacylglycerols, in breast cancer tumour tissue. Additionally, we were able to detect previously unreported or underreported fatty acids groups i.e. odd-chain fatty acids, branched-chain fatty acids and very long chain fatty acids. These groups possess beneficial, pro-health activities, or are worth considering as potential biomarkers of breast cancer. Presently, most of the studies focused on fatty acid composition in biological material of breast cancer patients often consider only limited number of classes of lipids at a time. This results in incomplete information about the fatty acids composition. Therefore, we propose the examination of fatty acids profile in whole lipidome in normal breast glands and tumour tissues of breast cancer patients. For realization of this task, we will use gas chromatography-mass spectrometry (GC-MS) method to analyse fatty acid profiles in total lipid extracts and separately in different lipid classes both neutral and polar. The fatty acids will also be analysed in total lipids of serum of breast cancer patients and healthy control group. Results obtained in this project will be used in correlation analysis of fatty acid profiles with biochemical markers and breast cancer.

Realization of the tasks proposed in this project will not only expand the state of the knowledge about changes in fatty acid composition associated with breast cancer in tumour tissues, but also, by examining the serum of patients and healthy subjects, allow us to identify new potential lipid biomarkers, which are minimally invasive – analysis by blood tests. Additionally, results obtained in this study may uncover lipid alterations useful to pursue in development of new therapeutic strategies based on lipid metabolism. The development of effective treatment and diagnosis of breast cancer requires the complete understanding of pathological processes occurring during cancer development and progression, therefore the data gathered in this study, will contribute to research in this direction.