According to data from the National Cancer Registry, the most common malignant tumour among men in Poland is lung cancer (21.4% of cases and 31.2% of deaths). By contrast, lung cancer among women is in second place in terms of the number of existing cases (8.6%), and in first place when it comes to mortality (15% mortality).

The main cause of lung cancer is the exposure of the organism to harmful, carcinogenic chemical substances. It is believed that the most common and most important risk factor for all histological types of lung cancer, responsible for the development of about 85% of the cases, is smoking. The treatment strategy of patients with non-small-cell lung carcinoma (NSCLC) is determined for each case individually depending on the tumour stage. The main disadvantage of the use of standard chemotherapy is the low selectivity in relation to cancer cells, because the substances used in the treatment of lung cancer are also harmful to healthy unchanged cells.

The demand for drugs against cancer is still high, and the therapeutics currently used in anticancer therapy, in addition to the desired therapeutic effects, cause a number of severe side effects that drastically lower the patient's quality of life. The latest available therapies, which use antibodies, are very expensive. Because of that, new drugs, equally effective but with low toxicity and no side effects, are still being sought.

According to numerous experimental studies, miRNA molecules are characterized by very low, if not zero, cytotoxicity in relation to the healthy cells and organs of the patient. As is the case for colon cancer, where international studies have identified the relationship between the expression of a specific type of miRNA and the prognosis and selection of the treatment of patients with this type of cancer, in the case of lung cancer it will be possible to determine the group of miRNA molecules that could help in its prognosis and treatment.

The very fact that specific markers (miRNAs) or a characteristic methylation profile within the so-called CpG islands (crucial for the development of cancer genes) can be identified lays a solid foundation for modern anti-cancer targeted therapy, despite the relatively limited knowledge we still have about the role of these epigenetic factors in the pathogenesis of cancer. The prospect of the use of miRNAs interacting with the *SOX18* transcript in the treatment of lung adenocarcinoma and squamous cell lung cancer seems promising, since there are already many similar miRNA molecules with proven pro- or anti-cancer functions.

The variable levels of the miRNA molecules we are interested in may be detected in the blood of the patient, which increases the availability and universality of the use of these molecules in lung cancer diagnosis, as they provide information not only about the type, but also about the stage of the tumour.

A careful examination of the mRNA expression levels of *SOX7, SOX17, SOX18, SOX30* and the molecules miR-7a and miR-24-3p, as well as the methylation profile of the *SOX18* and *SOX30* gene promoters could be used in future diagnoses of adenocarcinoma and squamous-cell lung carcinoma, and could even become a key aspect in anti-cancer therapy.

The correlation between the expression profiles and the patients' survival rate points to the possibility of using miRNA and the methylation profile (both crucial in the pathogenesis of tumour genes) in cancer prognosis. For example, it has been shown there is a relation between the expression level of eight miRNAs and the survival of patients with lung adenocarcinoma. The prospect of using miRNA and DNA-demethylating drugs in anti-cancer therapy is also promising. As an example, it has been shown that miRNA inhibition could lead *in vitro* to a reduction in the proliferation of cancer cells.

The role of SOX family proteins members expression in NSCLC is still not fully understood, although taking into account previous studies, this protein may be a significant factor in the development and progression of NSCLC. Our preliminary studies show a disproportion in the amount of *SOX18* mRNA relative to the amount of protein. This may be associated with the regulation of the translation by the molecules miR-7a and miR-24-3p, together with a change in the methylation profile of the promoters of the SOX genes.

Thorough testing of these epigenetic processes will allow for a fuller understanding of the molecular basis of the development of NSCLC, and it may contribute in the future to the development of new targeted therapy based on SOX proteins.