Despite advances in oncology, cancer still represent a difficult therapeutic target. Only 20-75% of cancer patients respond to standard treatment, due to the individual characteristics of patients, tumor heterogeneity, diversity and environmental conditions. Currently used anticancer drugs are often ineffective because some cancer cells are resistant since the beginning of treatment, while others acquire it over time causing the formation of drug-resistant metastatic lesions.Accordingly to this fact, significantly increases need for more efficient diagnostic methods that will allow to making optimal therapeutic decisions for individual patients.

Breast cancer is an example of the tumor that despite advances in the diagnosis and adjuvant treatment still remains a leading cause of death among women. Although the mechanism of cytostatics action used in the standard treatment this type of cancer has been thoroughly characterized still are sought predictive factors and methods reducing the risk of chemotherapy complications. Advances in molecular genetics methods allowed the development of microarray technology, thanks to which molecular subtypes of breast cancer has been distinguished: luminal, basal and HER-2with pronounced differences in prognosis and response to treatment. Meanwhile, the DNA microarray analysis in our studies allowed us to identify the *PIP* gene, which is the only gene with clearly higher expression in patients with invasive ductal carcinoma (IDC), which corresponded to standard chemotherapy compared with a group of non-responders patients with lower level of expression PIP .

PIP–Prolactin-Induced Protein, is a glycoprotein present in many body fluids, as well as in the breast cyst fluid and in the breast and prostate cancers. PIP is widely used as a diagnostic biomarker for determining if a metastasis of unknown primary site comes from the breast tumor. Despite numerous reports indicating the potential role of PIP in the progression of breast cancer it is still lack of data unambiguously confirm its role in the etiology of this type of cancer, which prompts us to further research. So far obtained results of our experiments, performed on clinical material of IDC, allowed us to hypothesize that the low level or lack of PIP protein may positively correlate with resistance to cytotoxic drugs used in the standard treatment this type of cancer. The main objective of this project is to explain the mechanism, in which high level of PIP protein in the breast cancer increases the sensitivity of cancer cells to the cytostatic agents such as doxorubicin, 4-hydroksycyklofosfamid, etoposide and paclitaxel.

Accordingly to our observations we planned *PIP* gene silencing at the genomic level in selected breast cancer cell lines and assessment the impact of PIP protein expression on survival and cell susceptibility to apoptosis induced by different doses of cytostatics. This project involves also the *in vivo* studies conducting on the athymic mice BALB/c model to illustration the impact of the PIP expression level on: the potential of breast cancer cells to create tumors, the ability of cancer cells to metastasize and sensitivity to apoptosis induced by cytostatic. In addition, we will examine an extracellular effect of the recombinant PIP protein on the process of programmed cell death induced by cytotoxic drugs. To characterize the role of the PIP expression in the mechanism of multidrug resistance of breast cancer cells we will signify an impact of the PIP expression level on the expression of genes involved in the process of replication, transcription and repair by using DNA and proteins arrays, Western blot and PCR techniques.

The achieved results of the project can contribute to understanding the role of PIP protein in the progression of breast cancer, and possibly, will help to determine its prognostic and predictive value in making decision about the selection of treatment for this cancer, based on the personalized therapy. Leading of basic research is necessary to understand the potential role of the PIP expression in overcoming drug resistance of breast cancer cells. In the future, PIP can be used in genomic tests that allow to separate prognostic groups requiring different therapeutic strategy. As a result we obtain financial savings at the level of health care by reducing the cost of unnecessary chemotherapy, and the reduction of costs associated with adverse effects of the treatment of women undergoing wrong adjuvant therapy.